

88884

From: Pak, Michael  
Sent: Wednesday, March 12, 2003 2:51 PM  
To: STIC-Biotech/ChemLib  
Subject: 09/721,495 sequence search

Sequence search - 2 month amendment  
App. #: 09/721,495  
Result format: Paper.  
Title: Methods for identifying modulators of CCX CFR...

Please search:

Search commercial and interference database.  
SEQ ID NO:1-2

**Top 40 hits.**

Thanks,

Mike Pak  
Michael Pak  
Art Unit 1646  
Mailbox: CM1, Rm. 10D19 (SPE office, Bonnie Eyler)  
Office: CM1, Rm. 10E13  
703-305-7038

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Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 3/17  
Date Completed: 3/25  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

CRF

10D19



# WEST Search History

DATE: Monday, March 24, 2003

<u>Set Name</u> side by side	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u> result set
<i>DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ</i>			
L5	L4 and l1	1	L5
L4	gosling-j\$.in.	100	L4
L3	L1 and ckr	168	L3
L2	L1 and ccx	4	L2
L1	chemokine\$ near5 receptor\$	1722	L1

END OF SEARCH HISTORY





GenCore version 5.1.4\_p5\_4578  
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# OM protein - protein search, using sw model

Run on: March 17, 2003, 16:25:25 ; Search time 18 Seconds  
(without alignments)  
1869.280 Million cell updates/sec

Title: US-09-721-495B-2

Perfect score: 1819  
Sequence: 1 MALLNQSDTYEENWNG.....VEFPFDSRGPRPTSTSI 350

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 135 summaries

Database :

1: PIR 73: \*  
2: PIR1: \*  
3: PIR2: \*  
4: PIR3: \*  
5: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	1620	89.1	350	2	JN0621	G protein-coupled
2	659	36.2	378	2	B55735	Lymphocyte-specific
3	650	35.7	378	2	A55735	G protein-coupled
4	643	35.3	378	2	A45680	G protein-coupled
5	583	32.1	369	2	JC5068	G protein-coupled
6	537.5	29.5	360	2	A57160	chemokine (C-C) re
7	534.5	29.4	360	2	A53611	interleukin-8 rece
8	524	28.8	354	2	158186	probable G protein
9	522.5	28.7	355	2	JC4304	orphan G protein-c
10	522.5	28.7	360	2	JC4587	chemokine (C-C) re
11	518.5	28.5	354	2	B55733	G protein-coupled
12	511	28.1	358	2	A53752	interleukin-8 rece
13	501.5	27.6	355	2	J01231	neuropeptide Y/pep
14	500.5	27.5	352	2	A45747	neuropeptide Y/pep
15	499.5	27.5	352	2	S28787	chemokine (C-C) re
16	493.5	27.1	352	2	G00048	chemokine (C-C) re
17	492	27.0	360	2	JC2443	interleukin-8 rece
18	489.5	26.9	350	2	A39445	G protein-coupled
19	486	26.7	355	2	JC5067	macrophage inflamm
20	485	26.7	355	2	149339	chemokine (C-C) re
21	484.5	26.6	352	2	A41113	interleukin-8 rece
22	483.5	26.6	359	2	A48921	chemokine (C-C) re
23	482	26.5	374	2	138450	MIP-1 alpha recept
24	479.5	26.4	359	2	149341	interferon-inducib
25	476.5	26.2	367	2	JR0349	chemokine (C-C) re
26	474	26.1	355	2	A45177	interleukin-8 rece
27	471	25.9	356	2	S42096	G protein-coupled
28	470	25.8	383	2	SS5594	chemokine (C-C) re
29	461.5	25.4	355	2	G02436	chemokine (C-C) re

30	455.5	25.0	359	2	S44425	angiotensin II rec
31	452.5	24.9	359	2	JC1104	angiotensin II rec
32	452.5	24.9	359	2	JC2134	angiotensin II rec
33	450	24.7	359	2	S15403	angiotensin II rec
34	450	24.7	374	2	S32785	angiotensin II rec
35	446.5	24.5	359	2	A48857	MIP-1 alpha recept
36	445.5	24.5	356	2	149340	G protein-coupled
37	442.5	24.3	372	2	S2667	G protein-coupled
38	442.5	24.3	374	2	JC2628	angiotensin II rec
39	441	24.2	362	2	JN0694	angiotensin II rec
40	439	24.1	359	2	A42656	angiotensin II rec
41	438.5	24.1	359	2	JH0621	G protein-coupled
42	438.5	24.1	362	2	A39714	angiotensin II rec
43	437.5	24.1	327	2	S56162	angiotensin II rec
44	434	23.9	359	2	J01516	angiotensin II rec
45	428.5	23.6	359	2	139418	G protein-coupled
46	428.5	23.6	362	2	A30341	angiotensin II rec
47	428	23.5	359	2	151372	angiotensin II rec
48	427	23.5	359	2	JC1194	interleukin-8 rece
49	420	23.1	354	2	A23669	angiotensin II rec
50	411.5	22.6	363	2	A49092	angiotensin II rec
51	408.5	22.5	363	2	148261	angiotensin II rec
52	405.5	22.3	363	2	JC2543	angiotensin II rec
53	398.5	21.9	323	2	J02543	angiotensin II rec
54	395.5	21.7	354	2	T09353	bradykinin B2 rece
55	393	21.7	364	2	165989	G protein-coupled
56	373	20.5	333	2	165989	bradykinin recepto
57	371.5	20.4	366	2	COORTB2	N-formyl peptide c
58	365	20.1	364	2	A49542	FMPL-related recep
59	362	19.9	351	2	BA2009	G protein-coupled
60	358.5	19.7	371	2	UC5498	G protein-coupled
61	357	19.6	360	2	G02064	probable chemotr
62	353.5	19.4	371	2	UC5796	G protein-coupled
63	351	19.3	308	2	150241	bradykinin B2 rece
64	349.5	19.2	366	2	149519	N-formyl peptide r
65	348.5	19.2	352	2	A46520	N-formyl peptide r
66	343.5	18.9	350	2	A42009	FMPL-related recep
67	341	18.7	353	2	C42009	probable chemotr
68	340.5	18.7	395	2	S40685	G protein-coupled
69	338.5	18.6	380	2	JC2434	heptahelical P2Y-
70	336	18.5	370	2	UC5549	angiotensin recept
71	335	18.4	380	2	138435	kappa opioid recep
72	334.5	18.4	380	2	A48227	chemokine receptor
73	333	18.3	344	2	UC5942	intron 17 puriner
74	332.5	18.3	344	2	T09508	kappa opioid recep
75	331.5	18.2	380	2	S36143	bradykinin B1 rece
76	330.5	18.2	352	2	S60024	G protein-coupled
77	330.5	18.2	361	2	B45680	somatostatin recep
78	326.5	17.9	363	2	157955	somatostatin recep
79	326.5	17.9	364	2	JN0763	kappa opioid recep
80	326.5	17.9	380	2	JC2338	G protein-coupled
81	325	17.9	398	2	155450	somatostatin recep
82	324	17.8	388	2	155450	somatostatin recep
83	323	17.8	388	2	JN0605	kappa opioid recep
84	321.5	17.7	380	2	A55259	somatostatin recep
85	320	17.6	363	2	157940	mu opioid receptor
86	320	17.6	398	2	156517	mu opioid receptor
87	320	17.6	398	2	A57510	complement C5a ana
88	319	17.5	352	1	S27357	complement C5a ana
89	316	17.4	392	2	S65693	opioid receptor mu
90	316	17.4	400	2	156553	mu opiate receptor
91	315	17.3	375	2	UC5069	G protein-coupled
92	314.5	17.3	351	1	A37963	complement C5a ana
93	312	17.2	351	1	A46525	complement C5a ana
94	310	17.0	373	2	JC4737	brain-specific som
95	310	17.0	384	2	A47249	G protein-coupled
96	309.5	17.0	362	2	S33733	G protein-coupled
97	308.5	17.0	375	2	UC5509	G protein-coupled
98	308	16.9	355	2	UC5733	G protein-coupled
99	307.5	16.9	353	2	UC2492	G protein-coupled
100	307	16.9	373	2	A47556	ATP receptor P2u -
101	306.5	16.8	334	2	UC4681	bradykinin B1 rece
102	306.5	16.8	384	2	JC4629	somatostatin recep

103	305.5	16.8	391	2	A39297	somatostatin recep
104	304.5	16.7	353	2	A53858	bradykinin recep
105	304.5	16.7	391	2	A41795	somatostatin recep
106	304.5	16.7	391	2	C41795	somatostatin recep
107	304	16.7	359	2	UC5277	G protein-coupled
108	304	16.7	369	2	B41795	somatostatin recep
109	304	16.7	373	2	UC4162	P2Y receptor - bov
110	302.5	16.6	342	2	A40191	platelet-activatin
111	302.5	16.6	404	2	UC5784	adrenomedullin rec
112	302	16.6	369	2	UC2083	somatostatin recep
113	301.5	16.6	369	2	D41795	somatostatin recep
114	299.5	16.5	369	2	A45291	somatostatin recep
115	298.5	16.4	365	2	S68679	G protein-coupled
116	296.5	16.3	372	2	B48227	delta opioid recep
117	296	16.3	397	2	S66518	proteinase-activat
118	295	16.2	375	2	A54946	p-2u nucleotide re
119	294.5	16.2	346	2	S29248	somatostatin recep
120	294.5	16.2	372	2	S34592	delta opioid recep
121	293	16.1	328	2	UC4800	P2Y6 receptor - hu
122	293	16.1	342	2	S13638	platelet-activatin
123	293	16.1	370	2	S43087	orphan opioid rece
124	293	16.1	373	2	JB0087	delta opioid recep
125	292	16.1	367	2	I49022	kappa opioid recep
126	292	16.1	367	2	UC2421	opioid receptor ho
127	292	16.1	367	2	I56520	G protein-coupled
128	291.5	16.0	387	2	I69202	G protein-coupled
129	288.5	15.9	372	2	I38532	delta opioid recep
130	287	15.8	418	2	A46226	somatostatin recep
131	286.5	15.8	349	2	I59336	galanin receptor 1
132	285	15.7	362	1	Q08B22	HHR23 protein - hu
133	285	15.7	399	2	I48705	platelet-activat
134	283.5	15.6	341	2	S43252	platelet-activatin
135	281.5	15.5	341	2	S63666	platelet activatin

## ALIGNMENTS

RESULT 1  
 G protein-coupled receptor type B - bovine  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 19-May-2000  
 C/Accession: JN0621  
 R/Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.  
 Biochem. Biophys. Res. Commun. 194, 504-511, 1993  
 A/Title: Identification of novel members of G-protein coupled receptor superfamily expe  
 A/Reference number: JN0621; MUID:93326166; PMID:8392843  
 A/Accession: JN0621  
 A/Molecule type: mRNA  
 A/Residues: 1-350 <MAT>  
 A/Cross-references: GB:563848; NID:9399710; PIDN:AAB27547.1; PID:9399711  
 A/Experimental source: tongue taste papillae  
 C/Comment: This protein is involved in modulating taste sensitivity or regeneration of t  
 C/Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein  
 F/42-66/Domain: transmembrane #status predicted <TM1>  
 F/80-99/Domain: transmembrane #status predicted <TM2>  
 F/114-135/Domain: transmembrane #status predicted <TM3>  
 F/154-175/Domain: transmembrane #status predicted <TM4>  
 F/200-222/Domain: transmembrane #status predicted <TM5>  
 F/242-265/Domain: transmembrane #status predicted <TM6>  
 F/284-306/Domain: transmembrane #status predicted <TM7>  
 F/6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.1%; Score 1620; DB 2; Length 350;  
 Best Local Similarity 86.0%; Pred. No. 1.3e-131;  
 Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 M A L E O N S T D Y Y E E N M G Y D S O Y E L I C I K E D V E P F A K V L P V L T I V F V I G L A G N S 60  
 Db 1 M A V E Y N S T D Y Y E E N M G Y D S O Y E L I C I K E V A K F A K V L P A F P T I A I I G L A G N S 60

QY	61	M V A I A Y A Y K K O R T K D Y V I L N L A V A D L L L F T L P F M A V N A V H G V L K I M K I N T S A L Y T 120
Db	61	T V A I A Y A Y K K R I T D Y I L N L A V A D L F L T L P F M A V N A V H G V L K I M K I N T S A L Y T 120
QY	121	L N F V S G M Q F L A C I S I D R Y A V A V T K V S Q S G V K P C W I I C F C W M A A I L S I P O L V E Y T V N D 180
Db	121	V N F V S G M Q F L A C I S I D R Y A V A V T K A P S Q S G V K P C W I I C F C W A A I L S I P O L V E Y T V N H 180
QY	181	N A R C P I F P R Y I G T S M K A L I Q M L E I C I G V P F P L I M G C Y P I T A R T A T M K M N I K S R P L K 240
Db	181	K A R C V P I F P Y H I G T S M K A S I Q L E I C I G F I I P L I M A C Y F T A K T Y L I K M P I K K S O P L K 240
QY	241	V L T V I V I V I Q L P Y N I V K F C R A I D I I Y S L I T S C M S K M P D I A I Q V E S I A L F H S C L N P 300
Db	241	V L F T V I V I V I Q L P Y N I V K F C Q A I D I I Y S L I T D C M S K R M D V A I Q I E S I A L F H S C L N P 300
QY	301	I I Y V E M G A S F K N Y V M K V A K K G S W R R O S V E E P F D S E G P T E P T S F S I 350
Db	301	V I Y V E M G T S F K N Y I M K V A K K G S W R R O R Q N V E I P F E S E D A T E P T S F S I 350

## RESULT 2

B55735  
 lymphocyte-specific G protein-coupled receptor EB11 - human  
 N/Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1  
 C/Species: Homo sapiens (man)  
 C/Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 19-May-2000  
 C/Accession: B55735; S52443  
 R/Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.;  
 Genomics 23, 643-650, 1994  
 A/Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor  
 A/Reference number: A55735; MUID:95154835; PMID:7851893  
 A/Accession: B55735  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-378 <SCH>  
 A/Cross-references: GB:L1581; NID:9468319; PIDN:AAA74231.1; PID:9468320  
 R/Burgstahler, R.; Kempkes, B.; Staube, K.; Lippe, M.  
 submitted to the EMBL Data Library, February 1995  
 A/Description: The expression of the chemokine receptor BLR2/EB11 is specifically transac

A/Reference number: S52443  
 A/Accession: S52443  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 21-378 <BLR>  
 A/Cross-references: EMBL:X64702  
 C/Genetics:  
 A/Gene: GDB:CMKBR7; EB11; BLR2; CCR7  
 A/Cross-references: GDB:342065; OMIM:600242  
 A/Map position: 17q12-17q21.2  
 C/Superfamily: vertebrate rhodopsin  
 C/Keywords: G protein-coupled receptor

Query Match 36.2%; Score 659; DB 2; Length 378;  
 Best Local Similarity 38.7%; Pred. No. 4.8e-49;  
 Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 M A L E O N S T D Y Y E E N M G Y D S O Y E L I C I K E D V E P F A K V L P V L T I V F V I G L A G N S 60  
 Db 21 V C L C D E V T D Y I G D N T -- T V D Y T L F E S L C S K D V N F P A W F L P I M Y S I I C F G L G N G 77  
 QY 61 M V A I A Y A Y K K O R T K D Y V I L N L A V A D L L L F T L P F M A V N A V H G V L K I M K I N T S A L Y T 120  
 Db 78 L V L T Y I F K R L K M T D Y I L N L A V A D I L F L T L P F A Y A S A S W G V A F C K L I P A I Y K 137  
 QY 121 L N F V S G M Q F L A C I S I D R Y A V A V T K V S --- Q S G V K P C W I I C F C W M A A I L S I P O L V E Y 176  
 Db 138 M S F S G M L L I C I S I D R Y A V A V T K A P S Q S G V K P C W I I C F C W A A I L S I P O L V E Y T V N H 197  
 QY 177 T V N D N A ----- R C P I F P R Y I G T S M K A L I Q M L E I C I G V P F P L I M G C Y P I T A R T A T M K M P 231  
 Db 198 D L O R S S E Q A M R C S L I T E H -- V E A F T T I O V A Q M V I G F L V P L A M S F C V I I R T L L O A R 254

```

OY      232 NIKISRLPKLLTVIVIVIVIVOLPNYIVKPCRAIDIIISLTSCMSKRMIDIAIQVESI 291
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      255 NFERKAKKVIIAVVVVIVIFQLPYNGVLLAQTVANNFNITSICELSKQMLAIDVITSL 314
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      252 ALFHSCNLAPILYEVFGASFKYVMKVAKKYG-----SW-----RRQSVSEEPFD 337
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      315 ACVRCVVAFELFYAFPGVYFRNDLFLFLFDLGLGSGEQLRWMSSCRHIRSSMSVE----- 369
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY      338 SEGPTPEPTSTPS 349
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      370 ---AETTTTFS 377
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 3
A55735
G:protein-coupled receptor EB11 - mouse
S:species: Mus musculus (house mouse)
C:date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C:accession: A55735
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:reference number: A55735; MUID:95154835; PMID:7851893
A:accession: A55735
A:status: preliminary
A:molecule type: mRNA
A:residues: 1-378 <SCH>
A:cross-references: GB:LIJ1580; NID:9468340; PIDN:AAA74232.1; PID:9468341
C:superfamily: vertebrate rhodopsin
C:keywords: G protein-coupled receptor

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Query Match 35.7% Score 650; DB 2; Length 378;
Best Local Similarity 38.3%; Pred. No. 2,8e-48;
Matches 140; Conservative 67; Mismatches 125; Indels 34; Gaps 8;

QY 5 QNQSIDYYEENEMNGTYDYSOYEELCIKEDYREFAKFLPEVETIVVIGLAGNSMYVA 64
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 25 QGEVTDYIGENT--TDVETLYESVCEFKKDVNRKAFVLLPLMSVLCFVGLDNGLVIL 81
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 65 IYAYYKOKTKTDYTIINLAVADLLFTLPFWANAVAHGWLCKIMCKITSAIYTLNFV 124
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 82 TYIYFRLKLTMDTYILNLAVADILFLILPPMAISEAKSMIFGYVLCCKGIFGYKLSFF 141
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 125 SGMQFLACISIDRYAVAVTKVPSQSG-----VKRPMIICEVMAAILLSIQIYPTT 177
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 142 SGWLLLCISIDRYVAIVQAVSRHRRARVLLISK---LSCGIMMLFLPSITPELLYSG 198
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 178 VNDNA-----RCPIFRPRLTGTSMKAL--IQMLEICIGFVPEFLIMGVCEYITARTLMKM 230
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 199 LQKNSSEDTLRC-----SLVSAQVEKLTITQVAVQFGLVPMIAMSICYILLIRTLQQA 253
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 231 PNIKISRPKLKLTIVVIVIVITQLPYNIIVKFCRAIDIIYSLTSCNMSKMDIAIQVTES 290
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 254 RNFERRKAIKVIITAAVVVVIVFQLPYNGVVLAAQTAVANFNITNSCEBTKQNLIAADVYS 313
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 291 IALFHSCLNPLILVEMGASPKNYVMKAVAKKGYSMWRQ-----QSYEEFPFDSGPT 343
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 314 LASVRCVVNFFLAIFIGVKFRKDFKLPDGLGCTSGERLRHMSGCRHRNMSVSN--AE 371
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 344 PTSTFS 349
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 372 TTTTFS 377

RESULT 4
A45680
G protein-coupled peptide receptor EBI 1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45680
R:Birkenholz, M.; Josefson, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A,:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled R

```

A:Reference number: A45680; MUID:91188173; PMID:8383238  
A:Accession: A45680  
A:Status: Preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-378 <BIR>  
A:Cross-references: GB:L08176; NID:G183484; PID:G183485  
A:Experimental source: B-1ymphocytes  
A>Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBI:P.127095)  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 35.3%; Score 643; DB 2; Length 378;  
Best Local Similarity 39.0%; Pred.No. 1.1e-47;  
Matches 145; Conservative 62; Mismatches 127; Indels 38; Gaps 8

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QY      1 MMBEONQSDIDYEEENBNMGTVDYSQYELCI KEDREEFKVELPVELTIVFYIAGNS 60
DB      21 VCLCQDEVDVDDYIDGNT---TYDYLTFESLCSSKQDVRNFAMWLLPIMYSIICVGLLNG 77
QY      61 MVVAIAAYYKORTKTDVYILINLAADVADLLFTLPFWANAVAHGWVLGIMCKITSALYT 120
DB      78 LVVLYITYYKRLKTMIDYILINLAADVADILFLLTLPFWAASAASWVGWGHFKILIPAITYK 137
QY      121 LNFVSGMOFLACISIDRYAAVTKVPSQSGVGKPCWII--CFCYWMA--ALLSTPOLVEY 176
DB      138 MSFSGMILLCTISIRYAVAIQAVSAHRHARVLLISKUSCVGSALAVLSTIPELLYS 197
QY      177 TYVNDNA-----RCIPFPRLIGTSMKALIOMLEICIGFVVPFLIMGVCYFARTAKMP 231
DB      198 DLORSSSEQAMRSLTTEH--VEAFITIOAOWVIGFVLPLAMSGCYIVITITLQAR 254
QY      232 NIKISAPLKVLITVIVIVITOLPYNIIVKEPCRAIDIYSITSCNMSKMDIAIQVTEBI 291
DB      255 NFBRNKAIKYIIIAVVVVEIFQLPYNGVVALAQIVANFNITSTCELSKOJINIAADVYSL 314
QY      292 ALFHSCINPLIYVFMGASFKQIVYMKVAKKYG-----SW-----RQOSQSYEEPPFD 337
DB      315 ACVRCVCNPLVAFIVGKXFENDIFKLFQDGLCSQEQOLRQWSSCRHTRRSSMAYE----- 369
QY      338 SBGPTPTSTFS 349
DB      370 ---AETTTFS 377

```

```

RESULT 5
JC5068
G/protein-coupled receptor CKR-L3 - human
C/species: Homo sapiens (man)
C/date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C/accession: JC5068
R/aballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A/title: Molecular cloning and RNA expression of two new human chemokine receptor-like genes
A/reference number: JC5067; MUID:97040707; PMID:8886020
A/accession: JC5068
A/molecule type: DNA
A/residues: 1-369 <ZAB>
A/cross-references: EMBL:Z79784; NID:g1668737; PIDN:CAB02144.1; PID:g1668738
C/comment: This protein belongs to the family of alpha chemokine receptors.
C/genetics:
A/gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4
A/cross-references: GDB:5370639; OMIM:601835
A/map position: 6q27-6q27
C/superfamily: vertebrate rhodopsin
C/keywords: G protein-coupled receptor; transmembrane protein
F/42-66/Domain: transmembrane #status predicted <TM1>
F/79-99/Domain: transmembrane #status predicted <TM2>
F/115-136/Domain: transmembrane #status predicted <TM3>
F/160-180/Domain: transmembrane #status predicted <TM4>
F/212-233/Domain: transmembrane #status predicted <TM5>
F/250-271/Domain: transmembrane #status predicted <TM6>
F/292-315/Domain: transmembrane #status predicted <TM7>

```

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Query Match 32.1%; Score 583; DB 2; Length 369;
Best Local Similarity 36.1%; Pred. No. 1.6e-42;
Matches 121; Conservative 68; Mismatches 120; Indels 26; Gaps 7;

QY      8 STDYEEENEMNGTYDYSOYELICIKEDVREFAKVLPEFLITVFVIGLAGNSMVAIYA 67
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      18 NTSYVSVDSEH-----LLCSLGEVRFGRPLFPAIYSLICVFGLLGNILVVITFA 67
       ::||::||::||::||::||::||::||::||::||::||::||::||::||

QY     68 YRKQRKTGVYILNLAVDLLLTLPFPMAV-NAVHGWLGIKIMCKITSALYTTLNFSVG 126
       :|::||::||::||::||::||::||::||::||::||::||::||::||
Db     68 FYKASMSMDVYLNNIAADIPLFTLLPFWAASHAGAWFNSNATKLKGAIYNFNFG 127
       :|::||::||::||::||::||::||::||::||::||::||::||::||

QY     127 MQPLACISIDRYAAVKRPVS----OSGVRKPWIIICECWMMAAILSTPOLVF---YTVN 179
       |||::||::||::||::||::||::||::||::||::||::||::||::||
Db    128 MLTLCISMRIAYIAIQATSPRLSRITLPRSKILLVYWGLSVISSSPFNQNTNQ 187
       :|::||::||::||::||::||::||::||::||::||::||::||::||

QY     180 DNARCIPIPPRYIGTS---MKALIOMLEICIGFVPFLIMGVCYFITARTLMKNINIKI 235
       GSDVPC--EPKQTVESEPFRWKLIIMGLTEILFFGFPLPFMFIFCYFIIVKTLVQAQNSKR 244
Db    188 GSDVPC--EPKQTVESEPFRWKLIIMGLTEILFFGFPLPFMFIFCYFIIVKTLVQAQNSKR 244
       :|::||::||::||::||::||::||::||::||::||::||::||::||

QY     236 SRPKVLTFVYVFIYTOIPYNIYVRCRAIDIIYSLITSQNSKRMDAIOVTESIALPH 295
       :|::||::||::||::||::||::||::||::||::||::||::||::||
Db    245 HKAIRIYIAVLVFLCACQIPHNVLLVITYAN-LGKNRSCOSEKLIIGYTKYTEVLAFLH 303
       :|::||::||::||::||::||::||::||::||::||::||::||::||

QY     296 SCINPILLYFMGASFKNYYVMKYAKKXGWSRRQROS 330
       |::||::||::||::||::||::||::||::||::||::||::||::||
Db    304 CCINPVLYAFIIGOKFRNYFLFKLIKDMCVRRKKYS 338
       :|::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 6
A57160
Chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C>Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: A57160
J:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W
J: Biol. Chem. 270, 19495-19500, 1995
A>Title: Molecular cloning and functional expression of a novel CC chemokine receptor cl
A:Reference number: A57160; MUID:95570289; PMID:1642634
A:Accession: A57160
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POW>
A:Cross-references: GB:X85740; NID:g1370103; PIND:CAAS9743.1; PID:g971452
A>Note: source clone KS-5
C:Genetics:
A:Gene: GDB:CMKBRA
A:Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:46-65/Domain: transmembrane #status predicted <TM1>
F:76-97/Domain: transmembrane #status predicted <TM2>
F:113-113/Domain: transmembrane #status predicted <TM3>
F:151-175/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:243-264/Domain: transmembrane #status predicted <TM6>
F:291-308/Domain: transmembrane #status predicted <TM7>
F:29-276,110-187/Disulfide bonds: #status predicted
F:72-350/Binding site: phosphate (Ser) (covalent) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:181,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 29.5%; Score 537.5; DB 2; Length 360;
Best Local Similarity 35.8%; Pred. No. 1.2e-38;
Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps 6;

QY      10 DYVEENMGTYDYSOYELICIKEDVREFAKVLPEFLITVFVIGLAGNSMVAIYAY 69
       :|::||::||::||::||::||::||::||::||::||::||::||::||
Db      8 DTTLDESIYNNYLVESIPKPTCKGIRAKFGLPLPYLSLVFPGLLGNSVVVLVLFKY 67

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[illegible]

RESULT 7  
 A:Accession: A53611  
 Interleukin-8 receptor type B - human  
 C:Species: Homo sapiens (man)  
 C:Date: 07-Oct-1994 #sequence revision 12-Apr-1996 #ext\_change 05-Nov-1999  
 C:Accession: I37898; I38712; A53611; A39446  
 R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.  
 J. Biol. Chem. 269, 26381-26389, 1994  
 A:Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor type B  
 A:Reference number: I37898; PMID:95014476; PMID:7929358  
 A:Accession: I37898  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-360 <RES>  
 A:Cross-references: EMBL:U11869; NID:G511801; PIDN:AA60656.1; PID:G511803  
 A:Accession: I38712  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-15 <RE2>  
 A:Cross-references: EMBL:U11872; NID:G511808; PIDN:AAA64380.1; PID:G511809; EMBL:U11873; I1876; NID:G511816; PID:G511817; EMBL:U11877; NID:G511818; PID:G511819; EMBL:U11878; NID:R1879; H.; Lloyd, A.R.; Laurens, L.L.; Bonner, T.I.; Kelvin, D.J.  
 J. Biol. Chem. 269, 11065-11072, 1994  
 A:Title: Structure, genomic organization, and expression of the human interleukin-8 receptor type B  
 A:Reference number: A53611; PMID:94209273; PMID:7512557  
 A:Accession: A53611  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 6-360 <SPR>  
 A:Cross-references: GB:M99412; GB:LI9593  
 R:Murphy, P.M.; Tiffany, H.L.  
 Science 253, 1280-1283, 1991  
 A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor  
 A:Reference number: A39446; PMID:91368200; PMID:1891716  
 A:Accession: A39446  
 A:Status: preliminary  
 A:Molecule type: nucleic acid sequence not shown  
 A:Residues: 6-360 <MUR>  
 A:Cross-references: GB:M73969  
 C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, including  
 A:Gene: GDB:IL8RB, IL8RA  
 A:Cross-references: GDB:127868; OMIM:146928  
 A:Map position: 2q35-2q35  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; transmembrane protein  
 Query Match 29.4%; Score 534.5; DB 2; Length 360;  
 Best Local Similarity 33.2%; Pred. No. 2-2e-38;  
 Matches 120; Conservative 75; Mismatches 141; Indels 25; Gaps 8;

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Db 6 MESDSEDFEWKGEGLSNYSISSTIPFLDAPCEPESL-EINKYFVILYALVFLSL 64
QY 58 GNSMVAIYAYYKQRTKTDVYLINLAVALDILLFTLPFAVANAAGWVGKIMCKITSA 117
Db 65 GNSLVLVLISRVGRSVTDVLTNLALADLFLALTLPIWAASKVMGIMGTFLCKVSL 124
QY 118 LYTANFVSGMOFLACISIDRYVAN---TKVPSQSGVGKPCMIICFCVMAAILLSIPOLV 174
Db 125 LKEVNFYSGLIALLACISIDRYLATVHARTLTQRY--LVKFTLSIWGLSLDLVFL 182
QY 175 F---YTNVDNARCIPIPRYLQ---TSMKALIQMLEICIGFVVPFLIMGVCFITARTL 227
Db 183 FRRVYVSNVSPACY---EDMGNNNTANWRMLRLILPQSEGFVPLIMFCGFTLRTL 238
QY 228 MKMENIKISREPLKLLTVIVIVITQLPYNIYKFCRAIDIIYSITSCNMSKMDIAIQV 287
Db 239 FKAHMGQKGRAMRYFAVVLIFLLCWLIPYNIVLADTLMTQVIOETCERNHIDRALDA 298
QY 288 TESTALPHSCNPLIYVPMGASFKNYWKVAKKYGSMRQ---RQVSEFPPEDEGPTLP 344
Db 299 TEIIGIHSCLNPLIYAFYTGKFRHGLKTLIAIHGLISKDSLPRDSRPSFVSSGHTST 358
QY 345 T 345
Db 359 T 359

RESULT 8
158186
A:Title: G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: J58186
R:Harriison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A:Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and h
A:Reference number: 158186; MUID:94323113; PMID:8047298
A:Accession: J58186
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>
A:Cross-references: EMBL:U04808; NID:92588635; PIDN:AA87093.1; PID:9439861
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 28.8%; Score 524; DB 2; Length 354;
Best Local Similarity 36.9%; Pred. No. 1.8e-37;
Matches 113; Conservative 51; Mismatches 128; Indels 14; Gaps 4;

QY 22 YDSQYELICIKEDVREFAKVFLPVFLTVFVIGLAGSMVAIYAYYKQRTKTDVYL 81
Db 13 FEYDSDAEACYGDIVAFGTIFLSTFYSLVFTFGLVGLNLVLTATNSKKSITDIYL 72
QY 82 NLAVALDILLFTLPFAVANAAGWVGKIMCKITSAIYTNFVSGMOFLACISIDRYVAN 141
Db 73 NLAISDLFLVALTPFTHTLHSHBGLHNMCKLTAFPIGFPGIIFTIVISIDRYLAI 132
QY 142 TKVPS-----QSGVGKPCMIICFCVMAAILLSIPOLVFTVNDNARCIPIPRYLGT 194
Db 133 VLAANSNNRRTVQHG---TISLGWMAAILVASPQMFETKRXDN-ECLGDYEPVLOE 186
QY 195 SMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIKISREPLKLLTVIVIVITQ 254
Db 187 IWPVLNKESEVNILGFVPLILMSFCYFRIVRTLFSCNKKKARARILLVIVVFFLEMT 246
QY 255 PYNIVKFCRAIDIIYSITSCNMSKMDIAIOVTESIALFHSCLNPLIYVPMGASFKNY 314
Db 247 PYNIVIFLETLK-FYNFPSCGKMDRLRALSVTETVAFSHCCLNPLIYAFAGEKFRRL 305
QY 315 MKVAKK 320
Db 306 RHLNKK 311

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RESULT 9
JC4304
A:Title: orphan G protein-coupled receptor - human
N:Alternate names: V28 protein
C:Species: Homo sapiens (man)
C>Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C:Accession: JC4304
R:Report: C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to G
A:Reference number: JC4304; MUID:96011651; PMID:7590284
A:Accession: JC4304
A:Molecule type: mRNA
A:Residues: 1-355 <RAP>
A:Cross-references: GB:U0350; NID:9665580; PIDN:AA91783.1; PID:9665581
A:Experimental source: peripheral blood mononuclear cell
C:Comment: This protein is a cell-surface receptor which recognizes extracellular signals;
C:Comment: This protein is a key regulator of many immune and homeostatic responses, and
C:Genetics:
A:Gene: V28
A:Map position: 3pter-p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F:35-57/Domain: transmembrane #status predicted <TM1>
F:66-88/Domain: transmembrane #status predicted <TM2>
F:104-125/Domain: transmembrane #status predicted <TM3>
F:146-165/Domain: transmembrane #status predicted <TM4>
F:197-217/Domain: transmembrane #status predicted <TM5>
F:230-254/Domain: transmembrane #status predicted <TM6>
F:275-296/Domain: transmembrane #status predicted <TM7>

Query Match 28.7%; Score 522.5; DB 2; Length 355;
Best Local Similarity 36.4%; Pred. No. 2.4e-37;
Matches 112; Conservative 57; Mismatches 122; Indels 17; Gaps 5;

QY 22 YDSQYELICIKEDVREFAKVFLPVFLTVFVIGLAGSMVAIYAYYKQRTKTDVYL 81
Db 12 FEYDSDAEACYGDIVAFGTIFLSTFYSVIFALGVLNLVLTATNSKKSITDIYL 71
QY 82 NLAVALDILLFTLPFAVANAAGWVGKIMCKITSAIYTNFVSGMOFLACISIDRYVAN 141
Db 72 NLAISDLFLVALTPFTHTLHSHBGLHNMCKLTAFPIGFPGIIFTIVISIDRYLAI 131
QY 142 TKVPS-----QSGVGKPCMIICFCVMAAILLSIPOLVFTVNDNARCIPIPRYLGT 194
Db 132 VLAANSNNRRTVQHG---TISLGWMAAILVASPQMFETKRXDN-ECLGDYEPVLOE 185
QY 195 SMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIKISREPLKLLTVIVIVITQ 254
Db 186 IWPVLNKESEVNILGFVPLILMSYCFRIIQTLSCKNKKARAKTILVIVVFFLEMT 245
QY 255 PYNIVKFCRAIDIIYSITSCNMSKMDIAIOVTESIALFHSCLNPLIYVPMGASFKNY 314
Db 246 PYNIVIFLETLK-LYDFPSCGKMDRLRALSVTETVAFSHCCLNPLIYAFAGEKFRRL 304
QY 315 MKVAKKYG 322
Db 305 YHL---YG 309

RESULT 10
JC4587
A:Title: chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: JC4587
R:Hoogerwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A:Reference number: JC4587; MUID:96136324; PMID:8573157
A:Accession: JC4587

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Biochem. Biophys. Res. Commun. 179, 784-789, 1991

A>Title: Molecular characterization of the interleukin-8 receptor.

A|Reference number: JQ1231; MUID:91378994; PMID:1698400

A|Accession: JQ1231

A|Molecule type: DNA

A|Residues: 1-355 <BEC>

A|Cross-references: GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439

R|Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.

J|Immunol. 148, 1261-1264, 1992

A>Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.

A|Reference number: A46483; MUID:92148149; PMID:1737938

A|Accession: A46483

A>Status: preliminary

A|Molecule type: mRNA

A|Residues: 1-355 <LEP>

A|Cross-references: GB:M82873; NID:g165440; PIDD:AAA31376.1; PID:g165441

A|Experimental source: neutrophils

A|Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBP:81530)

C|Superfamily: vertebrate rhodopsin

C|Keywords: G protein-coupled receptor; transmembrane protein

Query Match            27.6%; Score 501.5; DB 2; Length 355;  
Best Local Similarity   33.1%; Pred. No. 1.5e-35;  
Matches 107; Conservative 70; Mismatches 127; Indels 19; Gaps 6;

OY      12   YYEENEMNGT-----VDYSQEYLICIKEDVREFAKVELPVFLTFIVFIAGNSMVAI     65  
     :::|||||||:|||||||:|||||||:|||||||:|||||||:  
DB      14   WEDEFSANATGMPPPEKDYSS--FCLVTQTINKKYVV---VIALVFLLSLGNSLWLV     68  
  
OY      66   YAYYYKKRKTKDITVLINLANAVDLLLFLLPFANAHAHGWLGKMCKTSALTALTNLVS     125  
     :::|||||||:|||||||:|||||||:|||||||:|||||||:  
DB      69   ILYSSRNRSVTDVIYNLTNLAMADLLPALTWIPNAWSKEKGMLFGPLCVKSIVEKNFYIS     128  
  
OY      126   GNQFAACISIDIRRYNAV---TKVPQSOSGVGPKCMIICFCVMAAILLSLPOLVEITYNDNA     182  
     :::|||||||:|||||||:|||||||:|||||||:|||||||:  
DB      129   GIILLACLISVDHYIAIHVRTRLTLQK--RHLYVKPICIGIMWLSTLSPFLFRQVFESPN     186  
  
OY      183   RCPIFPFRPYLG--TSMKRALIQMLEICIGFVVYPFLIMGVCYTARTLMKPNIKISRPL     239  
     :::|||||||:|||||||:|||||||:|||||||:|||||||:  
DB      187   NSSPVCYEDELGHNTAKRWLVRLILPHTEGFILPLLWMFEYGFTLRTRFOAHMGQRHAM     246  
  
OY      240   KYLLTVIVIFETQTPYNYNVKFRCRAIDIYLSITSNNMSKRDIAIQWTESIAPHSCLIN     299  
     :::|||||||:|||||||:|||||||:|||||||:|||||||:  
DB      247   RVTFPAVALFILCWDLPRNYLAADTMRTHTVGFTQCRRANDIRDALDATEILGIHLSCLN     306  
  
OY      300   PILVYFMGASFKRVYWKVAKYTG          322  
Db      307   PIIFYAFIGNFNRGFFLKLAARG         329  
  
RESULT 14  
A45747  
neuropeptide Y/heptide YY receptor Y3 - human  
N|Alternate names: fusin; HMR9; leukocyte-derived seven-transmembrane receptor LESTR, re-

C|Species: Homo sapiens (man)  
C|Date: 03-May-1994 #sequence revision 03-May-1994 #text change 05-Nov-1999  
C|Accession: A45747; ASJ103; T53006; I59444; I69203; S32761  
R|Federbspiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lewis,  
Genomics 16, 707-712, 1993  
A>Title: Molecular cloning of the cDNA and chromosomal localisation of the gene for a pu-  
A|Reference number: A45747; MUID:93315164; PMID:8325644  
A|Accession: A45747  
A|Molecule type: mRNA  
A|Residues: 1-352 <PED>  
A|Cross-references: GB:M92923; NID:g292516; PIDD:AAA16617.1; PID:g292517  
R|Joetscher, M.; Geisler, T.; O'Reilly, T.; Zwenhlen, R.; Baggiolini, M.; Moser, B.  
J. Biol. Chem. 269, 232-237, 1994  
A>Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly e-  
A|Reference number: A53103; MUID:94103215; PMID:8276799  
A|Accession: A53103  
A|Molecule type: mRNA  
A|Residues: 1-352 <LOB>

A:Cross-references: EMBL:X71635; NID:g297099; PIND:CHA50641.1; PID:g297100  
R:Herzog, H.; Hort, V.J.; Shine, J.; Selbie, L.A.  
A:Title: Molecular cloning, characterization, and localization of the human homolog to the  
DNA Cell Biol. 12, 465-471, 1993  
A:Reference number: 153006; MUID:93319629; PMID:8329116  
A:Accession: 153006  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-352 <RES>  
A:Cross-references: GB:L06797; NID:g414929; PIND:AAA03209.1; PID:g414928  
R:Jatini, E.B.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.; Lari  
Regul. Pept. 47, 247-258, 1993  
A:Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homolog  
A:Reference number: 159444; MUID:94052833; PMID:8234509  
A:Accession: 159444  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-352 <RES>  
A:Cross-references: GB:L01639; NID:g189313; PIND:AAA16594.1; PID:g189314  
R:Nomura, H.; Nielsen, B.W.; Matsushima, K.  
Int. Immunol. 5, 1239-1249, 1993  
A:Title: Molecular cloning of cDNAs encoding a Ld78 receptor and putative leukocyte chemokine  
A:Reference number: 154751; MUID:94092629; PMID:7505609  
A:Accession: 169203  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-352 <RES>  
A:Cross-references: GDB:D10924; NID:g219868; PIND:BA01722.1; PID:g219869  
C:Genetics:  
A:Gene: GDB:NPY3R; NPY3  
A:Cross-references: GDB:230002; OMIM:162643  
A:Map position: 2q21-2q21  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; transmembrane protein

27.5%; Score 500.5; DB 2; Length 352;  
 Query Match Similarity 34.6%; Pred. No. 1.8e-35;  
 Best Local Similarity 57; Mismatches 134; Indels 11; Gaps  
 Matches 107; Conservative

4.

A:Reference number: 528787; MUID:92100053; PMID:1661837  
 A:Accession: 528787  
 A:Molecule type: mRNA  
 A:Residues: 1-353 <RIM>  
 A:Cross-references: EMBL:566739  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 27.5%; Score 499.5; DB 2; Length 353;  
 Best Local Similarity 34.0%; Pred. No. 2,2e-35;  
 Matches 106; Conservative 60; Mismatches 126; Indels 15; Gaps 5;

QY 13 YEENMNGTVDYDQYELICIKEDVREFAKFLPVFLTVFVIGLAGNSMVVAIYAYKKQ 72  
 12 YTEDDL-GSGDYDSKKEPCFRENAHFRIPLPTVYSHIFLTGIVGNGLVILVNGYQKL 70  
 QY 73 RTKIDVYILNLAVDLLFLTPFAVNAVHGWLGIKMKITSLATLTAFVSGMQLAC 132  
 71 RSMIDKRLHLSVADLLFLTPFAVNAVHGWLGIKMKITSLATLTAFVSGMQLAC 130  
 QY 133 ISIDRYAVATKVPQSGVGKPC-----WICFCVMAAILSLPOLVF--YTVDNARC 184  
 131 ISIDRYALIVATNSQ---KPKRLAEKVYVGVWLPRAVLLTIPDLIFADIKEDERYIC 187  
 QY 185 IPIPRYIGSMKALIQMLEICIGFVVPFLIMGVCFYFARTLMKMPNIKISRLKVLTT 244  
 188 DRFPSPDL--WLVFQFQIHVGLLPGIYILSCYCIISKLSHSGYQKRKALKTTVI 244  
 QY 245 VVIVPIVQLPYNIYKPCRAIDIIYSLTSCMSKMDIAIQTESIALPHSCINPILTY 304  
 245 LILTFACMLPYIIGISIDSLTLEITIQGCEFEFSTVHKMISTEALAFPHCCINPILTY 304  
 QY 305 FPMGASF 311  
 305 FLGAKFK 311  
 Db

RESULT 16  
 G00048  
 C:Species: Macaca fascicularis (crab-eating macaque)  
 C:Date: 11-Apr-1997 #sequence\_revision 11-Apr-1997 #text\_change 26-Aug-1999  
 C:Accession: G00048  
 R:Ratsumi, M.  
 A:Reference number: H00048  
 A:Accession: G00048  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-352 <TAT>  
 A:Cross-references: GB:D86579; NID:g1468948; PID:g1468949  
 C:Superfamily: vertebrate rhodopsin

Query Match 27.1%; Score 493.5; DB 2; Length 352;  
 Best Local Similarity 34.0%; Pred. No. 7.3e-35;  
 Matches 105; Conservative 59; Mismatches 134; Indels 11; Gaps 4;

QY 8 STDYVEENMNGTVDYDQYELICIKEDVREFAKFLPVFLTVFVIGLAGNSMVVAIYA 67  
 8 TSDNYTE---MGSQDSDSIKEPCFRENAHFRIPLPTVYSHIFLTGIVGNGLVILVNG 64  
 Db  
 QY 68 YKKORTKIDVYILNLAVDLLFLTPFAVNAVHGWLGIKMKITSLATLTAFVSGM 127  
 65 YOKKLSMTDKRLHLSVADLLFLTPFAVNAVHGWLGIKMKITSLATLTAFVSGM 124  
 Db  
 QY 128 QFLACTSIDRYAVATKVPQSGVGKPC--WICFCVMAAILSLPOLVFYV--NDNA 182  
 125 LILAFSLDRLYALIVATNSQRPKRLAEKVYVGVWLPRAVLLTIPDLIFADISEADDY 184  
 Db  
 QY 183 RCIPDIPRYIGSMKALIQMLEICIGFVVPFLIMGVCFYFARTLMKMPNIKISRLKVL 242  
 185 ICORFYNLDMV---VVFQFQIHVGLLPGIYILSCYCIISKLSHSGYQKRKALKTT 241  
 Db

QY 243 LTVIVIVITOLPYNIYKPCRAIDIIYSLTSCMSKMDIAIQTESIALPHSCINPIL 302  
 242 VILILAFACMLPYIIGISIDSLTLEITIQGCEFEFSTVHKMISTEALAFPHCCINPIL 301  
 Db  
 QY 303 YPMGASF 311  
 302 YAFGLAKFK 310  
 Db

Query Match 27.0%; Score 492; DB 2; Length 360;  
 Best Local Similarity 33.5%; Pred. No. 1e-34;  
 Matches 107; Conservative 62; Mismatches 122; Indels 28; Gaps 8;

QY 17 EMNGTVDYDQYELICIKEDVREFAKFLPVFLTVFVIGLAGNSMVVAIYAYKKORTK 76  
 19 EYTFPFY-DVGACCHKPDVQKQIAGOLPLPYSLVTFGFQGNLVLLINCKKLCIT 77  
 Db  
 QY 77 DYTILNLAVDLLFLTPFAVNAVHGWLGIKMKITSLATLTAFVSGMQLACISID 136  
 78 DYTILNLAISDLFLTPFAVNAVHGWLGIKMKITSLATLTAFVSGMQLACISID 137  
 Db  
 QY 137 RYVAVATK-----PSQSGVGKPCWIIICFCVMAAILSLPOLVFYVNDNAR---CIP 186  
 138 RYLAIVAVAFVAKRATYFGV---VTSVITWLVAVAFVPGIIFKCKQKEDSVYVCGP 192  
 Db  
 QY 187 IPR---YLGISMKALIQMLEICIGFVVPFLIMGVCFYFARTLMKMPN-IKISRLKVL 242  
 193 YFPGMNNFHTIMRNI-----LGLVLPILIVICSGIILTKLRCRNEKRRARAVI 245  
 Db  
 QY 243 LTVIVIVITOLPYNIYKPCRAIDIIYSLTSCMSKMDIAIQTESIALPHSCINPIL 302  
 246 FTIMIVIVFVTPYNIYKPCRAIDIIYSLTSCMSKMDIAIQTESIALPHSCINPIL 304  
 Db

Query Match 27.0%; Score 492; DB 2; Length 360;  
 Best Local Similarity 33.5%; Pred. No. 1e-34;  
 Matches 107; Conservative 62; Mismatches 122; Indels 28; Gaps 8;

QY 17 EMNGTVDYDQYELICIKEDVREFAKFLPVFLTVFVIGLAGNSMVVAIYAYKKORTK 76  
 19 EYTFPFY-DVGACCHKPDVQKQIAGOLPLPYSLVTFGFQGNLVLLINCKKLCIT 77  
 Db  
 QY 77 DYTILNLAVDLLFLTPFAVNAVHGWLGIKMKITSLATLTAFVSGMQLACISID 136  
 78 DYTILNLAISDLFLTPFAVNAVHGWLGIKMKITSLATLTAFVSGMQLACISID 137  
 Db  
 QY 137 RYVAVATK-----PSQSGVGKPCWIIICFCVMAAILSLPOLVFYVNDNAR---CIP 186  
 138 RYLAIVAVAFVAKRATYFGV---VTSVITWLVAVAFVPGIIFKCKQKEDSVYVCGP 192  
 Db  
 QY 187 IPR---YLGISMKALIQMLEICIGFVVPFLIMGVCFYFARTLMKMPN-IKISRLKVL 242  
 193 YFPGMNNFHTIMRNI-----LGLVLPILIVICSGIILTKLRCRNEKRRARAVI 245  
 Db  
 QY 243 LTVIVIVITOLPYNIYKPCRAIDIIYSLTSCMSKMDIAIQTESIALPHSCINPIL 302  
 246 FTIMIVIVFVTPYNIYKPCRAIDIIYSLTSCMSKMDIAIQTESIALPHSCINPIL 304  
 Db



OY 303 YVFMGASFKNYVMKAKKY 321  
 Db 305 YAFVGEKFRRLYSVFRRKH 323

## RESULT 18

A39445  
 Interleukin-8 receptor type A - human  
 N:Alternate names: interleukin-8 receptor, high-affinity  
 C:Species: Homo sapiens (man)  
 C:Date: 22-Jan-1993 #sequence revision 12-Apr-1996 #text\_change 05-Nov-1999  
 C:Accession: I37449; I38710; I38711; A39445  
 C:Molecule type: DNA  
 R:Holmes, W.E.; Lee, J.; Xuang, W.J.; Rice, G.C.; Wood, W.I.  
 J. Biol. Chem. 269, 26381-26389, 1994  
 A:Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor type A and human interleukin-8 receptor gene (IL8RA) maps to the 2q33-q36 region  
 A:Reference number: I37449; MUID:93252387; PMID:8486366  
 A:Accession: I37449  
 A:Molecule type: DNA  
 A:Residues: 1-350 <RES>  
 A:Cross-references: EMBL:X65858; NID:g312046; PIDN:CAA46688.1; PID:g312047  
 R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.  
 J. Biol. Chem. 269, 26381-26389, 1994  
 A:Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor type A and human interleukin-8 receptor gene (IL8RA) maps to the 2q33-q36 region  
 A:Reference number: I37449; MUID:93252387; PMID:8486366  
 A:Accession: I38710  
 A:Molecule type: DNA  
 A:Residues: 1-350 <RES>  
 A:Cross-references: EMBL:U11870; NID:g511804; PIDN:AAA64378.1; PID:g511805  
 A:Accession: I38711  
 A:Molecule type: DNA  
 A:Residues: 1-16 <RES>  
 A:Cross-references: EMBL:U11871; NID:g511806; PIDN:AAA64379.1; PID:g733002  
 R:Holmes, W.E.; Lee, J.; Xuang, W.J.; Rice, G.C.; Wood, W.I.  
 Science 253, 1278-1280, 1991  
 A:Title: Structure and functional expression of a human interleukin-8 receptor.  
 A:Reference number: A39445; MUID:91368199; PMID:1840701  
 A:Accession: A39445  
 A:Molecule type: mRNA  
 A:Residues: 1-275, 'T', 277-350 <HOL>  
 A:Cross-references: GB:M68932; NID:g186363; PIDN:AAA59159.1; PID:g186370  
 C:Genetics:  
 A:Gene: GDB:IL8RA  
 A:Cross-references: GDB:135039; OMIM:146929  
 A:Map position: 2035-2035  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 26.9%; Score 489.5; DB 2; Length 350;  
 Best Local Similarity 34.6%; Pred. No. 1.6e-34;  
 Matches 107; Conservative 63; Mismatches 120; Indels 19; Gaps 7;

OY 23 DYSQVELICKEDEAFAPVLPVLTIVFVIGLAGNSWVAIYAYKKQRTKDTVILN 82  
 Db 26 DYSQVELICKEDEAFAPVLPVLTIVFVIGLAGNSWVAIYAYKKQRTKDTVILN 80  
 OY 83 LAAVADLLFLTPFPMAVNAHVGLKIMCKITSAIYTNFVSGMQLACISIDRYAV- 141  
 Db 81 LAAVADLLFLTPFPMAVNAHVGLKIMCKITSAIYTNFVSGMQLACISIDRYAV- 140  
 OY 142 --TKVPSQSGVKPCWIIICFCVMAAAILISIPOLV--YTVDNARCTPIPRVLG--- 193  
 Db 141 HAARTLTQK--RHIVKFCVCGWGLSMNLISLPFLFRQAVHPNNSS--PVCYEVIGNDT 195  
 OY 194 TSKKALIQMLEICIGFVAVPLIIVGVCFTIARTLMKMPINKISRPKVLILFVIVITQ 253  
 Db 196 AKRRAVRLIPIHTPGFVLPVLMFCIGFTLRILFKAHGQCKRMRVFAVVLIFLLCM 255  
 OY 254 LPYIVVFCRAIDIIYSLITSCNMSKMDIAIOVTSIALFHSCLNPIIYVFMGASFKNY 313  
 Db 256 LPYIVVFCRAIDIIYSLITSCNMSKMDIAIOVTSIALFHSCLNPIIYVFMGASFKNY 315  
 OY 314 VMKAKKYG 322

Db 316 FLKILAMHG 324

## RESULT 19

G protein-coupled receptor CKR-L1 - human  
 N:Alternate names: chemokine receptor-like protein TBR1; GPR-CY6  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Jan-1997 #sequence revision 31-Jan-1997 #text\_change 21-Jul-2000  
 C:Accession: J05067; G02776; G02387  
 R:Zaballios, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.  
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996  
 A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like genes  
 A:Reference number: J05067; MUID:97040707; PMID:8886020  
 A:Accession: J05067  
 A:Molecule type: DNA  
 A:Residues: 1-355 <ZAB>  
 A:Cross-references: EMBL:Z79782; NID:g1668735; PIDN:CAB02142.1; PID:g1668736  
 R:Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.  
 submitted to the EMBL Data Library, June 1996  
 A:Reference number: H01714  
 A:Accession: G02776  
 A:Molecule type: DNA  
 A:Status: translated from GB/EMBL/DBJ  
 A:Residues: 1-355 <NAP>  
 A:Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979  
 R:Bonner, T.I.  
 submitted to the EMBL Data Library, January 1996  
 A:Reference number: H01154  
 A:Accession: G02387  
 A:Molecule type: DNA  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Residues: 1-355 <BON>  
 A:Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057  
 C:Comment: This protein belongs to the family of beta chemokine receptors.  
 C:Genetics:  
 A:Gene: GDB:CKR8; CKRBL2; TBR1; CKR-L1  
 A:Cross-references: GDB:6053733; OMIM:601834  
 A:Map position: 3p21-3p21  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; transmembrane protein  
 F:36-63/Domain: transmembrane #status predicted <TM1>  
 F:73-94/Domain: transmembrane #status predicted <TM2>  
 F:108-129/Domain: transmembrane #status predicted <TM3>  
 F:147-171/Domain: transmembrane #status predicted <TM4>  
 F:200-222/Domain: transmembrane #status predicted <TM5>  
 F:239-260/Domain: transmembrane #status predicted <TM6>  
 F:281-304/Domain: transmembrane #status predicted <TM7>

Query Match 26.7%; Score 486; DB 2; Length 355;  
 Best Local Similarity 31.4%; Pred. No. 3.2e-34;  
 Matches 109; Conservative 73; Mismatches 121; Indels 44; Gaps 8;

OY 9 TDYVYENEMNGYDYSQVELICKEDEAFAPVLPVLTIVFVIGLAGNSWVAIYAY 68  
 Db 13 TDYVYENEMNGYDYSQVELICKEDEAFAPVLPVLTIVFVIGLAGNSWVAIYAY 62  
 OY 69 YKQRTKDTVILNLAADLLFLTPFPMAVNAHVGLKIMCKITSAIYTNFVSGMQL 128  
 Db 63 YKQRTKDTVILNLAADLLFLTPFPMAVNAHVGLKIMCKITSAIYTNFVSGMQL 122  
 OY 129 FLACISIDRYAVV--KVP--QSGVSKPCWIIICFCVMAAAILISIPOLVETVNDN 181  
 Db 123 FLACISIDRYAVV--KVP--QSGVSKPCWIIICFCVMAAAILISIPOLVETVNDN 177  
 OY 182 ARCPIDPRY-----LGTSMKALIQMLEICIGFVAVPLIIVGVCFTIARTLMKMPIN 233  
 Db 178 ARCPIDPRY-----LGTSMKALIQMLEICIGFVAVPLIIVGVCFTIARTLMKMPIN 231  
 OY 234 KISRPLKVLTVVIVITQLPYIVVFCRAIDIIYSLITSCNMSKMDIAIOVTSIAL 293  
 Db 232 KISRPLKVLTVVIVITQLPYIVVFCRAIDIIYSLITSCNMSKMDIAIOVTSIAL 290

QY 294 FHSCINPILYVFMGASFKYVKKVAKK-----YGSMRQROSVEE 333  
 DB 291 THCCNVPYVAFVGEKFKKHSEIFQKSCSQIFNYLNGKMPRESCEK 337

## RESULT 20

149339

macrophage inflammatory protein-1 alpha receptor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
 C:Accession: 149339

R:Gao, J.L.; Murphy, P.M.  
 J. Biol. Chem. 270, 17494-17501, 1995

A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine

A:Reference number: 149339; MUID:95340546; PMID:7542241

A:Accession: 149339

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-355 <RES>

A:Cross-references: EMBL:U28404; NID:9881547; PIDN:AAA89153.1; PID:9881548

C:Superfamily: vertebrate rhodopsin

Query Match 26.7%; Score 485; DB 2; Length 355;  
 Best Local Similarity 31.2%; Pred. No. 3.9e-34;

Matches 114; Conservative 69; Mismatches 142; Indels 40; Gaps 12;

QY 3 LEONQSTDYVEEENKMGTYDSQYELICIKEDREFAKFLVFLVFLTVIGLAGNSW 62  
 DB 1 MEISDFEANTPTTE---FDYGD-STPCOKTAVRAGAGLPLPLSLVFLISVGNVLV 55

QY 63 VAIYAYKKORTKTVYILNLAVALLLFTLPFWA-VNAHGVNLGKIMCKITSAIYTL 121  
 DB 56 ILVLMQHRRLQSMSTSYLFNLAVSDLVFLFTLPFWIDYKLDKDMIFGDAMCKLISGFYTL 115

QY 122 NPFSGMQLACISIDRVAVTKV-----PSQSGVKPCWIIICFCVMAAILSTPOLV 174  
 DB 116 GLYSEIFILLTIDRLALVAHVAFIRAVTTLGI-----ITSITWLAIALASNPALY 170

QY 175 FYTVN--DNARCIPIPRRYLGTSMKALIQMLEI-CIGFVPLVINGVCYFARTIMK 230  
 DB 171 FFAQWQEFHRTQSPHPR-YKSLKQMRPQALKNLGLITLPLVWITICAGIIRILKR 229

QY 231 PNKISRPLKVLTVIVLVTVLPVINYKFCRAI-DIYSLTSCNMSKMDIALQVTE 289  
 DB 230 PSERKAVAVLIPALITLFLFWTPYMLSVFSAFQDVLF--NCEQSKHLDLMAQVTE 287

QY 290 SILFHSCLNPILYVFMGASFKYVKKVAKK-----GSMRQROSVVEFPDSEPTER 344  
 DB 288 VIAVTHCCNVPYVAFVGEKFKKHSEIFQKSCSQIFNYLNGKMPRESCEK 338

QY 345 TSTFS 349  
 DB 339 TSTIS 343

RESULT 21

A43113

chemokine (C-C) receptor 5 - human  
 N:Alternate names: C-C CR-5; CCR5  
 C:Species: Homo sapiens (man)  
 C:Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 20-Jun-2000  
 C:Accession: A43113; S71808; A58832; G02653; A58833  
 R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.  
 Biochemistry 35, 3362-3367, 1996  
 A:Title: Molecular cloning and functional expression of a new human CC-chemokine receptor  
 A:Reference number: A43113; MUID:96241590; PMID:8639485  
 A:Accession: A43113

A:Molecule type: mRNA

A:Residues: 1-352 <SAM1>

A:Cross-references: GB:91492; NID:91262810; PIDN:CAA62796.1; PID:91262811

R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Sargoud

M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pe

Nature 382, 722-725, 1996

A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of  
 A:Reference number: S71808; MUID:96345670; PMID:8751444

A:Accession: S71808

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 182-206/207-230 <SAM2>

A:Accession: A58832

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-184; 'IKDSHLGAGPAAAGHLLGNPKNSAVSK' <SAM3>

A:Cross-references: GB:X93933; NID:91524062; PIDN:CAA67767.1; PID:91524063

A:Note: this frameshift mutation results in a non-functional receptor but confers a degree

nd may have had a selective advantage by conferring resistance to feline plague infect

R:Combadiere, C.; Ahuja, S.K.; Tillet, H.L.; Murphy, P.M.  
 J. Leukoc. Biol. 60, 147-152, 1996

A:Title: Cloning and functional expression of CC CR5, a human monocyte CC chemokine rec

A:Reference number: A58832; MUID:96295970; PMID:8699119

A:Accession: A58832

A:Molecule type: mRNA

A:Residues: 1-352 <COM1>

A:Cross-references: GB:U57840; NID:91502408; PIDN:AAB17071.1; PID:91502409

A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes

R:Combadiere, C.  
 submitted to the EMBL Data Library, May 1996

A:Reference number: H01541

A:Accession: G02653

A:Status: translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-89; 'L', '91-352 <COM2>

A:Cross-references: EMBL:U57840

R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.  
 J. Biol. Chem. 271, 17161-17166, 1996

A:Title: Molecular cloning and functional characterization of a novel human CC chemokine

A:Reference number: A58833; MUID:96291862; PMID:8663314

A:Accession: A58833

A:Molecule type: mRNA

A:Residues: 1-352 <RAP>

A:Cross-references: GB:U54994; NID:91457945; PIDN:AAC05058.1; PID:91457946

C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A0574), MIP-1beta (see

C:Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C

A:Gene: GDB:CMKBR5; CCR5; CR-5; CC-CR-5; CCR5; ChemR13

A:Map position: 3p21-3p21

C:Function:

A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES

A:Note: probably acts to control granulocyte proliferation and differentiation

C:Superfamily: vertebrate rhodopsin

C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran

F:32-56/Domain: transmembrane #status predicted <TM2>

F:67-87/Domain: transmembrane #status predicted <TM2>

F:103-124/Domain: transmembrane #status predicted <TM3>

F:142-166/Domain: transmembrane #status predicted <TM4>

F:193-218/Domain: transmembrane #status predicted <TM5>

F:236-257/Domain: transmembrane #status predicted <TM6>

F:285-300/Domain: transmembrane #status predicted <TM7>

F:20-269,101-178/Disulfide bonds: #status predicted

F:268/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted

F:340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 26.6%; Score 484.5; DB 2; Length 352;  
 Best Local Similarity 32.8%; Pred. No. 4.3e-34;  
 Matches 114; Conservative 69; Mismatches 128; Indels 37; Gaps 11;

QY 22 YDSQY-ELICIKEDVREFAKFLPVFLTVFVIGLAGNSMVAIYAYKKORTKTVYI 80  
 DB 10 YDINYYTSEPCQKINWQIAARLLPLYSILVIFPGVGNMVLILLINCKRUKSMYDYL 69

QY 81 LNLAVADLLFLTPWAVNAHGVNLGKIMCKITSAITLAFVSGMQLACISIDRYVA 140  
 DB 70 LNLATSDLEFLTLTPWAVNAHGVNLGKIMCKITSAITLAFVSGMQLACISIDRYVA 129

QY 141 VTKV-----PSQGVGKPCWIIICPCWMAAILSLIPOLVF-----YTVNDNARC 184  
 Db 130 VHAHFAFKARTVFGV-----VTSVITWVAFAVSLPGIIIFRSQEGHAHY-----C 178  
 QY 185 IPIPRYLGTSMKALIMLEICT-GFVPEPLNGVCYFTIARTLMKPN-IKTSRPLKLV 242  
 Db 179 SSHP-YSQYQFWKQFOTKLIVLIGLVLPLVWVTCYSGILKTLRCKRKHRRVRL 237  
 QY 243 LTVIVIVLQLPYNIKFCRAIDIIYSLTSCMSKMDIAIQTESIALFSCINPIL 302  
 Db 238 FTITVIVFLFAPRNIVLLANTFOEFGL-NCSSSRLLQANQVTTGLMTCINPIL 296  
 QY 303 YVFMGAFKYNVVKAKYGSWRQR-QSVEEPFDESGTEPTSTFS 349  
 Db 297 YAFGEKFRNVLIVFQKHIAKRCCKSI-----FOEAPERASSVYT 340  
 RESULT 22  
 A48921  
 Interleukin-8 receptor type B - mouse  
 N:Alternate names: G-protein coupled receptor Gpcr16  
 C:Species: Mus musculus (house mouse)  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Nov-1999  
 C/Accession: A48921; A53677; 149348; 15421; A48909; 153774  
 R/Cerretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert, Genomics 18, 410-413, 1993  
 A>Title: The murine homologue of the human interleukin-8 receptor type B maps near the A:Reference number: A48921; MUID:94117014; PMID:8288247  
 A/Accession: A48921  
 A/Molecule type: DNA  
 A/Residues: 1-359 <CR>  
 A/Cross-references: GB:L23637; NID:9435093; PIDN:AAA9305.1; PID:9435094  
 R/Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.  
 J. Biol. Chem. 269, 18263-18266, 1994  
 A>Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding A:Reference number: A53677; MUID:94308043; PMID:7518426  
 A/Accession: A53677  
 A/Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A/Molecule type: DNA  
 A/Residues: 1-359 <SUZ>  
 A/Cross-references: GB:L26549  
 A/Note: sequence extracted from NCBI backbone (NCBI:P:149812)  
 R/Lee, J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.  
 J. Immunol. 155, 2158-2164, 1995  
 A>Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.  
 A:Reference number: 149348; MUID:95363183; PMID:7636264  
 A/Accession: 149348  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-359 <RES>  
 A/Cross-references: EMBL:U31207; NID:950174; PIDN:AC52239.1; PID:950175  
 R/Borric, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.  
 J. Biol. Chem. 269, 29355-29358, 1994  
 A>Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression A:Reference number: 155421; MUID:95050766; PMID:7961909  
 A/Accession: 155421  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-359 <RES>  
 A/Cross-references: GB:L13239; NID:9233665; PIDN:AAA62109.1; PID:9233666  
 R/Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G. Genomics 18, 175-184, 1993  
 A>Title: Identification, chromosomal location, and genome organization of mammalian G-PD A:Reference number: A48909; MUID:94116980; PMID:8288218  
 A/Accession: A48909  
 A/Status: preliminary; nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 145-258 <ML>  
 A/Cross-references: GB:L20337; NID:9438800; PIDN:AAA16853.1; PID:9438801  
 R/Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K. Gene 142, 297-300, 1994  
 A>Title: Cloning of a cDNA encoding a mouse homolg of the interleukin-8 receptor.  
 A:Reference number: 153774; MUID:94252584; PMID:8194768

A/Accession: 153774  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-359 <RB3>  
 A/Cross-references: GB:D17630; NID:9493671; PIDN:BA04536.1; PID:9493672  
 C/Genetics:  
 A/Gene: 118rb  
 A/Introns: #status absent  
 C/Superfamily: vertebrate rhodopsin  
 C/Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein  
 F:49-74/Domain: transmembrane #status predicted <TM1>  
 F:84-106/Domain: transmembrane #status predicted <TM2>  
 F:120-141/Domain: transmembrane #status predicted <TM3>  
 F:163-182/Domain: transmembrane #status predicted <TM4>  
 F:213-234/Domain: transmembrane #status predicted <TM5>  
 F:251-271/Domain: transmembrane #status predicted <TM6>  
 F:308-328/Domain: transmembrane #status predicted <TM7>  
 Query Match 26.6%; Score 483.5; DB 2; Length 359;  
 Best Local Similarity 30.4%; Pred. No. 5.4e-34;  
 Matches 112; Conservative 73; Mismatches 136; Indels 47; Gaps 7;  
 QY 10 DYVEENENNGTYDYSOYE-----LICIKK--DVREKAVFLPVFLTIVEVIGLA 57  
 Db 7 DKFNIEDPFGSDLDIFNYSNGMPSILPDAPCHSENLEINSAYVIVVLT--LSLV 63  
 QY 58 GNSMVVAIYAYKKQRTQDVTIINLAVALDLLFTLPPMAVNAVHGVVLKIMCKITSA 117  
 Db 64 GNSLVMLVILYNRSTCSVDVLLMLAIALDLFFALTLLPMAASKNGWTFGSTLCKIRSY 123  
 QY 118 LYTINPVSQGLACISIDRYAVAVKVP8---QSGVGKPCWIIICPCWMAAILSLIPOL 173  
 Db 124 VKEVTFYSSVLLACISMDRYALIVHASTLQKHLYK--FVIAIMLSVILALPIL 180  
 QY 174 V-----FYTVNDNARCIPIFRYLTGSMKALIQMLEICGFVVPFLIMGVC 219  
 Db 181 ILRNPKNVNLSTLVCEVDGNNT-----SRLRVLRILPQTRGFVPLIMIFC 229  
 QY 220 YFTIARTLMKMPNIRKISRLPKVLLVVIYFIYTOLPYNIKFCRAIDIIYSLTSCMSK 279  
 Db 230 YGFTLRITLFKAHQGHRRAMRVIFAVVLFLLCWLPPYMLVLTDTIMTKLKEICERD 289  
 QY 280 RMDIAIQTESIALFPCINPILYVFMGAFKYNVVKAKYGSWRQRQSVVEEPFDE 339  
 Db 290 DIDKALNATEIILGFHSCINPILTIYAFIQGFHGLKLTWATYGLVSKERLAKGRSPVS 349  
 QY 340 GPTEPTST 347  
 Db 350 SSSANTST 357  
 RESULT 23  
 138450  
 chemokine (C-C) receptor 2, splice form A - human  
 N:Alternate names: C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chem  
 C/Species: Homo sapiens (man)  
 C/Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 13-Aug-1999  
 C/Accession: 138450  
 R/Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.V.; Coughlin, S.R. Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
 A>Title: Molecular cloning and functional expression of two monocyte chemoattractant prot A:Reference number: A53477; MUID:94195921; PMID:8146186  
 A/Accession: 138450  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-374 <RES>  
 A/Cross-references: EMBL:U03882; NID:9472555; PIDN:AAA19119.1; PID:9472556  
 C/Genetics:  
 A/Gene: GDB:CMKBR2  
 A/Cross-references: GDB:337364; OMIM:601267  
 A/Map position: 3p21-3p21  
 C/Superfamily: vertebrate rhodopsin  
 C/Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane





Oy 299 NPILYFVGASFK-----NYWKAAYKXYSRROQSVSEPPF---DSEGPTEPT 345  
 Db 336 NPVIAFVGEKFRRLHYFHTYVAIYLCYK-----IPFLSGDEGKEGPT 381

## RESULT 29

chemokine (C-C) receptor 3 - human  
 G02436

N/Alternate names: C-C CKR-3  
 C/Species: Homo sapiens (man)

C/Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 04-Mar-2000

C/Accession: G02436; A57237

R/Ponath, P.D.  
 Submitted to the EMBL Data Library, February 1996

A/Reference number: H01272

A/Accession: G02436

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-355 <PON>

A/Cross-references: EMBL:U69727; NID:G1477560; PIDN:AAB09726.1; PID:G1477561

R/Combiadere, C.; Ahuja, S.K.; Murphy, P.M.

J. Biol. Chem. 270, 16491-16494, 1995

A/Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.

A/Reference number: A57237; MUID:95348056; PMID:7622448

A/Accession: A57237

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>

A/Cross-references: GB:U28694; NID:G1199579; PIDN:AAC50469.1; PID:G1199580

A/Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.

C/Genetics:

A/Gene: GDB:CMKBR3

A/Cross-references: GDB:579624; OMIM:601268

A/Map position: 3p21-3p21

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F/36-60/Domain: transmembrane #status predicted <TM1>

F/71-91/Domain: transmembrane #status predicted <TM2>

F/108-129/Domain: transmembrane #status predicted <TM3>

F/147-171/Domain: transmembrane #status predicted <TM4>

F/205-223/Domain: transmembrane #status predicted <TM5>

F/240-261/Domain: transmembrane #status predicted <TM6>

F/288-305/Domain: transmembrane #status predicted <TM7>

F/324-273, 106-183/Disulfide bonds: #status predicted

F/345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 25.4%; Score 461.5; DB 2; Length 355;

Best Local Similarity 31.8%; Pred. No. 4, 1e-32;

Matches 99; Conservative 63; Mismatches 114; Indels 35; Gaps 10;

Oy 24 YSOVELICIKEDVREPAKFLPVFLTIVFVIGLAGNSMVAIYVYKKQRTKDVYILN 83

Db 17 YDVGLLCEKADTALMAQFVPLYSIVFVGLGNVAVVMIILKYRLIMINIVLNL 76

Oy 84 AVADLLFLTPFAVNAV--HGWLGIKIMCKITSALTYTNFVSGMOFLACISIDRVAV 141

Db 77 AISDLPLVLTIPFV--IHVVRGHNVFPGHCKLSGFYHGVSEIFITLITDRILAI 135

Oy 142 TKV-----PSQGVGKPCWIIICFYVMAAILISIPOLVFTYV--DNARCIPIFP-- 189

Db 136 VHAFAVLRARTRVFGV-----ITSIVMGALVALALPEFIYETBELFEETLCSALYPED 190

Oy 190 -----RLIGISMKALLIOMLEICIGFVVPFLIMGVCYFITTARTLMKNITISRPKLULT 244

Db 191 TVYSWRHFHT-----LMTITFCL--VPLVMAICYGIIKTLIRCSKKRYAIRILFV 243

Oy 245 VVIYFVITQLPYNIIVKCRAT--DIYSLITSQNMCKEMDIAIOVTESIALFHSGLNDIIV 303

Db 244 IMAVFIFWTPYNIIVAILLSISQSLIFG--NDCERTKALDLVMTVEIATVIAISHCCMPVIT 301

Oy 304 VFMGASFKNYV 314

Db 304 VFMGASFKNYV 314

Db 302 AFVGERFRKYL 312

## RESULT 30

angiotensin II receptor type 1 - dog  
 S44425

C/Species: Canis lupus familiaris (dog)

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Nov-1999

C/Accession: S44425

R/Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.

FEBS Lett. 343, 146-150, 1994

A/Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor w

A/Reference number: S44425; MUID:94222188; PMID:8168620

A/Accession: S44425

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-359 <BUR>

A/Cross-references: PIDN:AAB30674.1; PID:G546569

A/Experimental source: liver

C/Superfamily: vertebrate rhodopsin

Query Match 25.0%; Score 455.5; DB 2; Length 359;

Best Local Similarity 31.2%; Pred. No. 1, 4e-31;

Matches 103; Conservative 70; Mismatches 130; Indels 27; Gaps 8;

Oy 31 CIKEDVREPAKFLPVFLTIVFVIGLAGNSMVAIYVYKKQRTQDYIINLAVADLL 90

Db 18 CPKGRHNYIFPMITPLYSIIFVGIKNSLVIVYIYVMTLKVASFLNLALADLCF 77

Oy 91 LFTLPPAVNAV--HGWLGIKIMCKITSALTYTNFVSGMOFLACISIDRVAVATKPSQS 148

Db 78 LITLPLMAVYTYMEYRMPFNGVYLCKIASASVFNLYASVPLTCLSIDRYVAIVH--PKMS 136

Oy 149 GVGKP---CWIIICFVMAAILISIPOL-----VFTYVNDNARCIPIPRVYGTSMKALIQ 201

Db 137 PVRRTMLAKVCIILIIWLAGLASLPTIIHRNVFEIENITVCAFYHESQNSTLPGLG 196

Oy 202 MLEICIGFVVPFLIMGVCYFITTARTLMKNITISRP-----LKVLTIVVFTVITOLPY 256

Db 197 LKNILGFLPFLITLITSTYTLTKLRAVEIQKPKPNNDIFKIMAVLFFPFSWPH 256

Oy 257 NIVKCFRAIDITYSL--ITSCNMSKEMDIAIOVTESIALFHSGLNDIIVFMGASFKNYV 314

Db 257 QFTF---LDVLIQGIHDKKIDIVDTAMPITFCIAYFNNCLNPLPYGLKKFKYF 313

Oy 315 MKV-----AKYGSWRROQSVSEPPF 337

Db 314 IQLTKYIPKAKSHSLSTKMTLSYRPSD 343

## RESULT 31

angiotensin II receptor type 1 - human  
 J01404

N/Alternate names: angiotensin II receptor 1A

C/Species: Homo sapiens (man)

C/Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 21-Jul-2000

C/Accession: J01404; J01402; J01403; J01404; J01405; J01406; J01407; J01408; J01409; J01410; J01411; J01412; J01413; J01414; J01415; J01416; J01417; J01418; J01419; J01420; J01421; J01422; J01423; J01424; J01425; J01426; J01427; J01428; J01429; J01430; J01431; J01432; J01433; J01434; J01435; J01436; J01437; J01438; J01439; J01440; J01441; J01442; J01443; J01444; J01445; J01446; J01447; J01448; J01449; J01450; J01451; J01452; J01453; J01454; J01455; J01456; J01457; J01458; J01459; J01460; J01461; J01462; J01463; J01464; J01465; J01466; J01467; J01468; J01469; J01470; J01471; J01472; J01473; J01474; J01475; J01476; J01477; J01478; J01479; J01480; J01481; J01482; J01483; J01484; J01485; J01486; J01487; J01488; J01489; J01490; J01491; J01492; J01493; J01494; J01495; J01496; J01497; J01498; J01499; J01500; J01501; J01502; J01503; J01504; J01505; J01506; J01507; J01508; J01509; J01510; J01511; J01512; J01513; J01514; J01515; J01516; J01517; J01518; J01519; J01520; J01521; J01522; J01523; J01524; 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 A; Title: Cloning and characterization of a human angiotensin II type 1 receptor.  
 A; Reference number: JH0574; MUID:9231907; PMID:1567413  
 A; Accession: JH0574  
 A; Molecule type: mRNA  
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 A; Experimental source: Liver  
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 A; Reference number: JH0267; MUID:92198490; PMID:1550596  
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 A; Molecule type: mRNA  
 A; Residues: 1-359 <TAK>  
 A; Experimental source: Liver  
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 A; Reference number: A44014; MUID:92375105; PMID:1508224  
 A; Accession: A44014  
 A; Status: Preliminary  
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QY 91 LFTLFPNAVNAV--HGWLGIKIMCKITSAIYLNLFVSGQFACISIDRYVAATKPSOS 148  
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 DB 197 LTKNIIIGFLFPLIITLSTYLLWKALKKAYEIQKNRPNDIIFKILIAIVLFFFSWVPH 256

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QY 315 MKV-----AKYGSWRQROSVVEFPD--SEGPTETSTFSI 350  
 DB 314 LQLLKTIPKAKSHSNLSTKMSTLSYRPEDNVSSSTKRPACFEV 358

RESULT 32  
 JC2134

angiotensin II receptor type 1A - rat  
 N; Alternate names: AT1a receptor; AT3 receptor  
 C; Species: Rattus norvegicus (Norway rat)  
 C; Date: 28-Aug-1985 #sequence revision 07-Oct-1994 #text\_change 24-Nov-1999  
 C; Accession: UC2134; S15404; S20424; J01055  
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 A; Title: Synthetic cDNA encoding the rat AT1a receptor: a useful tool for structure-funct  
 A; Reference number: UC2134; MUID:94197726; PMID:8147879  
 A; Accession: UC2134  
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 A; Reference number: S15404; MUID:91251901; PMID:2041570  
 A; Accession: S15404  
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 A; Reference number: S20423; MUID:92183879; PMID:1544458  
 A; Accession: S20424  
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 A; Title: Rat angiotensin II receptor: cDNA sequence and regulation of the gene expression  
 A; Reference number: JQ1055; MUID:91254291; PMID:2043116  
 A; Accession: JQ1055  
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Query Match 24.9%; Score 452.5; DB 2; Length 359;  
 Best Local Similarity 30.1%; Pred. No. 2.5e-31;  
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QY 31 CKEEDVREFAKVFLEPLTIVFVIGLGNMVAIYAYKKQRTKDYIINLAVALDLL 90  
 DB 18 CPKAGRHNYIFVMIPTLXIIFVVGIFGNSLVVIYFYFMKLTVA SVFLNLALADLCF 77

QY 91 LFTLFPNAVNAV--HGWLGIKIMCKITSAIYLNLFVSGQFACISIDRYVAATKPSOS 148  
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 DB 257 QITFT---LDVLIQIGIIRDCRIADIVDAMPITTCIAFNNCLNPLFYGFLGKKFKYF 313











GenCore version 5.1.4 ps 4578  
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## OM protein - protein search, using sw model

Run on: March 17, 2003, 16:26:11 ; Search time 15 Seconds

(without alignments)  
686.535 Million cell updates/sec

Title: US-09-721-495b-2

Perfect score: 1819

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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Listing first 135 summaries

Database : Issued Parents AA:\*

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6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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4	659	36.2	358	3	US-09-299-843A-19
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7	659	36.2	358	1	US-08-153-848-15
8	659	36.2	378	3	US-09-299-843A-15
9	659	36.2	378	4	US-09-251-545-1
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32	583	32.1	374	4	US-09-534-185-48	Sequence 4, Appl
33	581	31.9	342	4	US-09-116-498-4	Sequence 6, Appl
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 109 486 26.7 355 4 US-09-534-185-56 Sequence 56, Appl1  
 110 485 26.7 352 4 US-09-045-583-52 Sequence 52, Appl1  
 111 485 26.7 352 4 US-09-534-185-52 Sequence 52, Appl1  
 112 484.5 26.6 352 4 US-09-087-232A-13 Sequence 13, Appl1  
 113 484.5 26.6 352 4 US-08-861-105-14 Sequence 14, Appl1  
 114 484.5 26.6 352 4 US-08-575-967A-2 Sequence 2, Appl1  
 115 484.5 26.6 352 4 US-09-517-605-5 Sequence 5, Appl1  
 116 484.5 26.6 352 4 US-08-833-752-5 Sequence 5, Appl1  
 117 482 26.5 344 3 US-08-466-343D-9 Sequence 9, Appl1  
 118 482 26.5 374 1 US-08-450-393A-2 Sequence 2, Appl1  
 119 482 26.5 374 5 US-08-446-669-2 Sequence 2, Appl1  
 120 482 26.5 374 5 PCT-US95-00476-2 Sequence 2, Appl1  
 121 478 26.3 378 4 US-09-045-583-5 Sequence 5, Appl1  
 122 478 26.3 378 4 US-09-534-185-5 Sequence 5, Appl1  
 123 477.5 26.3 352 3 US-08-466-343D-2 Sequence 2, Appl1  
 124 474 26.1 355 1 US-08-012-988A-2 Sequence 2, Appl1  
 125 474 26.1 355 1 US-08-450-393A-5 Sequence 5, Appl1  
 126 474 26.1 355 4 US-08-446-669-5 Sequence 5, Appl1  
 127 474 26.1 355 5 PCT-US95-00476-5 Sequence 5, Appl1  
 128 474 26.1 355 4 US-08-833-752-9 Sequence 9, Appl1  
 129 471 25.9 355 4 US-08-575-967A-4 Sequence 4, Appl1  
 130 464.5 25.5 355 4 US-08-847-296B-1 Sequence 1, Appl1  
 131 464.5 25.5 355 4 US-09-045-583-54 Sequence 54, Appl1  
 132 464.5 25.5 355 4 US-09-534-185-54 Sequence 54, Appl1  
 133 464.5 25.5 358 2 US-08-458-970A-11 Sequence 11, Appl1  
 134 452.5 24.9 358 4 US-09-045-583-53 Sequence 53, Appl1  
 135 451.5 24.8 355 4 US-09-045-583-53

## ALIGNMENTS

## RESULT 1

US-08-966-316-16  
 ; Sequence 16, Application US/08966316  
 ; Patent No. 5932445  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Reddy, Roopa  
 ; APPLICANT: Murthy, Lynn E.  
 ; APPLICANT: Mathur, Preete  
 ; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/966,316  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0424 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 350 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: UTRNOT11  
 CLONE: 2547002  
 US-08-966-316-16  
 Query Match 100.0%; Score 1819; DB 2; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1,7e-147;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MALEQNSTDYENENNGTYDSQYELICKEDEYREPAKVFPLVITVYGLAGNS 60  
 1 MLEQNSTDYENENNGTYDSQYELICKEDEYREPAKVFPLVITVYGLAGNS 60  
 1 MVAIYAYKKRKTQDYIINLAVADLLFTLPFMAVNAVHGVIGIKICKITSAIYT 120  
 61 MVAIYAYKKRKTQDYIINLAVADLLFTLPFMAVNAVHGVIGIKICKITSAIYT 120  
 121 INFVSGMGLACISIDRYAVATKVPQSOGVGPCKIICFCVMAAILLSIQLVFYVND 180  
 121 INFVSGMGLACISIDRYAVATKVPQSOGVGPCKIICFCVMAAILLSIQLVFYVND 180  
 181 NARCIPPIPRYIGTSMKALIQMLEICIGFVYVPLIMGVCFITARTLMKNIKISRLK 240  
 181 NARCIPPIPRYIGTSMKALIQMLEICIGFVYVPLIMGVCFITARTLMKNIKISRLK 240  
 241 VLLTVIVIFIVQLPYNIVKFCRAIDIIYLSITSCNNSKRMIDIAIQTESIALPHSCNP 300  
 241 VLLTVIVIFIVQLPYNIVKFCRAIDIIYLSITSCNNSKRMIDIAIQTESIALPHSCNP 300  
 301 ILVFMGASFKNYVMKAKKYGSMWRQSVSEPPFSEGTPEPTSTFSI 350  
 301 ILVFMGASFKNYVMKAKKYGSMWRQSVSEPPFSEGTPEPTSTFSI 350

## RESULT 2

US-08-966-316-18  
 ; Sequence 18, Application US/08966316  
 ; Patent No. 5932445  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Reddy, Roopa  
 ; APPLICANT: Murthy, Lynn E.  
 ; APPLICANT: Mathur, Preete  
 ; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/966,316  
 ; FILING DATE: Herewith

```

/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0424 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 350 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: Genbank
/ CLONE: 399711
/ US-08-966-316-18

Query Match          89.1%; Score 1620; DB 2; Length 350;
Best Local Similarity 86.0%; Pred. No. 1,4e-130;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENENGTVDYSGYELICKEVDREPAVFLPVLTIVFVIGLAGNS 60
DB 1 MAVEYNQSTDYEEENENMDTHDYSGYEVICIKERKFAVFLPAFTTIAIIGLAGNS 60
QY 61 MVVAIYAAYKKORTKTDVYILNLAVADLLFLTPFWAVNAVHGVGLKIMCKITSAIYT 120
DB 61 TVVAIYAAYKKRRTKTDVYILNLAVADLLFLTPFWAVNAVHGVGLKIMCKITSAIYT 120
QY 121 LNFVSGMOFLACISIDRYAVATKVPBSQSGVKPCWIIICFCVWMAAILISIPQIVFYVND 180
DB 121 VNFVSGMOFLACISIDRYAVATKVPBSQSGVKPCWIIICFCVWMAAILISIPQIVFYVNH 180
QY 181 NARCIPIPRYLUGTSMKALIQMLEICIGFVVPFLIMGVCFITRTLMKMNKISRLK 240
DB 181 KARCPPIPRYHGTSMKASIQLEICIGFIIIPFLIMAVCFITKTLTKMNKIKKSQPLK 240
QY 241 VLTAVIYEIFYVLPYNYIVKFCRAIDIIYSLITSCNMSKMDIAIQVETSIATLHSCINP 300
DB 241 VLTAVIYEIFYVLPYNYIVKFCQALDIISLITDCMSKMDVAIQETSIATLHSCINP 300
QY 301 ILIYVFMGASFKNYVVKVAKKYSWRQROSYVEEFPDSEGEPTPTSTPSI 350
DB 301 VLIYFMGTSFKNYIMKVAKKYGSWRQROSYVEEFPDSEGEPTPTSTPSI 350

RESULT 3
US-08-153-848-19
/ Sequence 19, Application US/08153848
/ Patent No. 5759804
/ GENERAL INFORMATION:
/ APPLICANT: Godiska, Ronald
/ APPLICANT: Gray, Patrick W.
/ APPLICANT: Schweikart, Vicki L.
/ TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
/ NUMBER OF SEQUENCES: 64
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ ADDRESS: Bicknell,
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible

```

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/153,848
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/977,452
/ FILING DATE: 17-NOV-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5759804and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 31794
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 358 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-153-848-19

Query Match          36.2%; Score 659; DB 1; Length 358;
Best Local Similarity 38.7%; Pred. No. 9.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEQNSTDYEEENENGTVDYSGYELICKEVDREPAVFLPVLTIVFVIGLAGNS 60
DB 1 VCIQDEVTDDYIGDNT--TVDYTLFESLCKKQVRNFKAMFLPMISIIICFVGLGNG 57
QY 61 MVVAIYAAYKKORTKTDVYILNLAVADLLFLTPFWAVNAVHGVGLKIMCKITSAIYT 120
DB 61 LVVLTYYIKRLKMTMDYILNLAVADLLFLTPFWAVNAVHGVGLKIMCKITSAIYT 117
QY 121 LNFVSGMOFLACISIDRYAVATKVPBSQSGVKPCWIIICFCVWMAAILISIPQIVFY 176
DB 121 MSFSGMALLLCISIDRYAVATKVPBSQSGVKPCWIIICFCVWMAAILISIPQIVFY 177
QY 177 TVNDNA-----RCIPIPRYLUGTSMKALIQMLEICIGFVVPFLIMGVCFITRTLMKMP 231
DB 178 DLRSSSEQAMRCSLITTEH---VEARITIQVAMVIGFVPLPILANSFCVLIIRTLQAR 234
QY 232 NIKISRLKVLTVVIVFVITQLPYNYIVKFCRAIDIIYSLITSCNMSKMDIAIQVETSI 291
DB 235 NFERNAIKVILVAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIAVDYVSL 294
QY 292 ALFHSCINPILYVFMGASFKNYVVKVAKKYG-----SW-----RRQROSVREFFPD 337
DB 295 ACVRCVNPFLYAFIVGKVRNDLFKFKDGLCSQOLRQWSSCRHIRRSSMSVB----- 349
QY 338 SEGPTPTSTPS 349
DB 350 ----AETTTTS 357

RESULT 4
US-09-729-843A-19
/ Sequence 19, Application US/09299843A
/ Patent No. 6107475
/ GENERAL INFORMATION:
/ APPLICANT: Godiska, Ronald
/ APPLICANT: Gray, Patrick W.
/ APPLICANT: Schweikart, Vicki L.
/ TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
/ NUMBER OF SEQUENCES: 66
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ ADDRESS: Borun
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago

```

STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/299,843A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/088,337  
FILING DATE: 01-JUN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/153,848  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: JILL E. Uhl  
REGISTRATION NUMBER: 43,213  
REFERENCE/DOCKET NUMBER: 27866/32059B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-299-843A-19

Query Match 36.2%; Score 659; DB 3; Length 358;  
Best Local Similarity 38.7%; Pred. No. 9.7e-49;  
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALBQNSTDYVEENENGTVDYISQVELICIKEDVREPAKFLPVLTIVFVIGLAGNS 60  
DB 1 VCLQDEVTDYIGDNT--TVDTLLESLSCKSDVNFAMFLPIMYSIICFVGLGNG 57

QY 61 MVVAIYAYKKORTKTVYILNLAVALDLFLTPFAVNAVHGVGKIMCKITSAIYT 120  
DB 58 LVVLTIVYFKRLKMTDTYILNLAVALDLFLTPFAVNAVHGVGKIMCKITSAIYT 117

QY 121 LNFVSGMQLACISIDRYVAATKVP-----OSGVKPCWIIICFCVMAAALLSIPOLVFY 176  
DB 118 MSFSGMQLACISIDRYVAIVQAVSAHRARVLLISKSCVGIWTLATVLSIPELIYS 177

QY 177 TVNDNA-----RCIPFPRYLGTSMKALLIOMLEICIGFVVPFLIMGVCFITARTLMKMP 231  
DB 178 DLQSSSEQAMRCSLITEH--VEAFITIOVAQWVIGFVPLAMSFVCIYIIRTLQAR 234

QY 232 NIKISRLKVLTVVIVIVITOLPYNIIVKFCRAIDIIYSITSCNMSKRDIAIOVTEST 291  
DB 235 NFERNAKIKVIAVAVVIVIFQLPYNGVLAQTVANFNITSTCELSKQNLAIYDVYSL 294

QY 292 ALFHSCLNPILYVFMGSAFKYVVKVAKKYG-----SW-----RRQROSVEEFPD 337  
DB 295 ACVRCCVNPFLYAFIIGVFRNDLFKLPKDLGCLSQEOLRWSSCRHIRSSMSVE----- 349

QY 338 SEGPTREPTSES 349  
DB 350 ----AETTTFS 357

RESULT 5  
US-09-088-337B-19  
Sequence 19, Application US/09088337B

Patent No. 6348574  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
Gray, Patrick W.  
Schweikart, Vicki L.  
TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/088,337B  
FILING DATE: 01-JUN-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/153,848  
FILING DATE: 17-NOV-1993  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6348574and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-088-337B-19

Query Match 36.2%; Score 659; DB 4; Length 358;  
Best Local Similarity 38.7%; Pred. No. 9.7e-49;  
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALBQNSTDYVEENENGTVDYISQVELICIKEDVREPAKFLPVLTIVFVIGLAGNS 60  
DB 1 VCLQDEVTDYIGDNT--TVDTLLESLSCKSDVNFAMFLPIMYSIICFVGLGNG 57

QY 61 MVVAIYAYKKORTKTVYILNLAVALDLFLTPFAVNAVHGVGKIMCKITSAIYT 120  
DB 58 LVVLTIVYFKRLKMTDTYILNLAVALDLFLTPFAVNAVHGVGKIMCKITSAIYT 117

QY 121 LNFVSGMQLACISIDRYVAATKVP-----OSGVKPCWIIICFCVMAAALLSIPOLVFY 176  
DB 118 MSFSGMQLACISIDRYVAIVQAVSAHRARVLLISKSCVGIWTLATVLSIPELIYS 177

QY 177 TVNDNA-----RCIPFPRYLGTSMKALLIOMLEICIGFVVPFLIMGVCFITARTLMKMP 231  
DB 178 DLQSSSEQAMRCSLITEH--VEAFITIOVAQWVIGFVPLAMSFVCIYIIRTLQAR 234

QY 232 NIKISRLKVLTVVIVIVITOLPYNIIVKFCRAIDIIYSITSCNMSKRDIAIOVTEST 291  
DB 235 NFERNAKIKVIAVAVVIVIFQLPYNGVLAQTVANFNITSTCELSKQNLAIYDVYSL 294

QY 292 ALFHSCLNPILYVFMGSAFKYVVKVAKKYG-----SW-----RRQROSVEEFPD 337  
DB 295 ACVRCCVNPFLYAFIIGVFRNDLFKLPKDLGCLSQEOLRWSSCRHIRSSMSVE----- 349

QY 338 SEGPTEPTSTPS 349  
Db 350 ----AETTTTFS 357

RESULT 6  
PCT-US93-11153-19

Sequence 19, Application PC/TUS9311153

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.

APPLICANT: Schweikart, Vicki L.

TITLE OF INVENTION: Novel Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/11153

FILING DATE:

CLASSIFICATION:

Prior Application DATA:

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 358 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US93-11153-19

Query Match 36.2%; Score 659; DB 5; Length 358;  
Best Local Similarity 38.7%; Pred. No. 9.7e-49;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALFQNSTDYVYEEENMGTYDSQYELICIKEDREFPAKFLPVLPIVFIAGNS 60  
Db 1 VCLCQDEVTDDYIGDNT--TVDYTFESLCSKRDVANKFAMFLPIWYSIIICVGLLNG 57  
QY 61 MVVAIYAYKKORTKTVYIILNLAVALDLLLFTLPFWAVNAVHGVLGKIMKITSALYT 120  
Db 58 LVVLTYYFRKLTMTDTYILNLAVALDLLLFTLPFWAVNAVHGVLGKIMKITSALYT 117  
QY 121 LNFVSGMOFLACISIDRYVAIVTKVPS---QSGVGKPCWIIICCVMAAILISIPOLVFY 176  
Db 118 MSFSGMULLLCISIDRYVAIVQAVSAHRHRAVLLISKLSGVGIWLTATVLSIBELYS 177  
QY 177 TVVNDNA-----RCIPFPRIGTSMKALIQMLEICIGFVVPFELINGVCYFIARTLMKAP 231  
Db 178 DLGRSSSEQAKRCSLITH---VEAFITIQVAGMVGIFLPLAMSGFCLVLIIRTLQAR 234  
QY 232 NIKISRPLKLLTVIVFIYVITQLPYNIKFCRAIDIIYSLITSCKMSKMDAIOVTESI 291  
Db 233 NIKISRPLKLLTVIVFIYVITQLPYNIKFCRAIDIIYSLITSCKMSKMDAIOVTESI 291

Db 235 NEFNKAIRKIVIIAVVVFIVIPQLPYNQVLAQTVANFNITSSTCELSKQINADVTYSL 294  
QY 292 ALFHSCLNPILVFMGASFKYVMKAKYK-----SW-----RRORSVEPPFD 337  
Db 295 ACVRCVNPFLYAFIGVFRNDLPFLFDLGCLSQEQLRQWSSCRHIRSSMSV----- 349

QY 338 SEGPTEPTSTPS 349  
Db 350 ----AETTTTFS 357

RESULT 7

US-08-153-848-15

Sequence 15, Application US/08153848

Patent No. 5759804

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.

APPLICANT: Schweikart, Vicki L.

TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/153,848

FILING DATE:

CLASSIFICATION: 514

Prior Application DATA:

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 5759804and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 378 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-153-848-15

Query Match 36.2%; Score 659; DB 1; Length 378;  
Best Local Similarity 38.7%; Pred. No. 1e-48;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALFQNSTDYVYEEENMGTYDSQYELICIKEDREFPAKFLPVLPIVFIAGNS 60  
Db 21 VCLCQDEVTDDYIGDNT--TVDYTFESLCSKRDVANKFAMFLPIWYSIIICVGLLNG 77  
QY 61 MVVAIYAYKKORTKTVYIILNLAVALDLLLFTLPFWAVNAVHGVLGKIMKITSALYT 120  
Db 78 LVVLTYYFRKLTMTDTYILNLAVALDLLLFTLPFWAVNAVHGVLGKIMKITSALYT 137  
QY 121 LNFVSGMOFLACISIDRYVAIVTKVPS---QSGVGKPCWIIICCVMAAILISIPOLVFY 176  
Db 121 LNFVSGMOFLACISIDRYVAIVQAVSAHRHRAVLLISKLSGVGIWLTATVLSIBELYS 197

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Oy 177 IYNDNA-----RCIPIFRVLGTSMKALIONMEICIGVAVPELLMGVCYFLTAATLKMMP 23
Db 198 DLORSSSEQARCSLITEH---VEAFITIIQVAKMIGFVLELLMSFCYLLIIRTLQAR 254
Oy 232 NIKISRPFLKLLTVVIVEITVLQFPYNIYVFCRAIDIIYSLTSCNMSKRMADIAIQTESI 292
Db 255 NFERMKAIKVIIAVVVVEIFQLPFGNGVLAQTVANFNITSSTELSKQINIAVDVYSL 314
Oy 292 ALFHSCINAPILYVFMGASFKYVMKVAKKYG-----SW-----RRORQVEEPPFD 337
Db 315 ACVRCCVNPFPYAFYAGVFXRNDLFELFDLOGLCSOEOLRWSSCRHIRRSMSYE----- 369
Oy 338 SEGFTPEPTSTPS 349
Db 370 -----AETTTTTS 377

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RESULT 8
US-09-299-843A-15
Sequence 15 Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: JILL E. UHL
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IS-09-299-843A-15

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Query Match	36.2%;	Score 659;	DB 3;	Length 378;
Best Local Similarity	38.7%;	Pred. No. 1e-48;		
Matches 144;	Conservative 66;	Mismatches 124;	Indels 38;	Gaps 7

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QY 1 MALBQNSTDYVYENEMNGTYDSQYELLCIKEDYREBANKFLPVLPLTYVIGLQNS 60
Db 21 VCLQDEVTDDYIGDNT--TVDYTLFESCSKDDRNFRKFWPLMYSIIICFVTLING 77
QY 61 MVVAIYAYVYKKQRTKTDVYIILNLAVDDLFLPFWANANAHVWGLGKIMKITSALYT 120
Db 78 LVVLTYIYFRKTKMTDVTILNLAVADIFELTLPRMAISAQSNVFGVHFKCLFALYK 137
QY 121 LNFVSGQFLACISIDRYVAVTKPS---QSGVGKPCWIIICFCYMAAIIISIDQVY 176
Db 138 MSFSGMILLICISIDRYVAIVQVSAHHRHRAVLISILSCVGIWIIATVLSIDPELLYS 197
QY 177 TVNDNA-----RCPIEPFRYLGTSKMAILOMEICGFVYPLINGVCCTIARLMP 231
Db 198 DLQSSSEQAMRCSLITEH--VEAFITIQVOMQVGLFVPLPLAMSFCVLYITRLLQAR 254
QY 232 NIKISRLPKVLLTVYIVFIVTQLPYNIIVFRCDAIILYSILSCMSKRMDAIOVTESI 291
Db 255 NFEENKAIKVILAVVVEVIFQLPYGVVLAQVANFNITSTSCELSQNLNAVYVTSL 314
QY 292 ALFHSCLNPLIYFMGASEFNKYMKYAKKYG-----SW-----RRORSVEEPFD 337
Db 315 ACVCACVNPFLYAFIIGVFRNDLFKFLKDLGLCSQOLRQMSCHRIIRSSMSVE----- 369
QY 338 SEGEPTSTES 349
Db 370 ----AETTTTFS 377

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RESULT 9
US-09-251-545-1
: Sequence 1, Application US/09251545
: Patent No. 6153441
: GENERAL INFORMATION:
: APPLICANT: Edward R. Appelbaum
: APPLICANT: Henry M. Sarau
: APPLICANT: John R. White
: TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
: TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN
: TITLE OF INVENTION: AND CCR7 LIGAND AND INTERACTION THEREOF
: FILE REFERENCE: P50753
: CURRENT APPLICATION NUMBER: US/09/251,545
: CURRENT FILING DATE: 1999-02-17
: EARLIER APPLICATION NUMBER: 60/074,883
: EARLIER FILING DATE: 1998-02-17
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 378
: TYPE: PRT
: ORGANISM: Human
: US-09-251-545-1

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[illegible]



[illegible]

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Query Match	36.2%	Score 659;	DB 4;	Length 378;
Similarity	38.7%	Pred. No. 1e-48;		
Best Local				
Matches 144;	Conservative	66;	Mismatches 124;	Indels 38;
			Gaps	7

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QY      1 M A L E K O N S T D Y Y X E N N G M G T D Y S O Y E I C I C K E V R E A K F L E V F L T I J F V G I G L A N S    60
       . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
Db     21 V C L C O B E A V D D Y I G D N T - - - T W D Y T I F E S L G C K R O V R N K A M F L P I M Y S I I C F V G L G N G    77

QY      61 M V A I A Y A Y K Q K T K D V Y I L M A V D L L L E T L E P K A M A N H G V U G I C M K I T S A L Y T    120
       . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
Db     78 L V A T I Y F R E L T W M D Y T Y L M A V D I L F L T L P W A S A K S M V G V H C K I L A I Y K    13
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OY 121 LNFPSGQFPLACISIDBYVAVTKPS-----OSGQGRXCTWIIICCVMAAIIISIPOLVEY 176
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      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 177 TVNDNA-----RCPIEPFRVLIGTSMKALLIQMLEICIGFVVPFLMGVCYITARTLMKM 211
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 198 DLORSSSEQAMRCSLITEH---VEAFITIIQVQWVIGFVLPLAMSPCYVILITLLQAR 254
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 232 NIKISRPKVLTVVVIPIVQLPYNIYVFCRAIDIIYSITSCNNKSRMDIAIQTESI 291
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 235 NFERKKAIVIAVWVPIVQLPYNGVLAQIVANFNITSSCTEISKOLINADVYSL 314
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 292 ALFHSCLNPIIYVMGMSFKQYVWKVAKTIG-----SW-----RRQROSYEEPPD 333
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 315 ACVRCCVNPPIYAFIIGVFRNDLPKLPEDIGCISOEQLROMSSCRHIRKSSMSVE----- 365
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 338 SEGFTPEPTSES 349
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1 RESULT 11
2 PCT-US93-11153-15
3 ; Sequence 15, Application PC/US9311153
4 ; GENERAL INFORMATION:
5 ; APPLICANT: Godiska, Ronald W.
6 ; APPLICANT: Gray, Patrick W.
7 ; APPLICANT: Schweikart, Vicki L.
8 ; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
9 ; NUMBER OF SEQUENCES: 64
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
12 ; ADDRESSEE: Bicknell
13 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
14 ; CITY: Chicago
15 ; STATE: Illinois
16 ; COUNTRY: USA
17 ; ZIP: 60606
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: PCT/US93/11153
25 ; FILING DATE:
26 ; CLASSIFICATION:
27 ; PRIOR APPLICATION DATA:
28 ; APPLICATION NUMBER: US 07/977,452
29 ; FILING DATE: 17-NOV-1992
30 ; ATTORNEY/AGENT INFORMATION:
31 ; NAME: Noland, Greta E.
32 ; REGISTRATION NUMBER: 35,302
33 ; REFERENCE/DOCKET NUMBER: 31794
34 ; TELECOMMUNICATION INFORMATION:
35 ; TELEPHONE: (312) 474-6300
36 ; TELEFAX: (312) 474-0448
37 ; TELEX: 25-3856
38 ; INFORMATION FOR SEQ ID NO: 15:
39 ; SEQUENCE CHARACTERISTICS:
40 ; LENGTH: 378 amino acids
41 ; TYPE: amino acid
42 ; TOPOLOGY: linear
43 ; MOLECULE TYPE: protein
44 ; PCT-US93-11153-15

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Query Match	36.2%; Score 659; DB 5; Length 378;
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QY 1 M A L E D N O S T D Y Y E E N E N M G T Y D X O Y E L C I K E D V R E P A K F L P V E L T I V F I G L A G N S 60  
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Db 21 VCLCODEVTDDYIGDNT---TVDTYTLFESLCSKKDVRNFKAMFLPIWXSIIICFVGLLNG 77  
Qy 61 MVAIAYAYKKORTKTDVYIINLAVADLLFLTPFAVAVNAHGVGLKIMCKITSLYLT 120  
Db 78 LVVLYTYIFKRLKMTDYLNLAVADLLFLTLTPFAVAVNAHGVGLKIMCKITSLYLT 137  
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Qy 292 ALFHSCLNPILYVFMGASFKNYVMKAKKYG-----SW-----RROQSYEEFPFD 337  
Db 315 ACVRCVNPFLYAFIGVFRNDLFLFLFDJGCLSGEQLRQKSSCRHRRSSMSVE----- 369  
Qy 338 SEGPTPEPTSTFS 349  
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RESULT 12  
US-08-153-848-7  
Sequence 7, Application US/08153848  
Patent No. 5759804  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schweikart, Vicki L.  
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/153,848  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5759804and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ. ID NO.: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 410 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-153-848-7

Query Match 36.2%; Score 659; DB 1; Length 410;  
Best Local Similarity 38.7%; Pred. No. 1.1e-48;  
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;  
Db 1 MLEQONOSTDYIYENENNGYDYSQYELICIKEDREFAKVFLPVFLTIVFVIGLAGNS 60  
Qy 53 VCLCODEVTDDYIGDNT---TVDTYTLFESLCSKKDVRNFKAMFLPIWXSIIICFVGLLNG 109  
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Qy 287 NFERKAIKVIIVAVVVFIVQLPYNGVLAQTVANFNITSTCELSKQINIAVDVYSL 346  
Db 292 ALFHSCLNPILYVFMGASFKNYVMKAKKYG-----SW-----RROQSYEEFPFD 337  
Qy 347 ACVRCVNPFLYAFIGVFRNDLFLFLFDJGCLSGEQLRQKSSCRHRRSSMSVE----- 401  
Db 402 ---AETTTTFS 409

RESULT 13  
US-09-299-843A-7  
Sequence 7, Application US/09299843A  
Patent No. 6107475  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schweikart, Vicki L.  
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/299,843A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/088,337  
FILING DATE: 01-JUN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: J111 E. Dhl  
REGISTRATION NUMBER: 43,213  
REFERENCE/DOCKET NUMBER: 27866/32059B

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 410 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-299-843A-7

Query Match 36.2%; Score 659; DB 3; Length 410;  
Best Local Similarity 38.7%; Pred. No. 1,1e-48;  
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

1 MALEQNSTDYEEENENMGTYDSOYELICIKEDYREFAKVPFLPVLTVVIGLAGNS 60  
53 VCLCODEVTDDYIGDNT---TVDYTLFESLCSKQDVNRKAMFLPIMYSIICFVGLGNG 109

61 MVVAIYAYKKQRTKTDVYIINLAVADLLFLPFAVNAVHGVGLKIMCKITSALT 120  
110 LVLLTYIFRKLTMTDYLNLAVADLLFLPFAVNAVHGVGLKIMCKITSALT 169

121 INFVSGMQLACISIDRYAVATKVP-----QSGVGKPCWIIICFVMAAILSLPOLVFY 176  
170 MSFFSGMLLLCISIDRYAVAIQAVSAHRARVLLISKLSCVGIWILATVLSIPELLYS 229

177 TVNDNA-----RCIPFPRLYIGTSKALLIOMLEICIGFVVPFLMGVCYFTRTLMKMP 231  
230 DLQRSSSEQAMRCSLITEH---VEAFITIQVAVGVGLFVPLAMSFVYLIIRTLQAR 286

232 NIKSRPLKVLTVVIVFYVLPYNIKFCRAIDIIISLITSCNMSKMDIAIQVETSI 291  
287 NFERKAKIKVIAVVVVFYFQLPYNGVLAQTVANFNITSSCTELSKQNLAYDVYTSL 346

292 ALFHSCLNPLIYVFMGASFKNYVMKAKKYG-----SW-----RROQSVSEPPFP 337  
347 ACVRCVNPFLVAFIGVFRNDLFKLFKDLGCLSOEQLRQWSSCRHIRSSMSVE----- 401

338 SEGPTPTSTPS 349  
402 ----AETTTTFS 409

RESULT 14  
US-09-088-337B-7  
Sequence 7, Application US/09088337B  
Patent No. 6348574  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
Gray, Patrick W.  
Schweikart, Vicki L.  
TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/088,337B  
FILING DATE: 01-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/153,848  
FILING DATE: 17-NOV-1993  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6348574e1, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 410 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-088-337B-7

Query Match 36.2%; Score 659; DB 4; Length 410;  
Best Local Similarity 38.7%; Pred. No. 1,1e-48;  
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

1 MALEQNSTDYEEENENMGTYDSOYELICIKEDYREFAKVPFLPVLTVVIGLAGNS 60  
53 VCLCODEVTDDYIGDNT---TVDYTLFESLCSKQDVNRKAMFLPIMYSIICFVGLGNG 109

61 MVVAIYAYKKQRTKTDVYIINLAVADLLFLPFAVNAVHGVGLKIMCKITSALT 120  
110 LVLLTYIFRKLTMTDYLNLAVADLLFLPFAVNAVHGVGLKIMCKITSALT 169

121 INFVSGMQLACISIDRYAVATKVP-----QSGVGKPCWIIICFVMAAILSLPOLVFY 176  
170 MSFFSGMLLLCISIDRYAVAIQAVSAHRARVLLISKLSCVGIWILATVLSIPELLYS 229

177 TVNDNA-----RCIPFPRLYIGTSKALLIOMLEICIGFVVPFLMGVCYFTRTLMKMP 231  
230 DLQRSSSEQAMRCSLITEH---VEAFITIQVAVGVGLFVPLAMSFVYLIIRTLQAR 286

232 NIKSRPLKVLTVVIVFYVLPYNIKFCRAIDIIISLITSCNMSKMDIAIQVETSI 291  
287 NFERKAKIKVIAVVVVFYFQLPYNGVLAQTVANFNITSSCTELSKQNLAYDVYTSL 346

292 ALFHSCLNPLIYVFMGASFKNYVMKAKKYG-----SW-----RROQSVSEPPFP 337  
347 ACVRCVNPFLVAFIGVFRNDLFKLFKDLGCLSOEQLRQWSSCRHIRSSMSVE----- 401

338 SEGPTPTSTPS 349  
402 ----AETTTTFS 409

RESULT 15  
PCT-US93-11153-7  
Sequence 7, Application PC/TUS9311153  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
Gray, Patrick W.  
Schweikart, Vicki L.  
TITLE OF INVENTION: Novel Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Bicknell  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11153-7
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Query Match 36.2% Score 659; DB 5; Length 410;

Best Local Similarity 38.7% Pred. No. 1,1e-48;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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QY 1 MALEQNSTDYVYBENMNGTYDYSQYELICIKEDVREFAKVPFLVPLTIVFVIGLAGNS 60
DB 53 VCLQDEVTDDYIGDNT---TVDYTLFESLCSKDVNFAMFLPIVYSIICFVGLGNG 109
QY 61 MVAIVAYKKRKTKTDVYIINLAVALDLLLFTLPFAVAVNAVHGVLGKIMCTISALYT 120
DB 110 LVVLTYYFKRLKMTDYLINLAVALDILFLPLFMAVSAASWFGVHFCCLIFAIXK 169
QY 121 LNFVSGMPLACISIDRYVAATKVPSS---QSGVKPCWIIICFVMAAAILLSIPOLVEY 176
DB 170 MSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCGIMTLAVLSIPELIYS 229
QY 177 TVADNA-----RCIPRPYLGTSKMLIQMLEICIGFVVPFLIMGVCFITARTLMKP 231
DB 230 DLQSSSEQAMRCSLITEN---VEAFITIQAVIGFVPLPLAMSFVYLIIRTLQAR 286
QY 232 NIKISRLKVLTVVIVFYITOLPYNIIVKFCRAIDIIYSITSCNSKMDIAIQTESI 291
DB 287 NFERNKAIKVIIVAVVVFIFQLPYNGVLAQIVANFNITSSITCSELKQNLINAYDVYSL 346
QY 292 ALFHSCLNPLILYFMGASFKNYVMKAKKYG-----SW-----RRQROSEVEFPFD 337
DB 347 ACVRCCVNPFLYAFIVGKFRNDLFLKFLQGLCSQGLRQMSSCRHRRSSMSVE----- 401
QY 338 SEGPTPTSTPS 349
DB 402 ----AETTTTFS 409
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RESULT 16  
US-09-299-843A-66  
Sequence 66, Application US/09299843A  
Patent No. 6107475  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schwellkart, Vicki L.  
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive

```
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-66
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Query Match 35.7% Score 650; DB 3; Length 378;

Best Local Similarity 38.3% Pred. No. 6e-48;

Matches 140; Conservative 67; Mismatches 125; Indels 34; Gaps 8;

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QY 5 QNSTDYVYBENMNGTYDYSQYELICIKEDVREFAKVPFLVPLTIVFVIGLAGNSMVA 64
DB 25 QDEVTDDYIGDNT---TVDYTLFESVCFKDVNFAMFLPIVYSIICFVGLGNGVIL 81
QY 65 IYAYKKRKTKTDVYIINLAVALDLLLFTLPFAVAVNAVHGVLGKIMCTISALYTIN 124
DB 82 TYIFKRLKMTDYLINLAVALDILFLPLFMAVSAASWFGVHFCCLIFAIXK 141
QY 125 SGMQPLACISIDRYVAATKVPSSQSG-----VSGKPCWIIICFVMAAAILLSIPOLVEY 177
DB 142 SGMMLLCISIDRYVAIVQAVSAHRHARVLLISK---LSCVGIMTLAVLSIPELIYS 198
QY 178 VNDA-----RCIPRPYLGTSKMLIQMLEICIGFVVPFLIMGVCFITARTLMKP 230
DB 199 LQKSGEDTLRC-----SLVSAQVEALITIQAVMGFVPLPLAMSFVYLIIRTLQAR 253
QY 231 NIKISRLKVLTVVIVFYITOLPYNIIVKFCRAIDIIYSITSCNSKMDIAIQTES 290
DB 254 NFERNKAIKVIIVAVVVFIFQLPYNGVLAQIVANFNITSSITCSELKQNLINAYDVYS 313
QY 291 IALFHSCLNPLILYFMGASFKNYVMKAKKYGSROR-----QSEVEFPDSEGPT 343
DB 314 LASVRCCVNPFLYAFIVGKFRSDFLKFLQGLCSQGLRQMSSCRHRRSSMSVE---AE 371
QY 344 PTSTPS 349
DB 372 TTTTFS 377
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RESULT 17  
US-09-088-337B-66

Sequence 66, Application US/09088337B  
Patent No. 6348574  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
Gray, Patrick W.  
Schweikart, Vicki L.  
TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/088,337B  
FILING DATE: 01-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/153,848  
FILING DATE: 17-NOV-1993  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6348574and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 378 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 66:  
US-09-088-337B-66  
Query Match 35.7%; Score 650; DB 4; Length 378;  
Best Local Similarity 38.3%; Pred. No. 6e-48;  
Matches 140; Conservative 67; Mismatches 125; Indels 34; Gaps 8;

Db 314 LASVRCVNPFLYAFIVGFRSDLFKLFKDLGCLISQERLRHWSGRHVNNASVSNE--AE 371  
QY 344 PTSTFS 349  
Db 372 TTTTFS 377  
RESULT 18  
US-08-383-750-2  
Sequence 2, Application US/08383750  
Patent No. 5744301  
GENERAL INFORMATION:  
APPLICANT: Birkenbach, Mark  
Kieff, Elliot  
TITLE OF INVENTION: Epstein Barr Virus Induced Genes  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, N.W.,  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/383,750  
FILING DATE: Herewith  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Fox, Samuel L.  
REGISTRATION NUMBER: 30,353  
REFERENCE/DOCKET NUMBER: 0627.3300001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 378 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-383-750-2  
Query Match 35.3%; Score 643; DB 1; Length 378;  
Best Local Similarity 39.0%; Pred. No. 2.4e-47;  
Matches 145; Conservative 62; Mismatches 127; Indels 38; Gaps 8;

Db 315 ACVRCVNPFLAIFGVKFRNDIFKLFKDLGCLSQEQLRQMSCHIRRSSMSVE----- 369  
QY 338 SEGPTSTPS 349  
Db 370 ---AETTTTFS 377

RESULT 19  
US-08-383-751A-2  
; Sequence 2, Application US/08383751A  
; Patent No. 5753516  
; GENERAL INFORMATION:  
; APPLICANT: Heagy, Wytra E.  
; APPLICANT: Findberg, Robert W.  
; TITLE OF INVENTION: Identification and Uses of Opioid  
; TITLE OF INVENTION: Receptors  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: US  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/383,751A  
; FILING DATE: 03-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: DFCI:001/WIM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; TELEX: 79-0924  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 378 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-383-751A-2

Query Match 35.3%; Score 643; DB 1; Length 378;  
Best Local Similarity 39.0%; Pred. No. 2.4e-47;  
Matches 145; Conservative 62; Mismatches 127; Indels 38; Gaps 8;  
QY 1 MAEONOSTDYEEENMGTYDYSEYELICIKEDVEFAKFLPVLTVFVIGLAGNS 60  
Db 21 VCLQDEVTDDYIDNT---TVDYTLFESLCSKDDVNFAMFLPIMYSIICVGLLNG 77  
QY 61 MVAIYAYKKQRTKTDVYILNLAVALDLLLFTLPFAVNAVHGWLGIKMKITSALYT 120  
Db 78 LVVLTYIYFKRLKMTDTYILNLAVALDILFLTLFPWASAAKSWGVGFCKLIFAIK 137  
QY 121 LNVFSGMQLACISIDRYVAVTKVPSQSGVKRCWII--CFQVMA--ALLSIPLQVY 176  
Db 138 MSFSGMLLLCLISIDRYVAIVQAVSAHRRARVLLISKUSGSAIILTVLSIPELYS 197  
QY 177 TVNDNA-----RCIPFPRYLGTSKALIQMLEICIGFVVPFLIMGVCFYFARTLMKMP 231  
Db 198 DLQSSSEQMRGSLITEH---VEAFITIOVAGMVGFLVPLAMSFCYIVIRITLQAR 254  
QY 232 NIKISPLKALLTVVIVFIYTOPLPYNIVKFCRAIDIIYSILTSNNMSKMDIAIQVTEST 291  
Db 255 NFRNRKAIKIVIAVVFYFQLPYNGVVLQAVANFNITSSCTELSKQNLNADYVYSL 314  
QY 292 ALFHSCLNPLIYVFMGASFRQYMKAKKYG-----SW-----RRQOSVEBPPD 337

Db 315 ACVRCVNPFLAIFGVKFRNDIFKLFKDLGCLSQEQLRQMSCHIRRSSMSVE----- 369  
QY 338 SEGPTSTPS 349  
Db 370 ---AETTTTFS 377

RESULT 20  
US-08-352-678-2  
; Sequence 2, Application US/08352678  
; Patent No. 6043351  
; GENERAL INFORMATION:  
; APPLICANT: Birkenbach, Mark  
; APPLICANT: Kieff, Elliott  
; TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/352,678  
; FILING DATE: 30-NOV-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/980,518  
; FILING DATE: 25-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gates, Edward R.  
; REGISTRATION NUMBER: 31,616  
; REFERENCE/DOCKET NUMBER: B0801/7044  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-720-3500  
; TELEFAX: 617-720-2441  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 378 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-352-678-2

Query Match 35.3%; Score 643; DB 3; Length 378;  
Best Local Similarity 39.0%; Pred. No. 2.4e-47;  
Matches 145; Conservative 62; Mismatches 127; Indels 38; Gaps 8;  
QY 1 MALBONOSTDYEEENMGTYDYSEYELICIKEDVEFAKFLPVLTVFVIGLAGNS 60  
Db 21 VCLQDEVTDDYIDNT---TVDYTLFESLCSKDDVNFAMFLPIMYSIICVGLLNG 77  
QY 61 MVAIYAYKKQRTKTDVYILNLAVALDLLLFTLPFAVNAVHGWLGIKMKITSALYT 120  
Db 78 LVVLTYIYFKRLKMTDTYILNLAVALDILFLTLFPWASAAKSWGVGFCKLIFAIK 137  
QY 121 LNVFSGMQLACISIDRYVAVTKVPSQSGVKRCWII--CFQVMA--ALLSIPLQVY 176  
Db 138 MSFSGMLLLCLISIDRYVAIVQAVSAHRRARVLLISKUSGSAIILTVLSIPELYS 197  
QY 177 TVNDNA-----RCIPFPRYLGTSKALIQMLEICIGFVVPFLIMGVCFYFARTLMKMP 231  
Db 198 DLQSSSEQMRGSLITEH---VEAFITIOVAGMVGFLVPLAMSFCYIVIRITLQAR 254  
QY 232 NIKISPLKALLTVVIVFIYTOPLPYNIVKFCRAIDIIYSILTSNNMSKMDIAIQVTEST 291

Db 255 NPERNKAIKVIIVAVVVEIVFQLPYNGVLAQTVANFNITSTCELSKQINIAVDVYSL 314  
QY 292 ALFHSCINPLIYVFMGSAFKYVWKVAKKG-----SW-----RRQSVSEFPD 337  
Db 315 ACVRCVNPFLYAFGVKFRNDIFKLDGCLSGEQLRQWSSCRHTRSSMSV----- 369  
QY 338 SEGPTEPTSTFS 349  
Db 370 ----AETTTTFS 377

RESULT 21  
US-09-045-583-49

; Sequence 49, Application US/09045583  
; Patent No. 6287805  
; GENERAL INFORMATION:  
; APPLICANT: Graham, Gerard J. et al.  
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/045.583  
; FILING DATE: 20-MAR-98  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: MNI-044  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 378 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; US-09-045-583-49

Query Match 35.3%; Score 643; DB 4; Length 378;

Best Local Similarity 39.0%; Pred. No. 2.4e-47;  
Matches 145; Conservative 62; Mismatches 127; Indels 38; Gaps 8;

QY 1 MALBQNSTDYEEENMNGTVYSQYELICIKEDVREPAKFLPVFLTIYVYIGLAGNS 60  
Db 21 VCLQDEVTDDYIDNT--TVDYTLFESLCSKQDVNFKMFLEPIMYSIICVGLGNG 77  
QY 61 MVAIAIYAYYKQRTKTDVYIILNLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALT 120  
Db 78 LVVLTYYFRKLTMTDYLNLAVADILFLTLFPWAVSAKSWVGVHFCGLFAIYK 137  
QY 121 LNFVSGMFLACISIDRYAVAVTKVPSQSGVKRCWII--CFCVWMA--AIIISIPQLVFY 176  
Db 138 MEFPSGMLLLCISIDRYAVAIQVSAHHRARVLLISLSCVSGAIIATVLSIPELIYS 197  
QY 177 TVNDNA-----RCIPIFFPYLGTSMKALIQMLEICIGVYVPFLINGVCYFITARLTMCP 231  
Db 198 DLRSSSEQAMRCSLITEH---VEAFITIQVQWVIGFLVPLLAWSFCYLVITIRLLQAR 254

QY 232 NIKISRPKVLTVVIVEIVYQLPYNIYVFCRAIDIIYSLITSCNMSKRDIAIQWESI 291  
Db 255 NPERNKAIKVIIVAVVVEIVFQLPYNGVLAQTVANFNITSTCELSKQINIAVDVYSL 314  
QY 292 ALFHSCINPLIYVFMGSAFKYVWKVAKKG-----SW-----RRQSVSEFPD 337  
Db 315 ACVRCVNPFLYAFGVKFRNDIFKLDGCLSGEQLRQWSSCRHTRSSMSV----- 369  
QY 338 SEGPTEPTSTFS 349  
Db 370 ----AETTTTFS 377

RESULT 22  
US-09-534-185-49

; Sequence 49, Application US/09534185  
; Patent No. 6403767  
; GENERAL INFORMATION:  
; APPLICANT: Graham, Gerard J. et al.  
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
; Heptahelical Receptor Superfamily and Uses  
; Therefor  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/534.185  
; FILING DATE: 24-Mar-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/045.583  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: MNI-044  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 378 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
; US-09-534-185-49

Query Match 35.3%; Score 643; DB 4; Length 378;

Best Local Similarity 39.0%; Pred. No. 2.4e-47;  
Matches 145; Conservative 62; Mismatches 127; Indels 38; Gaps 8;

QY 1 MALBQNSTDYEEENMNGTVYSQYELICIKEDVREPAKFLPVFLTIYVYIGLAGNS 60  
Db 21 VCLQDEVTDDYIDNT--TVDYTLFESLCSKQDVNFKMFLEPIMYSIICVGLGNG 77  
QY 61 MVAIAIYAYYKQRTKTDVYIILNLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALT 120  
Db 78 LVVLTYYFRKLTMTDYLNLAVADILFLTLFPWAVSAKSWVGVHFCGLFAIYK 137  
QY 121 LNFVSGMFLACISIDRYAVAVTKVPSQSGVKRCWII--CFCVWMA--AIIISIPQLVFY 176

Db 138 MSFSGMILLICISIDRYVAIAVAVSARHRAVLLISKLSCVSAIATLAVLSIPELLYS 197  
Qy 177 TVNDA-----RCIPFPRYLGTSKALIQMLEICIGVVPFLMGVCYFTATLTKMP 231  
Db 198 DLORSSSSOAMKCSLITEH---VEAFITIOVAQWIGFVPLLMSPFCYLIITFTLLQAR 254  
Qy 232 NIKISRLKVLTVVIVFVITQLPYNIYVFCRAIDIIYSLITSQMSKMDIAIQVTESEI 291  
Db 255 NFERKAKVIAVAVVIVFVITQLPYNIYVFCRAIDIIYSLITSQMSKMDIAIQVTESEI 314  
Qy 292 ALFHSCLNPLIYVEMGASFKYVVKVAKKYG-----SW-----RRORSVEEPPFD 337  
Db 315 ACVRCVNPFLVAFVIGVFRNDIFKLPDLGCLSQEQLRQMSCRHRRSSMSVE----- 369  
Qy 338 SEGTEPTSTFS 349  
Db 370 ---AETTTTFS 377

## RESULT 23

PCT-US93-09636-2  
Sequence 2, Application PC/TUS9309636  
GENERAL INFORMATION:  
APPLICANT: Birkendach, Mark  
APPLICANT: Kieff, Elliot  
TITLE OF INVENTION: Epstein Barr Virus Induced Genes  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/09636  
FILING DATE: herewith  
CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 378 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-09636-2

Query Match 35.3%; Score 643; DB 5; Length 378;  
Best Local Similarity 39.0%; Pred. No. 2,4e-47;  
Matches 145; Conservative 62; Mismatches 127; Indels 38; Gaps 8;

Qy 1 MALEONOSTYVYENENGTVDYDYOYELICIKEDVREPAKVFPLVPLTVFVIGLAGNS 60  
Db 21 VCLQDEVTIDYIDNT---IVDTTLFESLCKSDVKNRPMFLPMYSITICFVGLGNG 77  
Qy 61 MVAIVAYYKORTKTDVYILNLAVADLLFTLPFWAVNAVHGVVLGIMCKITSALYAT 120  
Db 78 LVVLTLYIFPKLMTDTYILNLAVADLLFTLPFWAVNAVHGVVLGIMCKITSALYAT 137  
Qy 121 LNFVSGQFLACISIDRYVAVTKVPSQGVKPCWIT--CFCWMA--ALLSIPOLVEY 176  
Db 138 MSFSGMILLICISIDRYVAIAVAVSARHRAVLLISKLSCVSAIATLAVLSIPELLYS 197  
Qy 177 TVNDA-----RCIPFPRYLGTSKALIQMLEICIGVVPFLMGVCYFTATLTKMP 231  
Db 198 DLORSSSSOAMKCSLITEH---VEAFITIOVAQWIGFVPLLMSPFCYLIITFTLLQAR 254

Qy 232 NIKISRLKVLTVVIVFVITQLPYNIYVFCRAIDIIYSLITSQMSKMDIAIQVTESEI 291  
Db 255 NFERKAKVIAVAVVIVFVITQLPYNIYVFCRAIDIIYSLITSQMSKMDIAIQVTESEI 314  
Qy 292 ALFHSCLNPLIYVEMGASFKYVVKVAKKYG-----SW-----RRORSVEEPPFD 337  
Db 315 ACVRCVNPFLVAFVIGVFRNDIFKLPDLGCLSQEQLRQMSCRHRRSSMSVE----- 369  
Qy 338 SEGTEPTSTFS 349  
Db 370 ---AETTTTFS 377

## RESULT 24

US-09-266-464-2  
Sequence 2, Application US/09266464  
GENERAL INFORMATION:  
APPLICANT: Andrew, David P.  
APPLICANT: Zabel, Brian A.  
APPLICANT: Ponath, Paul D.  
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF  
FILE REFERENCE: LK98-16  
CURRENT FILING DATE: 1999-03-11  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 357  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-266-464-2

Query Match 35.0%; Score 637; DB 4; Length 357;  
Best Local Similarity 36.5%; Pred. No. 7,2e-47;  
Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps 4;

Qy 10 DYVEE-NEMNGTYDYSQYELICIKEDVREPAKVFPLVPLTVFVIGLAGNSMVAIYAY 68  
Db 4 DYGESESTSMEDYVNFNTDPCENKVRQASHPLPPLYLVFVIGLAGNSLVILYIY 63  
Qy 69 YKORTKTDVYILNLAVADLLFTLPFWAVNAVHGVVLGIMCKITSALYATLNFVSGMQ 128  
Db 64 CRYVMTMDMFLNLAIADLLFTVLPFWALTAADQWQFQFMCKVNVSNYKKNFSCVL 123  
Qy 123 FLACISIDRYVAVTKVPSQGVKPCW-----IICFCVMAALLSIPOLVFTVN 179  
Db 124 LTMCSVDYRIAIAQ-----AMRAHTWREKRLVSKWCFIIVLAALCIPILYSQIK 178  
Qy 180 DN---ARCIPIPRYLGTSKALIQMLEICIGVVPFLMGVCYFTATLTKMPNIKIS 236  
Db 179 EESGIALCTMYVPSDESKLSAVITLKVILGFPLFVMAACCTIIITHILIOAKKSKH 238  
Qy 237 RPLKVLTVVIVFVITQLPYNIYVFCRAIDIIYSLITSQMSKMDIAIQVTESEI 296  
Db 239 KALKVTITVLFVLSQPPYNCILLVOTIDAVAMFISNCAVSTNDICFVOTIARFHS 298  
Qy 297 CLNPLIYVEMGASFKYVVKVAKKYG 322  
Db 299 CLNPLIYVEMGASFKYVVKVAKKYG 324

## RESULT 25

US-08-153-848-24  
Sequence 24, Application US/08153848  
Patent No. 5759804  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schweikart, Vicki L.  
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 64



CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Bichnell  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/153,848  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5759804and, Greeta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-153-848-24

Query Match 34.9%; Score 635.5; DB 1; Length 359;  
Best Local Similarity 37.9%; Pred. No. 9.7e-47;  
Matches 140; Conservative 68; Mismatches 122; Indels 39; Gaps 10;

QY 5 QNOSTDYEEENMGVYDYSQYELICKEDVREFAKVFLEPFLITVFVIGLAGNSMVA 64  
DB 5 QDEVTSIDYIGENT--TVDYTLYESVCFKQVRFKAMFLPMYSVICFVGLGNGVL 61  
QY 65 IYAYYKQRTDVIYILNLAVALDILLFTLPFWANAVHGVLAGIKCKTSAIYTLNFV 124  
DB 62 TYIYFKRLKMTDVIYILNLAVALDILLFTLPFWANAVHGVLAGIKCKTSAIYTLNFV 121  
QY 125 SGMQFLACISIDRYVAIVTVPSQSG-----VGKPCWICFCVMAAILISIPQLVFT 177  
DB 122 SGMILLICISIDRYVAIVTVPSQSG-----LSCVGIWMLALFLSIPQLVFT 178  
QY 178 VDNA-----RCIPFPRLYIGTSMKAL--IOMLEICIGFVVPFLIMGVCFITARTLMK 230  
DB 179 LQKNSGEBTLRC-----SLVSAQVEALITIQVAVFGLVPMMLMSFCYLIITRLLOA 233  
QY 231 PNKISRPLKVLTVIVIVITOLPYNIVKFCRAI---DIYSLITSCNMSKMDIAIOV 287  
DB 234 RNFERNKAIKVIIVAVVIVIFQLPYNGVLAQTVANFNITNS--SCCETSQKQNIAYDV 291  
QY 288 TESIALFHSCLNPIIYVFMGASFKNYVMKAKYGSWROR-----QSVIEFPFDESG 340  
DB 292 TYSLASVACNPFYAIIVGKFRSDLFKLDGCLSGQERLRHMSCHVRNASSVSGME 350  
QY 341 PTEPTSTPS 349  
DB 351 AETTTTFS 358  
RESULT 26  
US-09-299-843A-24  
Sequence 24, Application US/09299843A  
Patent No. 6107475

GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schweikart, Vicki L.  
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/299,843A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/088,337  
FILING DATE: 01-JUN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/153,848  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Jill E. Uhl  
REGISTRATION NUMBER: 43,213  
REFERENCE/DOCKET NUMBER: 27866/320598  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX:  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-299-843A-24

Query Match 34.9%; Score 635.5; DB 3; Length 359;  
Best Local Similarity 37.9%; Pred. No. 9.7e-47;  
Matches 140; Conservative 68; Mismatches 122; Indels 39; Gaps 10;

QY 5 QNOSTDYEEENMGVYDYSQYELICKEDVREFAKVFLEPFLITVFVIGLAGNSMVA 64  
DB 5 QDEVTSIDYIGENT--TVDYTLYESVCFKQVRFKAMFLPMYSVICFVGLGNGVL 61  
QY 65 IYAYYKQRTDVIYILNLAVALDILLFTLPFWANAVHGVLAGIKCKTSAIYTLNFV 124  
DB 62 TYIYFKRLKMTDVIYILNLAVALDILLFTLPFWANAVHGVLAGIKCKTSAIYTLNFV 121  
QY 125 SGMQFLACISIDRYVAIVTVPSQSG-----VGKPCWICFCVMAAILISIPQLVFT 177  
DB 122 SGMILLICISIDRYVAIVTVPSQSG-----LSCVGIWMLALFLSIPQLVFT 178  
QY 178 VDNA-----RCIPFPRLYIGTSMKAL--IOMLEICIGFVVPFLIMGVCFITARTLMK 230  
DB 179 LQKNSGEBTLRC-----SLVSAQVEALITIQVAVFGLVPMMLMSFCYLIITRLLOA 233  
QY 231 PNKISRPLKVLTVIVIVITOLPYNIVKFCRAI---DIYSLITSCNMSKMDIAIOV 287  
DB 234 RNFERNKAIKVIIVAVVIVIFQLPYNGVLAQTVANFNITNS--SCCETSQKQNIAYDV 291  
QY 288 TESIALFHSCLNPIIYVFMGASFKNYVMKAKYGSWROR-----QSVIEFPFDESG 340

Db 292 TYSLASVRCVNPFLYAFVGVKFRSDLFKLPKDLGCLSGERLRHMSGCRHRNMSVSNME- 350  
Qy 341 PTEPTSTFS 349  
Db 351 -AETTTTFS 358

## RESULT 27

US-09-088-337B-24  
; Sequence 24, Application US/09088337B  
; Patent No. 6348574  
; GENERAL INFORMATION:  
; APPLICANT: Godiska, Ronald  
; Gray, Patrick W.  
; Schweikart, Vicki L.  
; TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/088,337B  
; FILING DATE: 01-Jun-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/153,848  
; FILING DATE: 17-NOV-1993  
; APPLICATION NUMBER: US 07/977,452  
; FILING DATE: 17-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6348574and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31794  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-09-088-337B-24

Query Match 34.9%; Score 635.5; DB 4; Length 359;  
Best Local Similarity 37.9%; Pred. No. 9.7e-47;  
Matches 140; Conservative 68; Mismatches 122; Indels 39; Gaps 10;  
Qy 5 QNOSTDYVEENMGTYDYSOYELCIKEDVREPAKVFLLPVFLTIYFVIGLAGNSMVVA 64  
Db 5 QDEVTSDYIGENT--TYDYTLYESVCFKQDVRFKAMFLPLMVSVCVGLGNGVIL 61  
Qy 65 IYAYYKQRTKTDVYILNLAVALDLLFTLPFWAVNAVHGVNLGKIMCKITSALYTLNFV 124  
Db 62 TYIYFKRLKTMDDTYLNLAVADILFLILPFWAYSEAKSWIFGVYLCGIGFYKLSFF 121  
Qy 125 SGMQFLACISIDRYAVAVTKVPSQSG-----VGKPCMIITFCVMMALILSTIQLVFYT 177  
Db 122 SGMILLICISIDRYAVAVTKVPSQSG-----LSCVGIWMLALFLSTIPELLVSG 178

Qy 178 VNDNA-----RCPIFPRLYLGTSKMAI--IQMLEICIGFVVPFLIMGVCFITARTLMKM 230  
Db 179 LQNSGEDTLRC-----SLVSAQVEALITITQVAVQVFPFLVPLMAMSPCYLIIIRTLHOA 233  
Qy 231 PNKISRLPLKLLTVYIVFVITQLPYNYVFCRAI---DIYSLITSQMSKRMADIAOV 287  
Db 234 RNFERKAKIKVIAVAVVFIQPLPYNGVLAQTVANFNITNS--SCETSKQNLAIYDV 291  
Qy 288 TESIALFHSCLNPILYVFGASFKYVMKAKKYSWROR-----QSYEEPFPDSEG 340  
Db 292 TYSLASVRCVNPFLYAFVGVKFRSDLFKLPKDLGCLSGERLRHMSGCRHRNMSVSNME- 350  
Qy 341 PTEPTSTFS 349  
Db 351 -AETTTTFS 358

## RESULT 28

PCT-US93-1153-24  
; Sequence 24, Application PC/TUS9311153  
; GENERAL INFORMATION:  
; APPLICANT: Godiska, Ronald  
; Gray, Patrick W.  
; APPLICANT: Schweikart, Vicki L.  
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; Bicknell  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/11153  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/977,452  
; FILING DATE: 17-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Noland, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31794  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US93-1153-24

Query Match 34.9%; Score 635.5; DB 5; Length 359;  
Best Local Similarity 37.9%; Pred. No. 9.7e-47;  
Matches 140; Conservative 68; Mismatches 122; Indels 39; Gaps 10;  
Qy 5 QNOSTDYVEENMGTYDYSOYELCIKEDVREPAKVFLLPVFLTIYFVIGLAGNSMVVA 64  
Db 5 QDEVTSDYIGENT--TYDYTLYESVCFKQDVRFKAMFLPLMVSVCVGLGNGVIL 61  
Qy 65 IYAYYKQRTKTDVYILNLAVALDLLFTLPFWAVNAVHGVNLGKIMCKITSALYTLNFV 124  
Db 62 TYIYFKRLKTMDDTYLNLAVADILFLILPFWAYSEAKSWIFGVYLCGIGFYKLSFF 121

QY 125 GCMQFLACISIDRYAVATKPSQSG-----VCKPCWIIICFCVMAAILLSTPOLVFT 177  
 DB 122 SGMILLICISIDRYAVATKPSQSG-----VCKPCWIIICFCVMAAILLSTPOLVFT 178  
 QY 178 VINDA-----RCIPFPRIYGTSMKAL--IOMLEICIGFVVPFLIMGVCFITARTLMK 230  
 DB 179 LQKSGEDTLRC-----SLVSAQVEALITIQVAVMGFGLVPLAMSFCLIIIRTLLOA 233  
 QY 231 PNKISRLKVLTLVIVFIVTQLPYNIYKRCRAI--DIYLSITSCNMSKMDIAIQV 287  
 DB 234 RNFERNKAIKVIIVAVVVFIFQLPYNGVLAQTVANFNITNS--SCCETSKOLNIAVDV 291  
 QY 288 TESTALHSCNPLIYVFMGASFKNYMKAKKYGSMRQR-----QSVVEEPFDPSEG 340  
 DB 292 TYSLASVRCVNPFLYAFIYGVKFRSDLFKLFKDLGCLSQEKLHMSCHRVNAYSME- 350  
 QY 341 PTEPTSTPS 349  
 DB 351 -AETTTTFS 358

RESULT 29  
 US-08-902-294-2  
 ; Sequence 2, Application US/08902294  
 ; Patent No. 5874252  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ZHU, YUAN  
 ; TITLE OF INVENTION: A NOVEL SPLICING VARIANT OF  
 ; TITLE OF INVENTION: THE EPSTEIN-BARR VIRUS-INDUCED G-PROTEIN COUPLED  
 ; TITLE OF INVENTION: RECEPTOR  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: RATNER & PRESTIA  
 ; STREET: P.O. BOX 980  
 ; CITY: VALLEY FORGE  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19482  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/902,294  
 ; FILING DATE: 29-JUL-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: PRESTIA, PAUL F  
 ; REGISTRATION NUMBER: 23,031  
 ; REFERENCE/DOCKET NUMBER: GP-70177  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-407-0700  
 ; TELEFAX: 610-407-0701  
 ; TELEX: 846169  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 361 amino acids  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-902-294-2

Query Match 33.3%; Score 606.5; DB 2; Length 361;  
 Best Local Similarity 37.1%; Pred. No. 2,9e-44;  
 Matches 138; Conservative 62; Mismatches 117; Indels 55; Gaps 8;  
 QY 1 MALEQNSIDYEEENMNGTYDYSEYELIICKEDVREFAKVLEPFLITIVFGLAGNS 60

DB 21 VCLQDEVTDDYIGDNT---TVDYTLFESLCSKQDVNFKAMFLPIMYSIIICFVGLGNG 77  
 QY 61 MVAIYAIYKKQRTDVIYIINTAVADLLLFTLPMAVNAVHGVLDKINCKTSAIYT 120  
 DB 78 LVVLYIYFKRKLTMDYLLNLAVADILFLTLTPEMAYSAKSNVF----- 124  
 QY 121 LNFVSGMFLACISIDRYAVATKPS-----QSGVCKPCWIIICFCVMAAILLSTPOLVFT 176  
 DB 125 ---SGMILLICISIDRYAVATKPS-----VCKPCWIIICFCVMAAILLSTPOLVFT 180  
 QY 177 TVNDA-----RCIPFPRIYGTSMKAL--IOMLEICIGFVVPFLIMGVCFITARTLMK 231  
 DB 181 DLQSSSEQAMKCSLTHE---VEAFITIQVAVMGFGLVPLAMSFCLIIIRTLLOA 237  
 QY 232 NIKISRLKVLTLVIVFIVTQLPYNIYKRCRAI--DIYLSITSCNMSKMDIAIQV 291  
 DB 238 RNFERNKAIKVIIVAVVVFIFQLPYNGVLAQTVANFNITNS--SCCETSKOLNIAVDV 297  
 QY 292 ALFHSCLNPLIYVFMGASFKNYMKAKKYG-----SW-----RRQSVVEEPFDP 337  
 DB 298 ACVRCVNPFLYAFIYGVKFRSDLFKLFKDLGCLSQEKLHMSCHRVNAYSME- 352  
 QY 338 SSGPTSTPS 349  
 DB 353 ---AETTTTFS 360

RESULT 30  
 US-09-178-637-2  
 ; Sequence 2, Application US/09178637  
 ; Patent No. 6001972  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ZHU, YUAN  
 ; TITLE OF INVENTION: A No. 6001972el Splicing Variant of  
 ; TITLE OF INVENTION: the Epstein-Barr Virus-Induced G-Protein Coupled Receptor  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: RATNER & PRESTIA  
 ; STREET: P.O. BOX 980  
 ; CITY: VALLEY FORGE  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19482  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/178,637  
 ; FILING DATE: 26-OCT-1998  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/902,294  
 ; FILING DATE: 29-JUL-1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: PRESTIA, PAUL F  
 ; REGISTRATION NUMBER: 23,031  
 ; REFERENCE/DOCKET NUMBER: GP-70177-1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-407-0700  
 ; TELEFAX: 610-407-0701  
 ; TELEX: 846169  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 361 amino acids  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-178-637-2

Query Match	33.3%	Score 606.5;	DB 3;	Length 361;
Best Local Similarity	37.1%;	Pred. No. 2.9e-44;		
Matches 138;	Conservative 62;	Mismatches 117;	Indels 55;	Gaps 8;

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Qy 1 MAEONOSTDYAYBENENKGYVDSQVELICIKEDVBEFAKVELPBLTVIVGLAGNS 60
Db 21 VCLCODEVTDIDYIGNT---TVDYTFESLCSKDOVRNFRAMFLPIWYSITICFGLGNG 77
Qy 61 MVVAIYAYKKQRTKTDYIILNLVADLLLETLTPFANVANHGVMVLGKIMCKTYSALT 120
Db 78 LVVLVIYIFFKRLMTDITDYLNLNAVADILFLTLIFPMAYSANXSVF----- 124
Qy 121 LNFVSGMOPFLACISIDRYAVATKVPB---OSGUKGRCWIIICFCVMMAILLSIPOLVFY 176
Db 125 ---SGMLLELCISIDRYAVAOVANSARHRARAYLLISKSCVGIMTIAVLVSIPELLYS 180
Qy 177 TVNDA-----RCPIPRVIGTSMKLLIOMLETCIGVNPDELIMGVCFELTRATKMP 231
Db 181 DLORSSSEQAMRCSLITEH---VEAFITTOAQWVIGFVLLMNSCYLVIITRLLOAR 237
Qy 232 NIKISRPFLKVLITVIVIVTOLPEYNIVKFCRADDIYSLTSCNMSKRMADIAIOVYESI 291
Db 238 NFERKAIKVILIAVVVIVIVQLOPPNGVLAQTYAANNINSSITELSKOINIAVDYISL 297
Qy 292 ALFHSCNLPILIVFMGASFKYIVMKVAKYV-----SW-----RROROSVEEFPFD 337
Db 298 ACVRCVNPFLYAFIGVFRNDLEKFLKDLGLCSQEOELRQWSSCRHIRRSSMSVE----- 352
Qy 338 SEGPTEPTSTPS 349
Db 353 ----AETTTTBS 360

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1      RESULT 31
2      US-09-045-583-48
3      : Sequence 48, Application US/09045583
4      : Patent No. 6287805
5      : GENERAL INFORMATION:
6      : APPLICANT: Graham, Gerard J. et al.
7      : TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
8      : NUMBER OF SEQUENCES: 56
9      : CORRESPONDENCE ADDRESS:
10     : ADDRESSEE: LAHIVE & COCKFIELD, LLP
11     : STREET: 28 State Street
12     : CITY: Boston
13     : STATE: Massachusetts
14     : COUNTRY: USA
15     : ZIP: 02109
16     : COMPUTER READABLE FORM:
17     : MEDIUM TYPE: Floppy disk
18     : COMPUTER: IBM PC compatible
19     : OPERATING SYSTEM: PC-DOS/MS-DOS
20     : SOFTWARE: Patent In Release #1.0, Version #1.25
21     : CURRENT APPLICATION DATA:
22     : APPLICATION NUMBER: US/09/045,583
23     : FILING DATE: 20-MAR-98
24     : CLASSIFICATION: 435
25     : PRIOR APPLICATION DATA:
26     : APPLICATION NUMBER:
27     : FILING DATE:
28     : ATTORNEY/AGENT INFORMATION:
29     : NAME: Mandagouras, Amy E.
30     : REGISTRATION NUMBER: 36,207
31     : REFERENCE/DOCKET NUMBER: MNI-044
32     : TELECOMMUNICATION INFORMATION:
33     : TELEPHONE: (617)227-7400
34     : TELEFAX: (617)742-4214
35     : INFORMATION FOR SEQ ID NO: 48:
36     : SEQUENCE CHARACTERISTICS:
37     : LENGTH: 374 amino acids
38     : TYPE: amino acid
39     : TOPOLOGY: linear
40     : MOLECULE TYPE: peptide

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FRAGMENT TYPE: internal  
US-09-045-583-48

	Query Match:	32.1%	Score	583;	DB	4;	Length	374;	
	Best Local Similarity	36.1%	Pred.	No. 3e-42;					
	Matches	121;	Conservative	68;	Mismatches	120;	Indels	26;	Gaps
Qy	8	STDYVYENEMNGTVDYSQYELEICIKEDVRERPAKVPFLPVLTITFVIGLGNMVAIYA	67						
Dd	23	NISYVSVDISM-----LLGSLGVRRQFSRLFPDIASVLICVGILGLITLVITTA	72						
Qy	68	YYKKORTKDVIYLNLAVADLLLLFTLPFAV-NAHGWLGKMKCITYSALYTLANFVG	126						
Dd	73	FYKARSMTDVIYLLMAIDILFVLTEPFMAVSHATAMWFSNATCLTLGIYAINFQG	132						
Qy	127	MOFLAISCIDRYAAVAKVPS-----OSGVGRCDWCIIICFWMMAILSPOLVF---YTAN	179						
Dd	133	MLLTICTSMDRYIAIQAOTKSFRLSRLLPRSKIIICLVANGLSVIITSSIFVNOKYTNQ	192						
Qy	180	DNARCIPIPERLYGTS---MKALLQMELICIGFVVEPLLIMGVCYPITARTLMKMENIKI	235						
Dd	193	GSDVC--EKXQQTSEPIRMKLMLLGLLELFGFFILFMNIPOYFIYKTVLVAQNRSR	249						
Qy	236	SRLPKVLLIVYVEIYVQLPINIVKFCRAIDIYLSLITSCMSRMDIALIQUTESALPH	295						
Dd	250	HKAIRVIIVVVLFACQIPHNMYLLVLAAN-LCKNRNSCOSEKLTIGYTKYTEVELAFIH	308						
Qy	296	SCANPLIYVMGASFNYMYMKAKKYGSWRBOROS	330						
Dd	309	CCLNPVALYAIQGRFNRFUKTLKLDJCMCVRRKYKS	343						

RESULT 32  
 US-09-534-185-48  
 ; Sequence 48, Application US/09534185  
 ; Patent No. 6403767  
 ;  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Graham, Gerard J. et al.  
 ; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
 ; Hepatohelical Receptor Superfamily and uses  
 ; Therefor  
 ;  
 ; NUMBER OF SEQUENCES: 56  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 ; STREET: 28 State Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
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 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/534,185  
 ; FILING DATE: 24-Mar-2000  
 ; CLASSIFICATION: <Unknown>  
 ;  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/045,583  
 ; FILING DATE: <Unknown>  
 ;  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mandragouras, Amy E.  
 ; REGISTRATION NUMBER: 36,207  
 ; REFERENCE/DOCKET NUMBER: MNT-044  
 ;  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617)227-7400  
 ; TELEFAX: (617)742-4214  
 ;  
 ; INFORMATION FOR SEQ ID NO: 48:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 374 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear







Db 237 MAVELLIQMPENLKKFIPSTHMEYYAMTSFFYT-----INVETALINVLACINPLVLYAF 250

Qy 306 MGASIKATVVMKAYAKKY-----SMRRQRQSVVEEPDPDSEGPTEPTSTFSI 350

Db 291 VSLKRRKKNFMKLVDIGCLPYLGVSHQKSSKEDNSK--TFASHNVVATSMFOL 342

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RESULT 39
US-09-517-605-9
: Sequence 9, Application US/09517605
: Patent No. 6391567
: GENERAL INFORMATION:
: APPLICANT: Litcman, Dan R.
: APPLICANT: Kwon, Douglas S.
: APPLICANT: Geljtenbeek, Theo
: TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
: TITLE OF INVENTION: CELLS
: FILE REFERENCE: 1049-1-017
: CURRENT APPLICATION NUMBER: US/09/517,605
: CURRENT FILING DATE: 2000-03-02
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 9
: LENGTH: 342
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-517-605-9

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Query Match	30.8%	Score 560;	DB 4;	Length 342;
Best Local Similarity	33.1%	Pred. No. 2.5e-40;		
Matches 117; Conservative	75;	Mismatches 130;	Indels 32;	Gaps 8

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QY      12 YXENBNNGTVDYQXVELICIKEDVREBAKFELEPVLLIVAVICLJANSNVAWIAAYKKK 71
Db      6 YHEDYGSSFNDSOEB---HÖDLÖFSKVFLLPOMLIVFVCGPVGNSLVIVISIFYHK 61

QY      72 ORTKIDVYILNADVADLLLFLLPFWMANAANGWLKIMCKITSALVYTLNFWNGMQLA 131
        :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      62 LOSLIDVLEFVNLPLDLYIVCTLPFWAAGHHEWFEQWCKSLLGITYITNFIYSMLLT 121

QY      132 CISIDRYAAVTKVPS--OSGVGKPCW--TICFCVMAAAILISTPOLVFYV--NDNARCI 185
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Db      122 CTTVDRFIVVAKATKAVYNOQAKRMWTKVSTLIVISLIVSLPQIITGVNFWLKDLC- 180

QY      186 PLPFRYLGTSMKALLIOMLEICIGFVVPVLINGVCYCFIARTLTMCPNPKISRLPKVLLTV 245
        :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      181 ----GYHDEAISTVLATOMTIGFELPLITIMVCCSVIUKITKLHAGGÖKRSUKIIFLV 236

QY      246 VVVFVLTOLPNIIVKECAIDIIYSLLTSCNMSKMDIAIÖVTESIALFHSCNLPILYVF 305
        :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      237 MAVFLLTÖPMLMKFISHTHEWYAMTSFHT-----INWTERIAIYLRACLNVPVIXAF 290

QY      306 MGASFKNYMKAKAYKYG-----SWRROQSVEEFPDSEGTBETSTFS1 350
        :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      291 VSLKRRKQKFWKVLKQIGCLPYIGVSHÖKMKSSDNDK--TFGASHNVLETISMFQL 342

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RESULT 40  
US-08-875-573-20  
; Sequence 20, Application US/08875573  
; Patent No. 6150132  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Timothy N.C.  
; APPLICANT: Power, Christine A.  
; TITLE OF INVENTION: A CHEMOKINE RECEPTOR ABLE TO BIND TO  
; TITLE OF INVENTION: MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: NIXON & VANDERHAYE P.C.  
; STREET: 1100 No. 6150132zh Glebe Rd. 8th floor  
; CITY: Arlington  
; STATE: VA  
;

COUNTRY: USA  
 ZIP: 22201-4741  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/875,573  
 FILING DATE: 31-OCT-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/GB96/00143  
 FILING DATE: 24-JAN-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9501683.8  
 FILING DATE: 27-JAN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Wilson, Mary J.  
 REGISTRATION NUMBER: 32,955  
 REFERENCE/DOCKET NUMBER: 1430-172  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-816-4000  
 TELEFAX: 703-816-4100  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 360 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-875-573-20

Query Match	29.5%	Score 537.5	DB 4	Length 360
Best Local Similarity	35.8%	Pred. No. 2	2e-38	
Matches 115	Conservative 63	Mismatches 124	Indels 19	Gaps 6

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Qy	70	KQOKRTDYVYIINTLAVADLLFTLPMAVAVAHVGLKIMCKITSAIYTLNPSGMOF	12
Db	68	KRLRSMTDYVYIINTLAIISDLLFVFSLPFGVYAADQWVFGJGLCKMISWYTLGVFSGIIF	12
Qy	130	LACISIDRYVAATKY-----PSOSGYKPCWJICECVMMAIILISIFQVLF---YVYN	17
Db	128	YMLMSIDRYLAIVHAFVSLRARTLYGV-----ITSLATSVAVFASLPGFLFSTCYIBER	18
Qy	180	DNACRPIFPRYIGISMALLOMLEI-CIGVVPFELMGVCYITARTLAKMPENKISRP	23
Db	183	NHTYCTKTKYS--LNSTWVKVSSLEINILGVJPLGIMFPCYSMIIRLHOCKMEKKKA	24
Qy	239	LKVLIVVYVEIYTOCPNIVYFCRAIDIYSILSCNMSKRDIAIQTESIALFHSCL	29
Db	241	VKMIEAVVVLFEFMTPNYIVLFEETL-VELVYQDCTFERIYDAIQATITLAVHCL	29
Qy	299	NPILYVEMGASFPKNYMKVAK	319
Db	300	NPILYVFLGKERKTYILOJFK	320

Search completed: March 17, 2003, 16:28:33  
Job time : 20 secs



GenCore version 5.1.4\_p5\_4578  
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## OM protein - protein search, using sw model

Run on: March 17, 2003, 16:18:10 ; Search time 37 seconds

(without alignments)  
1260.479 Million cell updates/sec

Title: US-09-721-495B-2

Perfect score: 1819  
Sequence: 1 MALEQNSQSDYDYENENMNG.....VERPPDSGPPETPTSTSI 350Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	20	AA157290 Human BGCKr protei
2	1819	100.0	350	20	AAV17435 Human signal pepti
3	1819	100.0	350	20	AAW93169 Human HflA041 prot
4	1819	100.0	350	21	AAAG9325 Human seven transm
5	1819	100.0	350	22	AAAG80119 Human CCR11 protei
6	1819	100.0	350	22	AAU08994 Human G protein-co
7	1819	100.0	350	22	AAAG67237 Amino acid sequenc
8	1819	100.0	382	22	AAAB62389 Amino chemokine re
9	1814	99.7	349	20	AAW93170 Human HflA041 prot
10	1814	99.7	350	20	AAV30125 A human seven-pass

11	1810	99.5	350	21	AAV17301 Human orphan G pro
12	1810	99.5	350	21	AAAB02835 Human G protein co
13	1808	99.4	350	21	AAAB37788 Human TSC7. Homo
14	1728	95.0	333	20	AAV57289 Human BGCKr parlia
15	1620	89.1	350	22	AAAG67238 Amino acid sequenc
16	1591	87.5	350	20	AAV57292 Mouse BGCKr protei
17	1275	70.1	246	20	AAV57292 Human BGCKr protei
18	1257	69.1	242	22	AAAG99949 Human expressed po
19	1212	66.6	263	20	AAV30126 A seven-pass trans
20	862	47.4	164	22	ABB11162 Human orphan GPCR
21	862	47.4	164	22	AAW79310 Human protein SEQ
22	824	45.3	159	21	AAAB41786 Human OREF ORF1550
23	761	41.8	175	22	AAAB17880 Novel central nerv
24	761	41.8	175	22	AAAB10276 Human expressed o
25	761	41.8	175	22	AAAB10276 Human cDNA SEQ ID
26	761	41.8	175	22	Novel human uterin
27	761	41.8	175	22	Human endocrine po
28	761	41.8	175	22	Renal and cardiov
29	761	41.8	175	22	Novel human neopla
30	659	36.2	358	15	AAAB51745 Human 7TM receptor
31	659	36.2	358	21	AAAB21689 Human 7 transmembr
32	659	36.2	358	23	AAU91231 Human V31 seven tr
33	659	36.2	378	21	AAW48724 Human 7TM receptor
34	659	36.2	378	21	AAAB21688 Human CCR7 protein
35	659	36.2	378	21	AAAB21688 Human CCR7. Homo
36	659	36.2	378	22	AAAB50859 Human 7 transmembr
37	659	36.2	378	22	AAAB50859 Putative seven tra
38	659	36.2	410	15	AAAB51743 Polypeptide sequen
39	659	36.2	410	15	Genomic clone of 7
40	659	36.2	410	21	Novel 7 transmembr
41	659	36.2	410	22	Novel human diagn
42	659	36.2	569	22	Putative seven tra
43	656	36.1	378	15	Human mutant G pro
44	655	36.0	378	21	Human G protein-co
45	653	35.9	378	21	7TM receptor prote
46	650	35.7	378	21	Mouse 7 transmembr
47	650	35.7	378	21	Human CCR9a protei
48	643	35.3	369	22	Epstein Barr virus
49	643	35.3	378	15	G-protein coupled
50	643	35.3	378	19	Epstein Barr virus
51	643	35.3	378	19	Human CC chemokine
52	637	35.0	357	21	Human G protein-co
53	637	35.0	357	21	Human CCR9b protei
54	637	35.0	357	22	Non-endogenous hum
55	637	35.0	357	22	Seven transmembran
56	635.5	34.9	359	15	Murine 7TM recepto
57	635.5	34.9	359	19	Mouse 7 transmembr
58	635.5	34.9	359	21	Human CCR6a protei
59	635.5	34.9	359	21	Human CCR6b protei
60	631	34.7	357	21	Human CCR6a protei
61	626.5	34.4	356	23	Human chemokine (C
62	606.5	33.3	361	22	African green mon
63	583	32.1	374	22	Green monkey SIV t
64	583	32.1	374	23	Pig-tailed macaque
65	581	31.9	342	20	A7 times membrane
66	581	31.9	342	19	STPL33 protein seq
67	581	31.3	342	22	Human HMBB014 prot
68	569	31.3	342	20	Platelet factor-4
69	569	31.3	342	20	Human HIV/SIV rece
70	566.5	31.1	351	22	Human CXCR6 protei
71	560	30.8	342	22	Human CXCR6 protei
72	560	30.8	342	22	Amino acid sequenc
73	560	30.8	342	22	Amino acid sequenc
74	560	30.8	342	22	Amino acid sequenc
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77	560	30.8	342	22	Amino acid sequenc
78	560	30.8	342	22	Amino acid sequenc
79	560	30.8	342	22	Amino acid sequenc
80	537.5	29.5	360	17	Chemokine receptor
81	537.5	29.5	360	21	A human CCR4 chemo
82	537.5	29.5	360	21	Human CCR4 protein
83	537.5	29.5	360	22	Amino acid sequenc

84 537.5 29.5 361 22 ABB11966 Human CCR4 homolog  
85 537 29.5 1064 16 AAR70124 IL8-R type 2-GBP 1  
86 535.5 29.4 355 23 AAU80485 Gorilla CXCR2 rece  
87 534.5 29.4 355 14 AAR33420 Human IL-8 recepto  
88 534.5 29.4 355 17 AAB09990 Human IL-8 recepto  
89 534.5 29.4 355 23 AAU80482 Human CXCR2 recept  
90 534.5 29.4 355 23 AAU80483 Chimpanzee CXCR2 r  
91 534.5 29.4 355 23 AAU80487 Orangutan CXCR2 re  
92 534.5 29.4 360 13 AAR82273 Sequence in a low  
93 534.5 29.4 360 16 AAR80758 Interleukin 8 rece  
94 534.5 29.4 360 22 AAG80121 Human CXCR2 protei  
95 534.5 29.4 360 23 AAU10557 Human Interleukin  
96 534.5 29.4 399 22 ABG13609 Novel human diagn  
97 534.5 29.4 399 22 ABB12024 Human IL-8R B homo  
98 533.5 29.3 355 23 AAU80484 Chimpanzee CXCR2 r  
99 529.5 29.1 355 23 AAU80488 Orangutan CXCR2 re  
100 529.5 29.1 360 16 AAR80953 Recombinant high a  
101 527 29.0 384 20 AAU41681 Human D6 protein.  
102 527 29.0 384 22 AAG80128 Human D6 protein.  
103 527 29.0 384 23 AAO21639 Protein of the CCB  
104 526.5 28.9 355 23 AAU80486 Gorilla CXCR2 rece  
105 526.5 28.9 360 23 AAU10558 Human Interleukin  
106 526.5 28.9 362 21 AAB01449 Rodent GPR2 protei  
107 525.5 28.9 355 23 AAU80490 Rhesus macaque CX  
108 525 28.9 362 22 AAG80118 Human CCR10 protei  
109 524 28.8 362 22 ABB07734 Human C-C chemokin  
110 522.5 28.7 355 15 AAR53748 Seven transmembran  
111 522.5 28.7 355 19 AAM48722 Human V28 seven tr  
112 522.5 28.7 355 21 AAB21692 Human 7TM receptor  
113 522.5 28.7 355 21 AAB21693 Human G protein-co  
114 522.5 28.7 355 21 AAU90642 Human CX3CR1 prote  
115 522.5 28.7 355 22 AAG80126 Human CX3C chemoki  
116 522.5 28.7 355 22 AAB82786 Human 7 transmembr  
117 522.5 28.7 355 23 AAU91234 Human 7 transmembr  
118 522.5 28.7 355 23 AAU91235 Human 7 transmembr  
119 522.5 28.7 355 23 AAU84327 Protein CX3CR1 dif  
120 522 28.7 365 21 AAU97077 Primate (human) ch  
121 521 28.6 355 21 AAM48086 Human dendritic ce  
122 518.5 28.5 355 21 AAU90677 Human mutant G pro  
123 518.5 28.5 355 23 AAU80492 Baboon CXCR2 recep  
124 518.5 28.5 362 21 AAB01448 Primate GPR2 amino  
125 516 28.4 355 18 AAM29179 Rat CC chemokine r  
126 515.5 28.3 361 23 ABB07735 Human C-C chemokin  
127 511 28.1 358 16 AAR80952 Recombinant high a  
128 508 27.9 355 23 AAU80489 Rhesus macaque CX  
129 507.5 27.9 355 23 AAU80491 Vervet monkey CXCR  
130 503.5 27.7 356 20 AAM97362 G-protein coupled  
131 501.5 27.6 355 13 AAR28272 Sequence in a high  
132 501.5 27.6 355 16 AAR80950 Recombinant high a  
133 500.5 27.5 352 16 AAR88812 Human monocyte PF4  
134 500.5 27.5 352 16 AAR80757 Chemokine superfam  
135 500.5 27.5 352 20 AAY39993 Human CXCR4 protei

## ALIGNMENTS

RESULT 1  
ID AAY57290 standard; Protein: 350 AA.

XX AC AAY57290;  
XX DT 05-JUN-2000 (first entry)  
XX DE Human BGCR protein.  
XX KM BGCR protein; G-protein coupled receptor; human; chemokine; exocytosis;  
XX KM cell proliferation; anti-inflammation; anti-inflammatory; anti-angiogenic; antitumor; HIV;  
XX KM anti-allergic; antiviral.  
XX OS Homo sapiens.  
XX

PN WO9952945-A2.  
XX 21-OCT-1999.  
PD 16-APR-1999; 99WO-US08395.  
XX 16-APR-1999; 98US-0061753.  
XX 16-APR-1999; 98US-0061753.  
XX 16-APR-1999; 99US-0061753.  
XX (MILL-) MILLENIUM PHARM INC.  
XX Gonzalo JA, Gutierrez-Ramos JC;  
XX WPI; 1999-620375/53.  
XX N-PSDB; AA290528.  
PT New nucleic acid encoding human BGCR receptor, used e.g. for  
PT modulating inflammation and tumor growth  
XX Claim 8; Fig 2A-B; 123pp; English.  
XX The invention relates to a human BGCR protein, a G-protein coupled  
XX receptor. The BGCR protein can be expressed by standard recombinant  
XX methodology. BGCR are receptor proteins possibly involved in modulation  
XX of proinflammatory or stimulatory functions of chemokines; cell  
XX proliferation, migration, adhesion and targeting, and exocytosis. The  
XX BGCR nucleic acids and derived proteins (or their variants), antibodies  
XX and modulators are potentially useful for modulating inflammation;  
XX chemotactic activity of leucocytes; angiogenesis; cell proliferation;  
XX tumor growth; allergic reactions and entry of human immune deficiency  
XX virus into cells; for therapeutic or prophylactic purposes. They are also  
XX used for diagnosis and in drug-screening assays. The present sequence  
XX represents the full-length human BGCR protein.  
SQ Sequence 350 AA;  
Query Match 100.0%; Score 1819; DB 20; Length 350;  
Best Local Similarity 100.0%; Pred. No. 1.9e-195;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLEONQSDYYEENENNGTYDSQYELLCKEYREFAVFLPVLTIVFVIGLAGNS 60  
DB 1 MLEONQSDYYEENENNGTYDSQYELLCKEYREFAVFLPVLTIVFVIGLAGNS 60  
QY 61 MVVAIYAYKKORTDYIINLAVALDLFLTPFMAVNAVHGVIGKIMCKITSALYT 120  
DB 61 MVVAIYAYKKORTDYIINLAVALDLFLTPFMAVNAVHGVIGKIMCKITSALYT 120  
QY 61 MVVAIYAYKKORTDYIINLAVALDLFLTPFMAVNAVHGVIGKIMCKITSALYT 120  
DB 61 MVVAIYAYKKORTDYIINLAVALDLFLTPFMAVNAVHGVIGKIMCKITSALYT 120  
QY 121 INFVSGMOFLACISIDRYVAATKVPDSQSGVGPWCWIIICFVMAAILLSIPQLVFTYND 180  
DB 121 INFVSGMOFLACISIDRYVAATKVPDSQSGVGPWCWIIICFVMAAILLSIPQLVFTYND 180  
QY 121 INFVSGMOFLACISIDRYVAATKVPDSQSGVGPWCWIIICFVMAAILLSIPQLVFTYND 180  
DB 121 INFVSGMOFLACISIDRYVAATKVPDSQSGVGPWCWIIICFVMAAILLSIPQLVFTYND 180  
QY 181 NARCTPIPRRYIGTSMKALIQMLEICGFVVPFLIMGCVYITARTLMKNITISRLK 240  
DB 181 NARCTPIPRRYIGTSMKALIQMLEICGFVVPFLIMGCVYITARTLMKNITISRLK 240  
QY 241 VLLTVIVFIYVITOLPYNIVKFCRAIDIIYSLITSCNNSKRDIAIQVETSLALFHSCLNP 300  
DB 241 VLLTVIVFIYVITOLPYNIVKFCRAIDIIYSLITSCNNSKRDIAIQVETSLALFHSCLNP 300  
QY 301 ILVFMGASFKYVYVKKVAKKYGSWRRQSVSEEPFDEGTEPTSTFSI 350  
DB 301 ILVFMGASFKYVYVKKVAKKYGSWRRQSVSEEPFDEGTEPTSTFSI 350

RESULT 2  
ID AAY17435 standard; Protein: 350 AA.  
XX AC AAY17435;  
XX DT 29-JUL-1999 (first entry)  
XX

DE Human signal peptide-containing protein SP-16.  
 XX  
 XX Human; signal peptide-containing protein; SP; cell proliferation;  
 KW cancer; neuronal disorder; immune response; detection.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W09924463-A2.  
 XX  
 XX 20-MAY-1999.  
 XX  
 XX 04-NOV-1998; 98WO-US23578.  
 XX  
 XX 07-NOV-1997; 97US-0966316.  
 XX  
 XX (INCY-) INCYTE PHARM INC.  
 XX  
 XX Au-Young J, Lal P, Mathur P, Murry LE, Reddy R;  
 PI WPI; 1999-337694/28.  
 XX  
 XX N-PSDB; AAX61288.  
 XX  
 XX cDNA clones encoding signal peptide-containing proteins  
 PT  
 XX  
 XX Claim 1; Fig 1; 83pp; English.  
 XX  
 XX The present sequence represents a human signal peptide-containing  
 CC protein (SP), designated SP-16. SP proteins can be used to stimulate  
 CC cell proliferation or to treat or prevent cancer. SP antagonists are  
 CC also used to treat or prevent cancer, and also for treating or  
 CC preventing neuronal disorders or immune responses. Polynucleotide  
 CC sequences complementary to the SP-encoding polynucleotides are useful  
 CC for the detection of SP-encoding nucleic acid molecules in biological  
 CC samples.  
 CC  
 XX  
 XX Sequence 350 AA;  
 SQ  
 Query Match 100.0%; Score 1819; DB 20; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-195;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAFBNOSTDYEEENEMNGTYDSQYELICIKEDVREPAKFLPVLITIVFIIGLAGNS 60  
 DB 1 MAFBNOSTDYEEENEMNGTYDSQYELICIKEDVREPAKFLPVLITIVFIIGLAGNS 60  
 QY 61 MVAIYAYKKKORTKTDVYIINLAVALDLILFTLPFAVNAVHGVNGLKIMCKTTSALYT 120  
 DB 61 MVAIYAYKKKORTKTDVYIINLAVALDLILFTLPFAVNAVHGVNGLKIMCKTTSALYT 120  
 QY 121 LNFVSGMOFLACISIDRYVAATKVSQSGVGRKCIICVMAAILLSIPOLVFYTVND 180  
 DB 121 LNFVSGMOFLACISIDRYVAATKVSQSGVGRKCIICVMAAILLSIPOLVFYTVND 180  
 QY 181 NARCIPIFRYVLTGSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIKISRLPK 240  
 DB 181 NARCIPIFRYVLTGSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIKISRLPK 240  
 QY 241 VILTVIVITVQLPYNIVKFCRAIDIIYSLTSCMSKRMIAIQVESTALFFSCINP 300  
 DB 241 VILTVIVITVQLPYNIVKFCRAIDIIYSLTSCMSKRMIAIQVESTALFFSCINP 300  
 QY 301 ILYVFMGASPKYVVMVAKKYSWROROSVEEFPDSGPTSTSTSI 350  
 DB 301 ILYVFMGASPKYVVMVAKKYSWROROSVEEFPDSGPTSTSTSI 350  
 RESULT 3  
 ID AAM93169 standard; Protein; 350 AA.  
 AC AAM93169;  
 XX  
 XX 24-MAY-1999 (first entry)

XX  
 DE Human HPIA041 protein.  
 XX  
 XX HPIA041; G-coupled receptor; disease susceptibility; diagnosis; immunise;  
 KW treatment; FIA041 protein; gene therapy; immune response; vaccine; HIV-2;  
 KW inoculate; bacterial; fungal; protozoan viral; infection; HIV-1; cancer;  
 KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;  
 KW hypotension; hypertension; urinary retention; osteoporosis; allergy;  
 KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;  
 KW benign prostatic hypertrophy; psychotic disorder; neurological disorder;  
 KW anxiety; manic depression; delirium; dementia; severe mental retardation;  
 KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;  
 KW linkage analysis; gene mapping; human.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX EP899332-A2.  
 XX  
 XX 03-MAR-1999.  
 XX  
 XX 17-FEB-1998; 98EP-0301170.  
 XX  
 XX 27-OCT-1997; 97US-0962922.  
 XX  
 XX 15-AUG-1997; 97US-0055895.  
 XX  
 XX (SMIK) SMITHKLINE BEECHAM CORP.  
 XX  
 XX Ellis CE;  
 PI WPI; 1999-144803/13.  
 XX  
 XX N-PSDB; AAX22557.  
 XX  
 XX New G-coupled receptor (HPIA041) polypeptide and polynucleotide -  
 PT useful as diagnostic reagents and for prevention and treatment of  
 PT cancer, HIV infections and Parkinson's disease  
 CC  
 XX  
 XX Claim 1; Page 22-23; 27pp; English.  
 XX  
 XX This sequence represents a G-coupled receptor, HPIA041 which is useful  
 CC for diagnosing susceptibility to diseases by detecting mutations in the  
 CC HPIA041 gene, and can diagnose diseases associated with HPIA041 protein  
 CC imbalance by determining HPIA041 polypeptide expression levels. Agonists  
 CC (agonist) or inhibitor (antagonist) HPIA041 activity, in addition to direct  
 CC administration of antisense sequences to prevent expression, or HPIA041  
 CC polynucleotides to treat conditions associated with a lack of HPIA041  
 CC protein. Gene therapy may also be used to affect endogenous HPIA041  
 CC polypeptide expression. HPIA041 antibodies are useful for inducing an  
 CC immune response to immunise and prevent disease, and for isolating  
 CC HPIA041 clones or purifying the polypeptides by affinity chromatography.  
 CC HPIA041 polypeptides can be administered directly or as a vaccine to  
 CC inoculate against disease. Diseases diagnosed, prevented and treated  
 CC include bacterial, fungal, protozoan and viral infections, particularly  
 CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's  
 CC disease; acute heart failure; hypotension; hypertension; urinary  
 CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;  
 CC asthma; allergies; benign prostatic hypertrophy; and psychotic and  
 CC neurological disorders, including anxiety, schizophrenia, manic  
 CC depression, delirium, dementia, severe mental retardation and dyskinesias  
 CC such as Huntington's disease or Gilles de la Tourette's syndrome. The  
 CC HPIA041 polypeptide is also useful for mapping the gene to a chromosome,  
 CC allowing gene inheritance to be studied through linkage analysis.  
 CC  
 XX  
 XX Sequence 350 AA;  
 SQ  
 Query Match 100.0%; Score 1819; DB 20; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-195;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAFBNOSTDYEEENEMNGTYDSQYELICIKEDVREPAKFLPVLITIVFIIGLAGNS 60  
 DB 1 MAFBNOSTDYEEENEMNGTYDSQYELICIKEDVREPAKFLPVLITIVFIIGLAGNS 60

```

Qy 61 MVVAIYAYKKQRTDVIYIINLAVADLLFLTPFMAVNAVHGMVLGKIMCKITSLALT 120
Db 61 MVVAIYAYKKQRTDVIYIINLAVADLLFLTPFMAVNAVHGMVLGKIMCKITSLALT 120
Qy 121 LNFVSGMQLACISIDRYVAATKVPSSGSGVKPCMIICFCVMAAIIISIPQVFTVND 180
Db 121 LNFVSGMQLACISIDRYVAATKVPSSGSGVKPCMIICFCVMAAIIISIPQVFTVND 180
Qy 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIKISRPLK 240
Db 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIKISRPLK 240
Qy 241 VLLTVIVFIVITQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNP 300
Db 241 VLLTVIVFIVITQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNP 300
Qy 301 ILVYFMGASFQNYVMKAKKYGSRQROSVSEPPFSEGTPTSTFSI 350
Db 301 ILVYFMGASFQNYVMKAKKYGSRQROSVSEPPFSEGTPTSTFSI 350

```

## RESULT 4

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AA194325
ID AA194325 standard; Protein; 350 AA.

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XX AC AA194325;
XX DT 11-AUG-2000 (first entry)
XX DE Human seven transmembrane receptor VSHK-1.
XX KM Human, seven transmembrane receptor; VSHK-1; signal transduction.
XX OS Homo sapiens.

```

```

PH Key Location/Qualifiers
FT Modified-site 6..8 /note= "potential N-glycosylation site"
FT Modified-site 19..21 /note= "potential N-glycosylation site"
FT Domain 42..66 /label= Transmembrane_domain
FT Domain 79..100 /label= Transmembrane_domain
FT Domain 114..135 /label= Transmembrane_domain
FT Domain 156..175 /label= Transmembrane_domain
FT Domain 199..221 /label= Transmembrane_domain
FT Domain 241..262 /label= Transmembrane_domain
FT Modified-site 276..278 /note= "potential N-glycosylation site"
FT Domain 287..308 /label= Transmembrane_domain

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XX PN WO200026369-A1.

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XX PD 11-MAY-2000.

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XX PF 03-NOV-1999; 99WO-US25848.

```

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XX PR 04-NOV-1998; 98US-0107112.
XX PR 06-JAN-1999; 99US-0114856.

```

```

XX PA (CHIR ) CHIRON CORP.

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XX PI Khoja H, Shymala V;

```

```

XX DR WPI; 2000-365618/31.

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XX DR N-PSDB; AA194325.

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PT Novel polypeptide comprising a new seven-transmembrane receptor protein
PT and its encoding polynucleotide, useful for the analysis of VSHK-1 -
PS Claim 3; Fig 1; 79pp; English.
XX
XX CC The present sequence is VSHK-1, a new seven transmembrane
CC receptor which contains seven membrane-spanning helical domains
CC that are linked by three intracellular and three extracellular loops. The
CC gene sequence encoding VSHK-1 was isolated from a cDNA library. In heart
CC tissue, where VSHK-1 is predominantly found, three RNA species were
CC identified: a 1.3kb; a 2.0kb; and a 5.0kb species. The polynucleotide
CC encoding the present sequence corresponds to the 2.0kb form. The 1.3kb
CC form may result from the use of an alternative polyadenylation site while
CC transcription of a 3.0kb intron at nucleotide 74 could account for the
CC 5.0kb species. VSHK-1 polynucleotides can be used as hybridisation probes
CC to detect and measure VSHK-1 mRNA. They may also be used to identify
CC substances that modulate the level of VSHK-1 mRNA. The VSHK-1 coding
CC sequence can be integrated into an expression vector for production of
CC VSHK-1 receptor polypeptides in host cells. The polypeptides can be used
CC to identify agents which modulate VSHK-1 receptor signal transduction
CC activity.

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```

SQ Sequence 350 AA;

```

```

Query Match 100.0%; Score 1819; DB 21; Length 350;
Best Local Similarity 100.0%; Pred. No. 1, 9e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MALEONOSTDYEEENENGTVDYSQYELICIKEDVREFAKVPFLVPLTIVFVIGLAGNS 60
Db 1 MALEONOSTDYEEENENGTVDYSQYELICIKEDVREFAKVPFLVPLTIVFVIGLAGNS 60
Qy 61 MVVAIYAYKKQRTDVIYIINLAVADLLFLTPFMAVNAVHGMVLGKIMCKITSLALT 120
Db 61 MVVAIYAYKKQRTDVIYIINLAVADLLFLTPFMAVNAVHGMVLGKIMCKITSLALT 120
Qy 121 LNFVSGMQLACISIDRYVAATKVPSSGSGVKPCMIICFCVMAAIIISIPQVFTVND 180
Db 121 LNFVSGMQLACISIDRYVAATKVPSSGSGVKPCMIICFCVMAAIIISIPQVFTVND 180
Qy 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIKISRPLK 240
Db 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIKISRPLK 240
Qy 241 VLLTVIVFIVITQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNP 300
Db 241 VLLTVIVFIVITQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNP 300
Qy 301 ILVYFMGASFQNYVMKAKKYGSRQROSVSEPPFSEGTPTSTFSI 350
Db 301 ILVYFMGASFQNYVMKAKKYGSRQROSVSEPPFSEGTPTSTFSI 350

```

## RESULT 5

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AA194325
ID AA194325 standard; Protein; 350 AA.

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XX AC AA194325;

```

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XX DT 17-JAN-2002 (first entry)

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XX DE Human CCR11 protein.

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```

XX KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
XX KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
XX KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
XX KW antineoplastic; antidiabetic; immunosuppressive; dermatological;
XX KW antineoplastic; antidiabetic.

```

```

XX OS Homo sapiens.

```

```

XX XX WO200172830-A2.

```

04-OCT-2001.

02-APR-2001; 2001WO-EP03708.

31-MAR-2000; 2000DE-1016013.

(TFP-) IPF PHARM GMBH.  
(FORS/) FORSMANN U.

Forsmann W, Adermann K, Heitland A, Spodberg N;  
WPI; 2001-626256/72.

Diagnostic agent containing two or more receptor-specific ligands,  
useful for detecting tumors, inflammation etc., also therapeutic use of  
ligand inhibitors -

Disclosure; Page 11; 26p; German.

This invention describes a novel diagnostic agent (A) comprising at least  
two different ligands (I) for receptors (II) that are implicated in  
disease. (A) are used for the diagnosis of tumors (especially colorectal  
or prostatic), organ rejection, inflammation and autoimmune diseases.  
Also inhibitors of (I) are used therapeutically against tumors (and their  
metastases), inflammation (particularly bronchial asthma or chronic bowel  
inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),  
where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,  
endocrine, motor or urogenital systems or skin are affected, and bone  
marrow diseases. The products of the invention are chemokine derivatives  
which have cytostatic, antiinflammatory, antiproliferative,  
immunosuppressive, dermatological, antirheumatic, anticholesteric,  
chemokines act on specific tumor and inflammatory cells through a  
constellation of chemokine receptors (CR), which control migration and  
proliferation of these cells. AAG80045-AAG80128 represent human chemokine  
fragments used to illustrate the method of the invention.

Sequence 350 AA:

Query Match 100.0%; Score 1819; DB 22; Length 350;  
Best Local Similarity 100.0%; Pred. No. 1.9e-195; Indels 0; Gaps 0;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLEQNSTDYEEENMGTYDYSQVELICIKEDVREFAKFLPFLTIYVIGLAGNS 60  
1 MLEQNSTDYEEENMGTYDYSQVELICIKEDVREFAKFLPFLTIYVIGLAGNS 60

61 MVAIYAYKKKORTKTDVYILNLAVALDLLFTLPFAVNAVHGVLGKIMCKITSALYT 120  
61 MVAIYAYKKKORTKTDVYILNLAVALDLLFTLPFAVNAVHGVLGKIMCKITSALYT 120

121 LNFVSGMOFLACISIDRYVAATKVPQSOGVKPCWITICFCVMAAAILLSIPOLVFTYND 180  
121 LNFVSGMOFLACISIDRYVAATKVPQSOGVKPCWITICFCVMAAAILLSIPOLVFTYND 180

121 LNFVSGMOFLACISIDRYVAATKVPQSOGVKPCWITICFCVMAAAILLSIPOLVFTYND 180

181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNKISRPLK 240  
181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNKISRPLK 240

241 VLLTVVIVFIYVQLPYNIVKFCRAIDIIYSILTSCKMSKMDIAIQVTESIALFHSCLNP 300  
241 VLLTVVIVFIYVQLPYNIVKFCRAIDIIYSILTSCKMSKMDIAIQVTESIALFHSCLNP 300

301 ILYVNGASPKYVYKVKYSGMROROSVEFPDSEPTSTFSI 350  
301 ILYVNGASPKYVYKVKYSGMROROSVEFPDSEPTSTFSI 350

301 ILYVNGASPKYVYKVKYSGMROROSVEFPDSEPTSTFSI 350

RESULT 6  
AA08994  
ID AA08994 standard; Protein; 350 AA.  
AC AA08994;  
XX

18-DEC-2001 (first entry)

Human G protein-coupled receptor, GPCR, 2398.

Human; GPCR; G protein-coupled receptor; 2398; cardiant;  
antithrombotic; analgesic; cytostatic; antiangiogenic;  
cardiovascular disorder; angiogenesis-related disorder;  
neural disorder; pain response disorder; inflammatory disorder;  
atherosclerosis; angina pectoris; myocardial infarction;  
ischemic heart disease; sudden cardiac death; obesity;  
hypertensive heart disease; diabetes; prostate cancer-related pain.

Homo sapiens.

Key Location/Qualifiers  
Region 125..141  
/label=G\_protein\_receptor\_signature

WO200164882-A2.

07-SEP-2001.

28-FEB-2001; 2001WO-US06543.

29-FEB-2000; 2000US-186059P.

(MILL-) MILLENNIUM PHARM INC.

Glucksmann MA, Galvan KM, Silos-Santiago I;  
N-PSDB; AAS14572.

Novel G protein coupled receptors and nucleic acids encoding them, for  
identifying agents for the treatment of cardiac disorders -

Claim 9; Fig 9; 209pp; English.

The invention relates to novel human G protein-coupled receptors (GPCR)  
named 1983, 52881, 2398, 45449, 50289 and 52872. The novel GPCRs and  
nucleic acids encoding them are useful for identifying agents for the  
treatment of cardiovascular disorders, angiogenesis-related disorders,  
neural disorders, pain response disorders and inflammatory disorders  
e.g. atherosclerosis, angina pectoris and myocardial infarction.  
ischemic heart disease, sudden cardiac death, hypertensive heart  
disease, diabetes, prostate cancer-related pain, diabetes and obesity.

The present sequence represents GPCR 2398.

Sequence 350 AA:

Query Match 100.0%; Score 1819; DB 22; Length 350;  
Best Local Similarity 100.0%; Pred. No. 1.9e-195; Indels 0; Gaps 0;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLEQNSTDYEEENMGTYDYSQVELICIKEDVREFAKFLPFLTIYVIGLAGNS 60  
1 MLEQNSTDYEEENMGTYDYSQVELICIKEDVREFAKFLPFLTIYVIGLAGNS 60

61 MVAIYAYKKKORTKTDVYILNLAVALDLLFTLPFAVNAVHGVLGKIMCKITSALYT 120  
61 MVAIYAYKKKORTKTDVYILNLAVALDLLFTLPFAVNAVHGVLGKIMCKITSALYT 120

121 LNFVSGMOFLACISIDRYVAATKVPQSOGVKPCWITICFCVMAAAILLSIPOLVFTYND 180  
121 LNFVSGMOFLACISIDRYVAATKVPQSOGVKPCWITICFCVMAAAILLSIPOLVFTYND 180

121 LNFVSGMOFLACISIDRYVAATKVPQSOGVKPCWITICFCVMAAAILLSIPOLVFTYND 180

181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNKISRPLK 240  
181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNKISRPLK 240

241 VLLTVVIVFIYVQLPYNIVKFCRAIDIIYSILTSCKMSKMDIAIQVTESIALFHSCLNP 300  
241 VLLTVVIVFIYVQLPYNIVKFCRAIDIIYSILTSCKMSKMDIAIQVTESIALFHSCLNP 300

QY 301 ILYVFGASFKNYVMKAKKYSWRORSVEEPPDESGTEPTSTSI 350  
 DB 301 ILYVFGASFKNYVMKAKKYSWRORSVEEPPDESGTEPTSTSI 350

RESULT 7  
 AAG67237  
 ID AAG67237 standard; Protein, 350 AA.  
 AC AAG67237;  
 XX  
 DT 13-NOV-2001 (first entry)  
 XX  
 DE Amino acid sequence of human chemokine receptor CCR11.  
 XX  
 KW Human; chemokine receptor; CCR11; G protein coupled receptor;  
 KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;  
 KW asthma; angiogenesis; atherosclerosis vascular association disease;  
 KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;  
 KW left ventricular diastolic dysfunction; migraine; preterm labour;  
 KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;  
 KW myocardial infarction; congestive heart failure; endometritis;  
 KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2001.66598-A2.  
 PD 13-SEP-2001.  
 XX  
 PF 05-MAR-2001; 2001WO-US07073.  
 XX  
 PR 03-MAR-2000; 2000US-0186928.  
 PR 03-MAR-2000; 2000US-0187231.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Gray PM, Schwickart VL, Epp A, Raport CJ, Chantry D, Steiner B;  
 XX WPI: 2001-541918/60.  
 DR N-PSDB; AAF77711.  
 XX  
 XX An isolated polynucleotide encoding the chemokine receptor CCR11,  
 PT useful for treating rheumatoid arthritis, inflammatory bowel disease,  
 PT asthma, angiogenesis, atherosclerosis, cardiac arrhythmias, Raynaud's  
 PT phenomenon and migraine -  
 XX  
 PS Claim 13; Page 96-97; 110pp; English.  
 XX  
 CC The present sequence represents the human chemokine receptor CCR11.  
 CC CCR11 is a member of the G protein coupled receptor family. A CCR11  
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11  
 CC expression or biological activity, is useful for treating many  
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory  
 CC bowel disease, and asthma. They are also useful for treating  
 CC angiogenesis, atherosclerosis vascular association diseases which may  
 CC include but are not limited to hypertension, angina pectoris, cardiac  
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's  
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic  
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive  
 CC heart failure, endometritis, vasospasm, retinopathy, nephropathy, or  
 CC pulmonary vascular disease.  
 XX  
 SQ Sequence 350 AA:  
 Query Match 100.0%; Score 1819; DB 22; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-195;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 MVAIAYKKKORTKDYVILNLAVADLLLEPTLPEFANVAVHGVILGKIMCKITSALYT 120  
 DB 61 MVAIAYKKKORTKDYVILNLAVADLLLEPTLPEFANVAVHGVILGKIMCKITSALYT 120

QY 121 LNFVSGMQLACISIDRYAVATKVPSSGVGKPCWIIICFCVMAAILLSIPOLVETVND 180  
 DB 121 LNFVSGMQLACISIDRYAVATKVPSSGVGKPCWIIICFCVMAAILLSIPOLVETVND 180

QY 181 NARCIPIPPRYIGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIKISRLK 240  
 DB 181 NARCIPIPPRYIGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIKISRLK 240

QY 241 VLLTVIVFIVQLPNTIVKFCRAIDIIYSLLTSCNMSKMDIAIQVETSLAFHSCINP 300  
 DB 241 VLLTVIVFIVQLPNTIVKFCRAIDIIYSLLTSCNMSKMDIAIQVETSLAFHSCINP 300

QY 301 ILYVFGASFKNYVMKAKKYSWRORSVEEPPDESGTEPTSTSI 350  
 DB 301 ILYVFGASFKNYVMKAKKYSWRORSVEEPPDESGTEPTSTSI 350

RESULT 8  
 AAB62389  
 ID AAB62389 standard; Protein, 382 AA.  
 XX  
 AC AAB62389;  
 XX  
 DT 29-JUN-2001 (first entry)  
 XX  
 DE Human chemokine receptor CCX CKR polypeptide.  
 XX  
 KW Chemokine receptor; CCX CKR; chemokine; ELC; SLG; TECK; modulator;  
 KW antiinflammatory; immunosuppressive; cytostatic; antiallergic; human;  
 KW immunostimulant; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 351 /note= "encoded by TAA"  
 FT Misc-difference 353 /note= "encoded by TAA"  
 FT Misc-difference 365 /note= "encoded by TAA"  
 FT Misc-difference 371 /note= "encoded by TGA"  
 FT Misc-difference 371 /note= "encoded by TAA"  
 XX  
 PN WO200127146-A2.  
 XX  
 PD 19-APR-2001.  
 XX  
 PF 10-OCT-2000; 2000WO-US28067.  
 XX  
 PR 12-OCT-1999; 99US-0159015.  
 PR 13-OCT-1999; 99US-0159210.  
 PR 20-DEC-1999; 99US-0172979.  
 PR 28-DEC-1999; 99US-0173389.  
 PR 03-MAR-2000; 2000US-0186626.  
 XX  
 PA (CHEM-) CHEMOCENTRYX INC.  
 XX  
 PI Goelling J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;  
 XX WPI: 2001-281975/29.  
 DR N-PSDB; AAF57685.  
 XX  
 PT Isolated or recombinant chemokine receptor (designated CCX CKR)  
 PT polypeptide (PI) or its fragment, useful for identifying CCX CKR  
 PT modulators which can be used in the treatment of inflammation, allergy,  
 PT an autoimmune disease or cancer -  
 XX  
 PS Claim 4; Fig 1; 72pp; English.

XX The invention relates to an isolated or recombinant chemokine receptor  
 CC designated CCX CKR) polypeptide which binds to chemokines such as ELC,  
 CC SLK or TRCK. The CCX CKR polypeptide is useful for identifying CCX CKR  
 CC modulators. An agent that modulates the activity or expression of CCX CKR  
 CC in a cell or tissue in the mammal is useful in the treatment of a CCX CKR  
 CC -mediated condition such as inflammation, allergy, an autoimmune disease,  
 CC graft rejection, cancer, an infectious disease or an immunosuppressive  
 CC disease. The present sequence represents the human CCX CKR polypeptide.  
 CC  
 XX

XX Sequence 382 AA;

Query Match 100.0%; Score 1819; DB 22; Length 382;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-195;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALONOSTDYEEENMGTYDYSQYELICIKEDVEPAKFLPVFLITVFIYGLAGNS 60  
 DB 1 MALONOSTDYEEENMGTYDYSQYELICIKEDVEPAKFLPVFLITVFIYGLAGNS 60  
 QY 61 MVAIYAYYKQRTKTDVYIINLAVADLLFLTPFAVNAVHGWLGKIMCKTTSALYT 120  
 DB 61 MVAIYAYYKQRTKTDVYIINLAVADLLFLTPFAVNAVHGWLGKIMCKTTSALYT 120  
 QY 121 LNFVSGMFLACISIDRYVAATKVPSSGSGVKPCMIICFCVMAAILLSIPOLVFYTVND 180  
 DB 121 LNFVSGMFLACISIDRYVAATKVPSSGSGVKPCMIICFCVMAAILLSIPOLVFYTVND 180  
 QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFTRTKMKPNIKISPLK 240  
 DB 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFTRTKMKPNIKISPLK 240  
 QY 241 VLLTVVIFVITQLPYNTVVKRCRAIDIIYSLITSCNSKRDIAIQVTESTALFHSCLNP 300  
 DB 241 VLLTVVIFVITQLPYNTVVKRCRAIDIIYSLITSCNSKRDIAIQVTESTALFHSCLNP 300  
 QY 301 LLYVMGASFKNYVWKVAKKYGSMRQROSVVEFPDSEGPTSTPSI 350  
 DB 301 LLYVMGASFKNYVWKVAKKYGSMRQROSVVEFPDSEGPTSTPSI 350

RESULT 9  
 AAM93170  
 ID AAM93170 standard; Protein; 349 AA.

XX AC AAM93170;

XX DT 24-MAY-1999 (first entry)

XX DE Human HFI041 protein.

XX HFI041; G-coupled receptor; disease susceptibility; diagnosis; immunise;  
 XX treatment; FFI041 protein; gene therapy; immune response; vaccine; HIV-2;  
 XX inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;  
 XX diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;  
 XX hypotension; hypertension; urinary retention; osteoporosis; allergy;  
 XX angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;  
 XX benign prostatic hyperplasia; psychotic disorder; neurological disorder;  
 XX anxiety; manic depression; delirium; dementia; severe mental retardation;  
 XX dyskinnesia; Huntington's disease; Gilles de la Tourette's syndrome;  
 XX linkage analysis; gene mapping; human; ss.

XX OS Homo sapiens.

XX PN EP899332-A2.

XX PD 03-MAR-1999.

XX PF 17-FEB-1998; 98EP-0301170.

XX PR 27-OCT-1997; 97US-0962922.

XX PR 15-AUG-1997; 97US-0055895.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX Ellis CE;

XX WPI; 1999-144803/13.

XX N-PSDB; AAX22558.

PT New G-coupled receptor (HFI041) polypeptide and polynucleotide -  
 PT useful as diagnostic reagents and for prevention and treatment of  
 PT cancer, HIV infections and Parkinson's disease

XX Disclosure; Page 25-26; 27pp; English.

XX This sequence encodes a G-coupled receptor, HFI041 which is useful for  
 CC diagnosing susceptibility to diseases by detecting mutations in the  
 CC HFI041 gene, and can diagnose diseases associated with HFI041 protein  
 CC imbalance by determining HFI041 polypeptide expression levels. Agonists  
 CC and antagonists of the protein can be used in treatment to activate  
 CC (agonist) or inhibit (antagonist) HFI041 activity, in addition to direct  
 CC administration of antisense sequences associated with a lack of HFI041  
 CC polynucleotides to treat conditions associated with a lack of HFI041  
 CC protein. Gene therapy may also be used to affect endogenous HFI041  
 CC polypeptide expression. HFI041 antibodies are useful for inducing an  
 CC immune response to immunise and prevent disease, and for isolating  
 CC HFI041 clones or purifying the polypeptides by affinity chromatography.  
 CC HFI041 polypeptides can be administered directly or as a vaccine to  
 CC inoculate against disease. Diseases diagnosed, prevented and treated  
 CC include bacterial, fungal, protozoan and viral infections, particularly  
 CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's  
 CC disease; acute heart failure; hypotension; hypertension; urinary  
 CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;  
 CC asthma; allergic; benign prostatic hypertrophy; and psychotic and  
 CC neurological disorders, including anxiety, schizophrenia, manic  
 CC depression, delirium, dementia, severe mental retardation and dyskinesias  
 CC such as Huntington's disease or Gilles de la Tourette's syndrome. The  
 CC HFI041 polypeptide is also useful for mapping the gene to a chromosome,  
 CC allowing gene inheritance to be studied through linkage analysis.

XX Sequence 349 AA;

Query Match 99.7%; Score 1814; DB 20; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 7e-195;  
 Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALEONOSTDYEEENMGTYDYSQYELICIKEDVEPAKFLPVFLITVFIYGLAGNS 61  
 DB 1 ALEONOSTDYEEENMGTYDYSQYELICIKEDVEPAKFLPVFLITVFIYGLAGNS 60  
 QY 62 VVAIYAYYKQRTKTDVYIINLAVADLLFLTPFAVNAVHGWLGKIMCKTTSALYT 121  
 DB 62 VVAIYAYYKQRTKTDVYIINLAVADLLFLTPFAVNAVHGWLGKIMCKTTSALYT 120  
 QY 122 LNFVSGMFLACISIDRYVAATKVPSSGSGVKPCMIICFCVMAAILLSIPOLVFYTVND 181  
 DB 122 LNFVSGMFLACISIDRYVAATKVPSSGSGVKPCMIICFCVMAAILLSIPOLVFYTVND 180  
 QY 182 ARCIPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFTRTKMKPNIKISPLK 241  
 DB 182 ARCIPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFTRTKMKPNIKISPLK 240  
 QY 242 LLLTVVIFVITQLPYNTVVKRCRAIDIIYSLITSCNSKRDIAIQVTESTALFHSCLNP 301  
 DB 242 LLLTVVIFVITQLPYNTVVKRCRAIDIIYSLITSCNSKRDIAIQVTESTALFHSCLNP 300  
 QY 302 LLYVMGASFKNYVWKVAKKYGSMRQROSVVEFPDSEGPTSTPSI 350  
 DB 302 LLYVMGASFKNYVWKVAKKYGSMRQROSVVEFPDSEGPTSTPSI 349

RESULT 10  
 AAY30125  
 ID AAY30125 standard; Protein; 350 AA.

AC AAY30125;  
 XX  
 DT 14-OCT-1999 (first entry)  
 XX  
 DE A human seven-pass transmembrane receptor protein.  
 XX  
 KW Seven-pass transmembrane receptor; autoimmune disease;  
 KW white blood cell dysfunction.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09933876-A1.  
 XX  
 PD 08-JUL-1999.  
 XX  
 PF 24-DEC-1998; 98WO-JP05886.  
 XX  
 PR 24-DEC-1997; 97JP-0354537.  
 XX  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX  
 PI Ishimaru H, Koshio T, Ohno T;  
 XX  
 DR WPI; 1999-493806/41.  
 DR N-PSDB; AAX86674.  
 XX  
 PT New seven-pass transmembrane receptor protein useful for treating,  
 PT preventing or diagnosing autoimmune diseases  
 XX  
 PS Claim 1; Page 101-103; 118pp; Japanese.  
 XX  
 CC The present sequence represents a seven-pass transmembrane receptor  
 CC protein. The protein and its DNA can be used to screen substances  
 CC for the diagnosis, prevention and treatment of autoimmune diseases,  
 CC particularly those due to white blood cell dysfunction.  
 XX  
 SQ Sequence 350 AA;  
 Query Match 99.7%; Score 1814; DB 20; Length 350;  
 Best Local Similarity 99.7%; Pred. No. 7e-195; Indels 0; Gaps 0;  
 Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MALBQNSTDYVYENENNGTYDYSOYELICIKEDVREPAKFLPVLTIVFVIGLAGNS 60  
 DB 1 MALBQNSTDYVYENENNGTYDYSOYELICIKEDVREPAKFLPVLTIVFVIGLAGNS 60  
 QY 61 MVVAIVYVYKQRTKTVYIINLAVALDLLLFTLPFMAVNAVHGWVIGKIMCKITSLTYT 120  
 DB 61 MVVAIVYVYKQRTKTVYIINLAVALDLLLFTLPFMAVNAVHGWVIGKIMCKITSLTYT 120  
 QY 121 LNFVSGMQFLACISIDRYVAVTKVPSOSGVGKPCMIICFCVMAAIIISIPOLVFTVND 180  
 DB 121 LNFVSGMQFLACISIDRYVAVTKVPSOSGVGKPCMIICFCVMAAIIISIPOLVFTVND 180  
 QY 181 NARCIPIFPRLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIKISRPJK 240  
 DB 181 NARCIPIFPRLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIKISRPJK 240  
 QY 241 VLLTVVVFVLTOLPNIIVKFCRAIDIIYSLITSQNMKMDALIQVTESIALFHSCLNP 300  
 DB 241 VLLTVVVFVLTOLPNIIVKFCRAIDIIYSLITSQNMKMDALIQVTESIALFHSCLNP 300  
 QY 301 ILVYFMGASFKNYVMKAKYKGSWRQSVREPEPDSPTSTFSI 350  
 DB 301 ILVYFMGASFKNYVMKAKYKGSWRQSVREPEPDSPTSTFSI 350  
 RESULT 11  
 ID AAY71301 standard; Protein; 350 AA.  
 XX  
 AC AAY71301;  
 XX

DT 02-NOV-2000 (first entry)  
 XX  
 DE Human orphan G protein-coupled receptor hPPR1.  
 XX  
 KW Human; orphan G protein-coupled receptor; GPCR; hPPR1; drug screening;  
 KW transmembrane receptor; expressed sequence tag; EST; signal cascade.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200031258-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 13-OCT-1999; 99WO-US23687.  
 XX  
 PR 20-NOV-1998; 98US-0109213.  
 PR 16-FEB-1999; 99US-0120416.  
 PR 26-FEB-1999; 99US-0121852.  
 PR 12-MAR-1999; 99US-0123946.  
 PR 12-MAR-1999; 99US-0123949.  
 PR 28-MAY-1999; 99US-0136435.  
 PR 28-MAY-1999; 99US-0136437.  
 PR 28-MAY-1999; 99US-0136439.  
 PR 28-MAY-1999; 99US-0136567.  
 PR 28-MAY-1999; 99US-0137127.  
 PR 28-MAY-1999; 99US-0137131.  
 PR 29-SEP-1999; 99US-0156555.  
 PR 29-SEP-1999; 99US-0156633.  
 PR 29-SEP-1999; 99US-0156634.  
 PR 29-SEP-1999; 99US-0156653.  
 PR 01-OCT-1999; 99US-0157280.  
 PR 01-OCT-1999; 99US-0157281.  
 PR 01-OCT-1999; 99US-0157282.  
 PR 01-OCT-1999; 99US-0157293.  
 PR 01-OCT-1999; 99US-0157294.  
 PR 12-OCT-1999; 99US-0157294.  
 PR 12-OCT-1999; 99US-0416760.  
 PR 12-OCT-1999; 99US-0417044.  
 XX  
 PA (AREN-) ARENA PHARM INC.  
 XX  
 PI Chen R, Dang HT, Liaw CW, Lin I;  
 XX  
 DR WPI; 2000-400068/34.  
 DR N-PSDB; AAD01128.  
 XX  
 PT Novel human orphan G protein-coupled receptors and the encoding cDNAs  
 PT for use in the identification of G protein-coupled receptor agonists -  
 XX  
 PS Claim 42; Page 69-70; 102pp; English.  
 XX  
 CC The present amino acid sequence is the hPPR1, an endogenous human  
 CC orphan G protein-coupled receptor (GPCR), expressed in the pituitary  
 CC gland, heart, salivary gland, small intestine and testis. The hPPR1 cDNA  
 CC was identified using EST (expressed sequence tag) A359504 and 238667 as  
 CC a probe. The orphan GPCR of the invention, like all GPCRs has seven  
 CC transmembrane alpha helices with an extracellular N-terminus and an  
 CC intracellular C-terminus. However, no endogenous ligands has yet been  
 CC identified for the proteins of the invention. The orphan GPCRs may be  
 CC used in the identification of their endogenous ligands, and to screen  
 CC potential GPCR agonists and antagonists for use as pharmaceutical agents.  
 CC The proteins may also be used in the study of GPCR-mediated signalling  
 CC cascades, and to elucidate their precise role in normal and diseased  
 CC human conditions. Nucleic acid encoding human orphan GPCRs may be used  
 CC for tissue localisation expression analysis to provide information about  
 CC their function in healthy and pathological states.  
 XX  
 SQ Sequence 350 AA;  
 Query Match 99.5%; Score 1810; DB 21; Length 350;  
 Best Local Similarity 99.4%; Pred. No. 2e-194; Indels 0; Gaps 0;  
 Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



QY 1 MLEONOSTDYVEENEMNGTYDYSOYEELICIKEDVREFAKFLPVFLTIYVIGLAGNS 60  
 DB 1 MLEONOSTDYVEENEMNGTYDYSOYEELICIKEDVREFAKFLPVFLTIYVIGLAGNS 60  
 QY 61 MVAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAVHGVWLGKIMCKITSALYT 120  
 DB 61 MVAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAVHGVWLGKIMCKITSALYT 120  
 QY 121 LNFVSGMOFLACISIDRYAVATKVPSSGVGKPCWITICFCVMAAILLSIPOLVFTYVND 180  
 DB 121 LNFVSGMOFLACISIDRYAVATKVPSSGVGKPCWITICFCVMAAILLSIPOLVFTYVND 180  
 QY 181 NARCIPIFPYVLTGSMKALLOMELICIGFVVPFLMGVCYFTIARTLMKPNIKISRPK 240  
 DB 181 NARCIPIFPYVLTGSMKALLOMELICIGFVVPFLMGVCYFTIARTLMKPNIKISRPK 240  
 QY 241 VLTIVIVIFVITQLPYNIVKFCRAIDIIYSLITSCKMSKRMIDIAIQVTSIALFHSCLNP 300  
 DB 241 VLTIVIVIFVITQLPYNIVKFCRAIDIIYSLITSCKMSKRMIDIAIQVTSIALFHSCLNP 300  
 QY 301 ILVYFMGASFKNYVMKVAKKYGSWRQROSVVEFPDSEGTPEPTSTFSI 350  
 DB 301 ILVYFMGASFKNYVMKVAKKYGSWRQROSVVEFPDSEGTPEPTSTFSI 350

RESULT 12  
 ID AAB02835 standard; Protein; 350 AA.

XX AC AAB02835;

DT 22-AUG-2000 (first entry)

DE Human G protein coupled receptor hppri protein SEQ ID NO:24.

KM Human; G protein coupled receptor; GPCR; transmembrane receptor;  
 identification; agonist; screening; therapeutic; pharmaceutical;  
 mutant.

OS Homo sapiens.

XX PN MO200022131-A2.

XX PD 20-APR-2000.

XX PF 13-OCT-1999; 99WO-US24065.

XX PR 13-OCT-1998; 98US-0170496.

XX PR 12-NOV-1998; 98US-0108029.

XX PR 27-NOV-1998; 98US-0109213.

XX PR 16-FEB-1999; 99US-0120416.

XX PR 26-FEB-1999; 99US-0121852.

XX PR 12-MAR-1999; 99US-0123944.

XX PR 12-MAR-1999; 99US-0123945.

XX PR 12-MAR-1999; 99US-0123946.

XX PR 12-MAR-1999; 99US-0123948.

XX PR 12-MAR-1999; 99US-0123951.

XX PR 28-MAY-1999; 99US-0136436.

XX PR 28-MAY-1999; 99US-0136437.

XX PR 28-MAY-1999; 99US-0136439.

XX PR 28-MAY-1999; 99US-0137127.

XX PR 28-MAY-1999; 99US-0137131.

XX PR 30-JUN-1999; 99US-0137567.

XX PR 27-AUG-1999; 99US-0141448.

XX PR 03-SEP-1999; 99US-0152524.

XX PR 29-SEP-1999; 99US-0156633.

XX PR 29-SEP-1999; 99US-0156555.

XX PR 29-SEP-1999; 99US-0156634.

XX (AREN-) ARENA PHARM INC.

XX Behan DP, Lehmann-Brulmsma K, Chalmers DT, Chen R, Dang HT;  
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;  
 XX WPI, 2000-317986/27.  
 DR N-PSDB; AAA46029.  
 XX Non-endogenous, human G protein-coupled receptors for screening  
 PT receptor, inverse or partial agonists useful as therapeutic agents  
 PS Example 1; Page 99-100; 187pp; English.  
 XX

The present invention describes transmembrane receptors, preferably  
 CC human G protein coupled receptors (GPCR), for which the endogenous  
 CC ligand is unknown (orphan GPCR receptors). More specifically the present  
 CC invention relates to non-endogenous, constitutively activated versions  
 CC of a human GPCR. These non-endogenous human GPCRs can be useful for  
 CC the direct identification of candidate compounds as receptors agonists,  
 CC inverse agonists or partial agonists for use as pharmaceutical agents,  
 CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in  
 CC the exemplification of the present invention.

XX Sequence 350 AA;

Query Match 99.5%; Score 1810; DB 21; Length 350;  
 Best Local Similarity 99.4%; Pred. No. 2e-194;  
 Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLEONOSTDYVEENEMNGTYDYSOYEELICIKEDVREFAKFLPVFLTIYVIGLAGNS 60

DB 1 MLEONOSTDYVEENEMNGTYDYSOYEELICIKEDVREFAKFLPVFLTIYVIGLAGNS 60

QY 61 MVAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAVHGVWLGKIMCKITSALYT 120

DB 61 MVAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAVHGVWLGKIMCKITSALYT 120

QY 121 LNFVSGMOFLACISIDRYAVATKVPSSGVGKPCWITICFCVMAAILLSIPOLVFTYVND 180

DB 121 LNFVSGMOFLACISIDRYAVATKVPSSGVGKPCWITICFCVMAAILLSIPOLVFTYVND 180

QY 181 NARCIPIFPYVLTGSMKALLOMELICIGFVVPFLMGVCYFTIARTLMKPNIKISRPK 240

DB 181 NARCIPIFPYVLTGSMKALLOMELICIGFVVPFLMGVCYFTIARTLMKPNIKISRPK 240

QY 241 VLTIVIVIFVITQLPYNIVKFCRAIDIIYSLITSCKMSKRMIDIAIQVTSIALFHSCLNP 300

DB 241 VLTIVIVIFVITQLPYNIVKFCRAIDIIYSLITSCKMSKRMIDIAIQVTSIALFHSCLNP 300

QY 301 ILVYFMGASFKNYVMKVAKKYGSWRQROSVVEFPDSEGTPEPTSTFSI 350

DB 301 ILVYFMGASFKNYVMKVAKKYGSWRQROSVVEFPDSEGTPEPTSTFSI 350

RESULT 13

ID AAB37788 standard; Protein; 350 AA.

XX AC AAB37788;

DT 23-FEB-2001 (first entry)

XX DE Human TSC7.

XX Human; TSC; tuberous sclerosis complex; cytosolic; antimicrobial;  
 KM osteopathic; antitumor; antiaslomatic; antiallergic; neuroprotective;  
 KM cardiant; hypotensive; hypertensive; nootropic; anticonvulsant;  
 KM analgesic; tranquiliser; immunosuppressive; antiinflammatory;  
 KM gene therapy; TSC7; infection; cancer; autoimmune disorder;  
 XX Parkinson's disease; osteoporosis; neurological disorder.

XX OS Homo sapiens.

XX PN MO200064941-A2.

XX 02-NOV-2000.  
PD  
XX 21-APR-2000; 2000WO-US10979.  
PE  
XX 23-APR-1999; 99US-0130817.  
PR 20-APR-2000; 2000US-0556002.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Gould-Rothberg BE;  
XX  
DR WPI: 2000-679670/66.  
XX N-PSDB; AAC68722.  
PT Novel nucleic acid encoding G-protein coupled receptor for diagnosis  
PT and treatment of conditions associated with disorder in a G-protein  
PT mediated pathway such as cancer, neurological disorders and infections  
PT  
PS Claim 12; Page 8; 132pp; English.  
XX  
XX The present sequence is human tuberous sclerosis complex 7 (TSC7).  
CC TSC7 polynucleotides and polypeptides are useful for determining the  
CC presence or predisposition to a disease associated with altered levels of  
CC TSC7. TSC7 polynucleotides, polypeptides and antibodies specific for the  
CC polypeptide are useful for treating or preventing pathological conditions  
CC associated with the disorder in a G-protein mediated pathway. They are  
CC useful for diagnosing a hyperproliferative condition such as a neoplasm  
CC or dermatological condition. TSC7 nucleic acids and polypeptides are  
CC useful in the treatment of microbial infections, pain, cancer, anorexia,  
CC asthma, autoimmune disorders, Parkinson's disease, acute heart failure,  
CC hypotension, osteoporosis, multiple sclerosis, angina pectoris,  
CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy  
CC and psychotic and neurological disorders, including schizophrenia,  
CC dementia, severe mental retardation and dyskinesias, such as  
CC Huntington's disease and/or other pathologies and disorders. TSC7  
CC polypeptides are also useful as immunogens to produce antibodies and as  
CC vaccines.  
XX  
SQ Sequence 350 AA;  
Query Match 99.4%; Score 1808; DB 21; Length 350;  
Best Local Similarity 99.4%; Pred. No. 3.3e-194;  
Matches 348; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MALRQNSTDYRYEENMGTYDYSOYELICIKEDVREFAKFLPVLITVFIYGLAGNS 60  
DB 1 MALRQNSTDYRYEENMGTYDYSOYELICIKEDVREFAKFLPVLITVFIYGLAGNS 60  
QY 61 MVAIYAYKKQRTKTDVYIINLAVADLLFLTFPMAVNAHGVNLGKIMCKITSALT 120  
DB 61 MVAIYAYKKQRTKTDVYIINLAVADLLFLTFPMAVNAHGVNLGKIMCKITSALT 120  
QY 121 LNFVSGMQLACISIDRYAVATKVPVSGVGKPCMIICFCWMAAILLSIPQLVFTVND 180  
DB 121 LNFVSGMQLACISIDRYAVATKVPVSGVGKPCMIICFCWMAAILLSIPQLVFTVND 180  
QY 181 NARCIPIFPRILGTSMAQLIOMLEICIGFVVPFLIMGVCFITARTLMKPNIKISRLK 240  
DB 181 NARCIPIFPRILGTSMAQLIOMLEICIGFVVPFLIMGVCFITARTLMKPNIKISRLK 240  
QY 241 VLTFTVVFVITQLPYNIIVKFCRAIDIIYSILITSCNMSKMDIAIQVTSIALFHSCLNP 300  
DB 241 VLTFTVVFVITQLPYNIIVKFCRAIDIIYSILITSCNMSKMDIAIQVTSIALFHSCLNP 300  
QY 301 ILVFMGASFKNYVMKAKKXGWRQROSVSEEPFDSSEPTSTFSI 350  
DB 301 ILVFMGASFKNYVMKAKKXGWRQROSVSEEPFDSSEPTSTFSI 350

ID AAY57289 standard; Protein; 333 AA.  
XX  
XX AAY57289;  
AC  
XX 05-JUN-2000 (first entry)  
XX  
XX  
XX Human BGCR partial amino acid sequence.  
DE  
XX  
XX BGCR protein; G-protein coupled receptor; human; chemokine; exocytosis;  
XX cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;  
XX anti-allergic; antiviral.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO952945-A2.  
PN  
XX 21-OCT-1999.  
PD  
XX  
XX 16-APR-1999; 99WO-US08395.  
PF  
XX  
XX 16-APR-1998; 98US-0061753.  
PR 16-APR-1999; 99US-0061753.  
XX  
XX (MILL-) MILLENIUM PHARM INC.  
PA  
XX  
XX Gonzalo JA, Gutierrez-Ramos JC;  
PI  
XX  
XX WPI: 1999-620375/53.  
DR  
XX N-PSDB; AA290527.  
DR  
XX  
XX New nucleic acid encoding human BGCR receptor, used e.g. for  
XX modulating inflammation and tumor growth -  
XX  
XX Claim 1; Fig 1A-B; 123pp; English.  
PS  
XX  
XX The invention relates to a human BGCR protein, a G-protein coupled  
XX receptor. The BGCR protein can be expressed by standard recombinant  
XX methodology. BGCR are receptor proteins possibly involved in modulation  
XX of proinflammatory or stimulatory functions of chemokines; cell  
XX proliferation, migration, adhesion and targeting, and exocytosis. The  
XX BGCR nucleic acids and derived proteins (or their variants), antibodies  
XX and modulators are potentially useful for modulating inflammation;  
XX chemotactic activity of leucocytes; angiogenesis; cell proliferation;  
XX tumor growth; allergic reactions and entry of human immune deficiency  
XX virus into cells, for therapeutic or prophylactic purposes. They are also  
XX used for diagnosis and in drug-screening assays. The present sequence  
XX represents the sequence of a partial human BGCR protein.  
XX  
SQ Sequence 333 AA;  
Query Match 95.0%; Score 1728; DB 20; Length 333;  
Best Local Similarity 100.0%; Pred. No. 3e-185;  
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 18 NNGTIDYSGYELICIKEDVREFAKFLPVLITVFIYGLAGNSMVAIYAYKKQRTKTD 77  
DB 1 NNGTIDYSGYELICIKEDVREFAKFLPVLITVFIYGLAGNSMVAIYAYKKQRTKTD 77  
QY 78 VTIINLAVADLLFLTFPMAVNAHGVNLGKIMCKITSALTINLNFVSGMQLACISIDR 137  
DB 78 VTIINLAVADLLFLTFPMAVNAHGVNLGKIMCKITSALTINLNFVSGMQLACISIDR 137  
QY 138 YVAVTKVPSGSGVGKPCMIICFCWMAAILLSIPQLVFTVNDNARCIPIFPRILGTSMK 197  
DB 138 YVAVTKVPSGSGVGKPCMIICFCWMAAILLSIPQLVFTVNDNARCIPIFPRILGTSMK 197  
QY 198 ALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIKISRLKVLTVVITQLPYN 257  
DB 198 ALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIKISRLKVLTVVITQLPYN 257  
QY 258 IYKFCRAIDIIYSILITSCNMSKMDIAIQVTSIALFHSCLNPILYVFMGASFKNYVMKV 317  
DB 258 IYKFCRAIDIIYSILITSCNMSKMDIAIQVTSIALFHSCLNPILYVFMGASFKNYVMKV 317

QY 318 AKKXGWRQROSVSEEPFDESGTEPTSTFSI 350  
 |||||  
 Db 301 AKKXGWRQROSVSEEPFDESGTEPTSTFSI 333

RESULT 15  
 AAG67238  
 ID AAG67238 standard; Protein; 350 AA.

XX AAG67238;  
 AC

XX 13-NOV-2001 (first entry)  
 DT

XX Amino acid sequence of bovine chemokine receptor CCR11.  
 DE

XX Human; chemokine receptor; CCR11; G protein coupled receptor;  
 KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;  
 KW asthma; angiodysplasia; arteriosclerosis vascular association disease;  
 KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;  
 KW left ventricular diastolic dysfunction; migraine; preterm labour;  
 KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;  
 KW myocardial infarction; congestive heart failure; endometriosis;  
 KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.

XX Bos sp.  
 OS

XX MO200166598-A2.  
 PN

XX 13-SEP-2001.  
 PD

XX 05-MAR-2001; 2001WO-US07073.  
 PF

XX 03-MAR-2000; 2000US-0186928.  
 PR

XX 03-MAR-2000; 2000US-0187231.  
 PR

XX (ICOS-) ICOS CORP.  
 PA

XX Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;  
 PI

XX WPI; 2001-541918/60.  
 DR

XX N-PSDB; AAH77712.  
 DR

XX An isolated polynucleotide encoding the chemokine receptor CCR11,  
 PT useful for treating rheumatoid arthritis, inflammatory bowel disease,  
 PT asthma, angiodysplasia, arteriosclerosis, cardiac arrhythmias, Raynaud's  
 PT phenomenon and migraine -  
 PS phenomenon and migraine -

XX Example 1; Page 99-100; 110pp; English.

XX The present sequence represents the bovine chemokine receptor CCR11.  
 CC CCR11 is a member of the G protein coupled receptor family. A CCR11  
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11  
 CC expression or biological activity, is useful for treating many  
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory  
 CC bowel disease, and asthma. They are also useful for treating  
 CC angiogenesis, arteriosclerosis vascular association diseases which may  
 CC include but are not limited to hypertension, angina pectoris, cardiac  
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's  
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic  
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive  
 CC heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or  
 CC pulmonary vascular disease.

XX Sequence 350 AA;  
 SQ

XX Query Match 89.1%; Score 1620; DB 22; Length 350;  
 XX Best Local Similarity 86.0%; Pred. No. 4.2e-173;  
 XX Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEFQNSTYTYEENMNTYDYSOVELICTEDYREFAKVLPEFLTVFVIGLAGNS 60  
 |||||  
 Db 1 MAVEYNOSTYTYEENMNDTHDSQLEVICIKBEVAKFAKVLPEFLTVFVIGLAGNS 60

QY 61 MVVAIYAYKKKORTKTDVYIINLAVALDLLFTLPFMAVNAVHGVIKINCKITSAIYT 120  
 |||||  
 Db 61 TVVAIYAYKKKRTKTDVYIINLAVALDLLFTLPFMAVNAVHGVIKINCKITSAIYT 120  
 QY 121 LNFVSGQFLACISIDRVAVATKVPSSQGVKPCWIIICCVMAAIIILSTPOLVFYTVND 180  
 |||||  
 Db 121 VNFVSGQFLACISIDRVAVATKVPSSQGVKPCWIIICCVMAAIIILSTPOLVFYTVNH 180  
 QY 181 NARCTPIPRRYLGTSMKALIQMLEICIGFVVVPLIMGVCFITARTLMKPNIKISRLK 240  
 |||||  
 Db 181 KARCVPIPRRYLGTSMKASIQMLEICIGFIIIPILMAVCYFIIKTLMKNINIKKSQPLK 240  
 QY 241 VLLTVVIVIVITQLEPYNIVKFCRAIDIIYSILTSCNMRKDIAIQVETSLALFSCINP 300  
 |||||  
 Db 241 VLFVTVIVIVITQLEPYNIVKFCQAIIDIIYSILTDCDMSKMDVAIQITESIALFHSCLNP 300  
 QY 301 ILVYFMGASFKNVYKVAKKXGWRQROSVSEEPFDESGTEPTSTFSI 350  
 |||||  
 Db 301 VLYVFMGTSFKNVIKVAKKXGWRQROSVSEEPFDESGTEPTSTFSI 350

RESULT 16  
 AAY57291  
 ID AAY57291 standard; Protein; 350 AA.

XX AAY57291;  
 AC

XX 05-JUN-2000 (first entry)  
 DT

XX Mouse BGCR protein.  
 DE

XX BGCR protein; G-protein coupled receptor; human; chemokine; exocytosis;  
 KW cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;  
 KW anti-allergic; antiviral.

XX Mus sp.  
 OS

XX Key Location/Qualifiers  
 FH MISC-difference 170  
 FT MISC-difference /note= "encoded by ATN"

XX MO9952945-A2.  
 PN

XX 21-OCT-1999.  
 PD

XX 16-APR-1999; 99WO-US08395.  
 PF

XX 16-APR-1998; 98US-0061753.  
 PR

XX 16-APR-1999; 99US-0061753.  
 PR

XX (MILL-) MILLENITUM PHARM INC.  
 PA

XX Gonzalo JA, Gutierrez-Ramos JC;  
 PI

XX WPI; 1999-620375/53.  
 DR

XX N-PSDB; AAZ50529.  
 DR

XX New nucleic acid encoding human BGCR receptor, used e.g. for  
 PT modulating inflammation and tumor growth -  
 PT modulating inflammation and tumor growth -

XX Disclosure; Fig 3; 123pp; English.

XX The invention relates to a human BGCR protein, a G-protein coupled  
 CC receptor. The BGCR protein can be expressed by standard recombinant  
 CC methodology. BGCR are receptor proteins possibly involved in modulation  
 CC of proinflammatory or stimulatory functions of chemokines; cell  
 CC proliferation, migration, adhesion and targeting, and exocytosis. The  
 CC BGCR nucleic acids are potentially useful for modulating inflammation;  
 CC and modulators are potentially useful for modulating inflammation;  
 CC chemotactic activity of leucocytes; angiogenesis; cell proliferation;  
 CC tumour growth; allergic reactions and entry of human immune deficiency  
 CC virus into cells, for therapeutic or prophylactic purposes. They are also

CC used for diagnosis and in drug-screening assays. The present sequence  
CC represents the mouse BGCKr protein.

XX Sequence 350 AA;

Query Match 87.5%; Score 1591; DB 20; Length 350;  
Best Local Similarity 85.1%; Pred. No. 7.6e-170;  
Matches 298; Conservative 26; Mismatches 26; Indels 0; Gaps 0;

QY 1 MALRQNSTDYVYENNNKGYDSQVLLICEDVRFAPVLPVLTIVFVGLAGNS 60  
DB 1 MALEINQSAEYVYENNNKGYDSQVLLICEDVRFAPVLPVLTIVFVGLAGNS 60  
QY 61 MVVAIYAYKKQRTKTDVYIINLAVADLLFTLPFMAVNAVHGVGLKINCKITSA 120  
DB 61 VVAIYAYKKQRTKTDVYIINLAVADLLFTLPFMAVNAVHGVGLKINCKITSA 120  
QY 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGVKPCWITFCVWMAAILLSIPQLVFT 180  
DB 121 VNFVSGMOFLACISIDRYVAATKVPSSGSGVKPCWITFCVWMAAILLSIPQLVFT 180  
QY 181 NARCIPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIKISR 240  
DB 181 NARCIPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIKISR 240  
QY 241 VLLTVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCKNSKMDIAIQVTSIALFHSCL 300  
DB 241 VLLTVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCKNSKMDIAIQVTSIALFHSCL 300  
QY 301 ILVYFMGASFPYNYMKYAKKYGSROROSVVEFPDSGPTPTSTFST 350  
DB 301 ILVYFMGASFPYNYMKYAKKYGSROROSVVEFPDSGPTPTSTFST 350

## RESULT 17

AAY57292  
ID AAY57292 standard; Protein; 246 AA.

XX AC AAY57292;  
XX DT 05-JUN-2000 (first entry)

DE Human BGCKr protein fragment (residues 58-303).

KW BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;  
KW cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;  
KW anti-allergic; antiviral.

XX OS Homo sapiens.

XX PN WO952945-A2.

XX PD 21-OCT-1999.

XX PF 16-APR-1999; 99WO-US08395.

XX PR 16-APR-1998; 98US-0061753.

XX PA 16-APR-1999; 99US-0061753.

XX PA (MILL-) MILLENIUM PHARM INC.

XX PI Gonzalo JA, Gutierrez-Ramos JC;

XX DR WPI; 1999-620375/53.

XX PT New nucleic acid encoding human BGCKr receptor, used e.g. for  
XX modulating inflammation and tumor growth  
XX PS Disclosure; Fig 10; 123pp; English.

XX CC The invention relates to a human BGCKr protein, a G-protein coupled  
XX CC receptor. The BGCKr protein can be expressed by standard recombinant  
XX CC methodology. BGCKr are receptor proteins possibly involved in modulation

CC of proinflammatory or stimulatory functions of chemokines; cell  
CC proliferation, migration, adhesion and targeting, and exocytosis. The  
CC BGCKr nucleic acids and derived proteins (or their variants), antibodies  
CC and modulators are potentially useful for modulating inflammation;  
CC chemottractant activity of leucocytes; angiogenesis; cell proliferation;  
CC tumour growth; allergic reactions and entry of human immune deficiency  
CC virus into cells, for therapeutic or prophylactic purposes. They are also  
CC used for diagnosis and in drug-screening assays. The present sequence  
CC represents a human BGCKr protein fragment.

XX SQ Sequence 246 AA;

Query Match 70.1%; Score 1275; DB 20; Length 246;  
Best Local Similarity 100.0%; Pred. No. 1.4e-134;  
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 GNSMVAIYAYKKQRTKTDVYIINLAVADLLFTLPFMAVNAVHGVGLKINCKITSA 117  
DB 1 GNSMVAIYAYKKQRTKTDVYIINLAVADLLFTLPFMAVNAVHGVGLKINCKITSA 60  
QY 118 LXTNFGSGMOFLACISIDRYVAATKVPSSGSGVKPCWITFCVWMAAILLSIPQLVFT 177  
DB 61 LXTNFGSGMOFLACISIDRYVAATKVPSSGSGVKPCWITFCVWMAAILLSIPQLVFT 120  
QY 178 VNDNARCIPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIKISR 237  
DB 121 VNDNARCIPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIKISR 180  
QY 238 PLKVLITVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCKNSKMDIAIQVTSIALFHSCL 297  
DB 181 PLKVLITVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCKNSKMDIAIQVTSIALFHSCL 240  
QY 298 LNPILY 303  
DB 241 LNPILY 246

## RESULT 18

AAM99949  
ID AAM99949 standard; Protein; 242 AA.

XX AC AAM99949;

XX DT 04-JAN-2002 (first entry)

DE Human expressed polypeptide SEQ ID NO 73.

KW Human; nootropic; neuroprotective; cytoskeletal; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;  
KW antineumatic; hepatotropic; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;  
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; neurotropic; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO20015387-A1.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01310.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214886.



in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from [ftp.wipo.int/pmb/published\\_pct\\_sequences](http://wipo.int/pmb/published_pct_sequences).

**SQ Sequence 242 AA;**

Query Match	69.1%;	Score 1257;	DB 22;	Length 242;
Best Local Similarity	100.0%;	Pred. No. 1.5e-132;		
Matches 242;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	109	KIMKCTISALTINLNFVSGMOFLACISIDRYAVAVTKVPQSQSVGRPMWICPCVMAAILL	168
Db	1	KIMKCTISALTINLNFVSGMOFLACISIDRYAVAVTKVPQSQSVGRPMWICPCVMAAILL	60
QY	169	SIPOLVFYTVANDNARCIPFPRYLGTSMKALIQMLETIGFVVPPLINGVCYFPTARTLM	228
Db	61	SIPOLVFYTVANDNARCIPFPRYLGTSMKALIQMLETIGFVVPPLINGVCYFPTARTLM	120
QY	229	KMPNKRISRPLKVLITVIVIFVITQLPNINVKFCRAIDIIYSLLTSCMSGRMDIAIQVT	288
Db	121	KMPNKRISRPLKVLITVIVIFVITQLPNINVKFCRAIDIIYSLLTSCMSGRMDIAIQVT	180
QY	289	ESIALFHSCLNPIIYVFENGASFKNYVMKVAKKYGSWRQRQSVEEPPDSGTEPTSTF	348
Db	181	ESIALFHSCLNPIIYVFENGASFKNYVMKVAKKYGSWRQRQSVEEPPDSGTEPTSTF	240
QY	349	SI 350	
Db	241	SI 242	

	RESULT 19
AAV30126	
ID	AAV30126 standard; Protein; 263 AA.
AC	AAV30126;
XX	
DT	14-OCT-1999 (first entry)
XX	
DE	A seven-pass transmembrane receptor protein fragment.
XX	
KW	Seven-pass transmembrane receptor; autoimmune disease; white blood cell dysfunction.
OS	Mus musculus.
XX	
PN	WO933876-A1.
XX	
PD	08-JUL-1999.
XX	
PF	24-DEC-1998; 98WO-UP05886.
XX	
PR	24-DEC-1997; 97JP-0354537.
PA	(ASAH ) ASahi KASEI KOgyo KK.
XX	
PI	Ishimaru H, Koshio T, Ohno T;
XX	
DR	WPI; 1999-493806/41.
DR	N-PsDB; AAX86675.
TT	New seven-pass transmembrane receptor protein useful for treating preventing or diagnosing autoimmune diseases

XX Claim 14; Page 106-108; 118pp; Japanese.

CC The present sequence represents a murine seven-pass transmembrane  
CC receptor protein fragment. The protein and its DNA can be used to  
CC screen substances for the diagnosis, prevention and treatment of  
CC autoimmune diseases, particularly those due to white blood cell  
CC dysfunction.

SQ Sequence 263 AA;

Query Match	66.6%;	Score 1212;	DB 20;	Length 263;
Best Local Similarity	85.9%;	Pred. No. 1.8e-127;		
Matches 226;	Conservative 19;	Mismatches 18;	Indels 0;	Gaps 0;

Qy	88	LLLLFTLPFMAVNAVHGMVGIKMTKTSALTLEFVSGNQPLACISIDRYAVTKVPSQ	147
Db	1	LLLLITLPFMAVNAVHGMILGKMKCKTSLXYTNFVSGNQPLACISIDRYAITAPSQ	60
Qy	148	SGVGKPCWIIICECVMAAAILLSTIPOLVFYVYVNDNARCLPIFPFRYLGTSKALLIOMLEICI	207
Db	61	SGAGSPCWIICCCVMAAAILLSTIPOLFVYVYVNDNARCTPIFPFHLGTSKAASTOMLEIGI	120
Qy	208	GFVVVPELIMGVCYETFTARTMKMKNITSRPLKVLVLVVVVFIVTOLPYNYVKECRAIDI	267
Db	121	GFVVVPELIMGVCYASTARALIKMKNIKSRPLKVLVAVVVFIVTOLPYNVKVFCAIDA	180
Qy	268	LYSLITSCKMSKRMDDIAIQVTESIALFHSCLNPLLYVFMGASFRKNYMKVAKKYGYSWRQ	327
Db	181	LYLLITSCKMSKRMDDVAIQVTESIALFHSCLNPLLYVFMGASFRKNYIMKAKKYGYSWRQ	240
Qy	328	RSVSEEPPEPDEGTEPTSTESI	350
Db	241	RQNVSEELPDEGTEPTSTETI	267

	RESULT	20
XX	AB1162	
ID	AB1162 standard; peptide; 164 AA.	
XX		
AC	AB1162;	
XX		
DT	11-JAN-2002 (first entry)	
XX		
DE	Human orphan GPCR homologue, SEQ ID NO:1532.	
XX		
KW	Human; cytokine; cell proliferation; cell differentiation; growth factor	
KW	haematopoiesis regulation; tissue growth; immunomodulator; activin;	
KW	inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;	
KW	proliferation; metastasis; cancer; tumour; haematopoietic disorder;	
KW	myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;	
KW	chronic inflammatory condition; proliferative retinopathy;	
KW	atherosclerosis; coronary heart disease; arterial ischaemia;	
KW	bone disorder; osteoporosis; vascular growth disorder;	
KW	tissue regeneration; wound healing; infection; immune disorder;	
KW	cell culture; drug screening; gene therapy; anti-inflammatory;	
KW	antiaesthetic; antiarthritis; haemostatic; antiarteriosclerotic;	
KW	cytostatic; osteopathic; vasotropic; cardiact; virucide; antibacterial;	
KW	antifungal; vulnery; antitumor;	
XX		
OS	Homo sapiens.	
XX		
PN	WO200157188-A2.	
PD		
PF	09-AUG-2001.	
XX		
PP	05-FEB-2001; 2001WO-US03800.	
PR	03-FEB-2000; 2000US-0496914.	
PR	27-APR-2000; 2000US-0560875.	
XX		
PA	(HYSE-) HYSEQ INC.	
XX		

PI Tang YT, Liu C, Drmanac RT;  
XX WPI; 2001-457740/49.  
DR N-PSDB; ABA08406.  
XX  
PT Human proteins and DNA encoding sequences useful for preventing,  
PT treating or ameliorating a medical condition in a mammalian subject  
PT e.g. arthritis and cancer -  
XX  
PS Claim 20; Page 151; 1963pp; English.  
XX  
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
CC invention also relates to vectors and recombinant host cells comprising a  
CC nucleotide of the invention, methods of producing the novel polypeptides,  
CC antibodies against the polypeptides, methods of detecting the nucleotides  
CC or polypeptides in a sample, and methods of identifying compounds which  
CC bind to polypeptides of the invention. Although novel, many of the  
CC polypeptides of the invention have homology to known proteins, thereby  
CC giving an insight into their probable biological activities, and hence  
CC potential therapeutic applications. The polypeptides of the invention may  
CC have various activities, including cytokine, cell proliferation or cell  
CC differentiation activities; stem cell growth factor activity;  
CC haematopoiesis regulatory activity; tissue growth activity;  
CC immunomodulatory activity; activin- or inhibin-related activities;  
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
CC thrombolytic activities; receptor or ligand activities; or may be  
CC involved in oncogenesis, cancer cell proliferation or metastasis.  
CC Depending on their biological activities, polypeptides and nucleotides of  
CC the invention are useful for preventing, treating or ameliorating medical  
CC conditions, e.g., by protein or gene therapy. Such conditions include  
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
CC proliferative retinopathy, atherosclerosis, coronary heart disease, and  
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
CC vascular growth. Polypeptides involved with tissue regeneration and  
CC repair (or nucleic acids encoding them) may be used to promote wound  
CC healing (e.g., of burns, incisions and ulcers), while those with  
CC immunomodulatory activities may be used in the treatment of viral,  
CC bacterial and fungal infections in addition to immune disorders.  
CC Polypeptides with growth factor activity may be used in cell cultures to  
CC promote cell growth. For example, such polypeptides may be used to  
CC manipulate stem cells in culture to give rise to neuroepithelial cells  
CC that can be used to augment or replace cells damaged by illness,  
CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
CC may also be used in the diagnosis of the above conditions, and in drug  
CC screening techniques. The present sequence represents a novel human  
CC polypeptide of the invention.  
XX  
SQ Sequence 164 AA;  
Query Match 47.4%; Score 862; DB 22; Length 164;  
Best Local Similarity 100.0%; Pred. No. 1.9e-88;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
DT 06-NOV-2001 (first entry)  
XX  
XX Human protein SEQ ID NO 2956.  
DE  
XX  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation.  
XX  
OS Homo sapiens.  
XX  
XX WO200157190-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 05-FEB-2001; 2001WO-US04098.  
XX  
XX 03-FEB-2000; 2000US-0496914.  
XX 27-APR-2000; 2000US-0560875.  
XX 20-JUN-2000; 2000US-0598075.  
XX 19-JUL-2000; 2000US-0620325.  
XX 01-SEP-2000; 2000US-0654936.  
XX 15-SEP-2000; 2000US-0663561.  
XX 20-OCT-2000; 2000US-0693325.  
XX 30-NOV-2000; 2000US-0728422.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
XX  
DR WPI; 2001-476283/51.  
DR N-PSDB; AAK52443.  
PT Nucleic acids encoding polypeptides with cytokine-like activities,  
PT useful in diagnosis and gene therapy -  
XX  
PS Claim 20; Page 213; 6221pp; English.  
XX  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to  
XX cytokine, cell proliferation or cell differentiation or which may induce  
XX production of other cytokines in other cell populations. The  
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or  
XX peptide therapy. The polypeptides have various cytokine-like activities,  
XX e.g. stem cell growth factor activity, haematopoiesis regulating  
XX activity, tissue growth factor activity, immunomodulatory activity and  
XX activin/inhibin activity and may be useful in the diagnosis and/or  
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and  
XX inflammation.  
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
XX (AAM80020) are omitted as the relevant pages from the sequence listing  
XX were missing at the time of publication.  
XX  
SQ Sequence 164 AA;  
Query Match 47.4%; Score 862; DB 22; Length 164;  
Best Local Similarity 100.0%; Pred. No. 1.9e-88;  
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 22  
 AAB41786  
 ID AAB41786 standard; Protein, 159 AA.  
 AC AAB41786;  
 XX  
 DT 08-FEB-2001 (first entry)  
 DE Human ORFX ORF1550 polypeptide sequence SEQ ID NO:3100.  
 XX  
 KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
 KW vulnerey; antipariatic; antiparkinsonian; nootropic; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;  
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 KW hypotensive; dermatological; immunosuppressive; antineoplastic;  
 KW antiviral; antibacterial; antifungal; antineumatic; antithyroid;  
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 KW cholesterol ester storage; systemic lupus erythematosus; infection;  
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KW thrombosis; contraceptive.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200058473-A2.  
 PD 05-OCT-2000.  
 DE 31-MAR-2000; 2000WO-US08621.  
 PF 31-MAR-1999; 99US-0127607.  
 PR 02-APR-1999; 99US-0127636.  
 PR 05-APR-1999; 99US-0127728.  
 PR 30-MAR-2000; 2000US-0540763.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 P1 Shinkets RA, Leach M;  
 XX  
 DR N-PSDB; AAC75995.  
 DR  
 XX  
 PT Novel nucleic acids and peptides derived from open reading frame X,  
 PT useful for treating e.g. cancers, proliferative disorders,  
 PT neurodegenerative disorders and cardiovascular disease -  
 XX  
 PS Claim 11; Page 2318-2319; 5507pp; English.  
 XX  
 CC AAC74446 to AAC7606 encode the proteins given in AAB40237 to AAB43397,  
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 CC sequences have activities such as: cytostatic; hepatotropic; vulnerey;  
 CC antipariatic; antiparkinsonian; nootropic; neuroprotective;  
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
 CC immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;  
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
 CC antiinflammatory; antibacterial; antiviral; antifungal; antineumatic;  
 CC antithyroid; and antianaemic. The sequences can be used for determining  
 CC the presence of or predisposition to, or preventing or treating  
 CC pathological conditions associated with an ORFX-associated disorder. The  
 CC nucleic acids can be used to express ORFX proteins in gene therapy  
 CC vectors. The proteins and nucleic acids may be used to treat cancers,  
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral  
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance

CC coagulation; to inhibit thrombosis; and as a contraceptive.  
 XX  
 SO Sequence 159 AA.  
 XX  
 Query Match 45.3%; Score 824; DB 21; Length 159;  
 Best Local Similarity 99.4%; Pred. No. 3.4e-84;  
 Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 61 MVAIAYKKKQRTKTDVYILNLAVALDLEFTLPFMVNAHGVNLGKIMKITSALYT 120  
 DB 2 MVAIAYKKKQRTKTDVYILNLAVALDLEFTLPFMVNAHGVNLGKIMKITSALYT 61  
 QY 121 LNFVSGMQLACISIDRYAVATKVPSSGVRKPCWIIICFCVMAAILLSIPOLVFYTVND 180  
 DB 62 LNFVSGMQLACISIDRYAVATKVPSSGVRKPCWIIICFCVMAAILLSIPOLVFYTVND 121  
 QY 181 NARCIPIFPFYIGTSMKALIQMLEICIGFVVPFLIMGV 218  
 DB 122 NARCIPIFPFYIGTSMKALIQMLEICIGFVVPFLIMGV 159  
 RESULT 23  
 AAB87280  
 ID AAB87280 standard; Protein, 175 AA.  
 AC AAB87280;  
 XX  
 DT 05-JUN-2002 (first entry)  
 DE  
 XX  
 DE Novel central nervous system protein #190.  
 XX  
 KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
 KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;  
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
 KW endocrine disorder; diabetes; cancer; leukemia; neovascularisation;  
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
 KW myocardial infarction; wound healing; cell proliferation; skin aging;  
 KW food additive; food preservative; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200155318-A2.  
 PD 02-AUG-2001.  
 DE 17-JAN-2001; 2001WO-US01332.  
 PF 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
 PR 02-MAR-2000; 2000US-0186350.  
 PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 07-JUL-2000; 2000US-0216880.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 11-JUL-2000; 2000US-0217496.  
 PR 14-JUL-2000; 2000US-0218290.  
 PR 26-JUL-2000; 2000US-0220963.  
 PR 26-JUL-2000; 2000US-0220964.  
 PR 14-AUG-2000; 2000US-0224518.  
 PR 14-AUG-2000; 2000US-0224519.  
 PR 14-AUG-2000; 2000US-0225213.  
 PR 14-AUG-2000; 2000US-0225214.  
 PR 14-AUG-2000; 2000US-0225266.



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PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225477.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226688.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234227.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 25-SEP-2000; 2000US-0234999.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0244674.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251038.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
PT WPI; 2001-581633/65.  
DR N-PSDB; ABK43610.  
XX  
XX New isolated nucleic acid encoding a protein for diagnosing,  
PT preventing, treating or ameliorating medical conditions and used as  
PT food additives or preservatives -  
XX  
XX  
PS Claim 9; SEQ ID No 798; 837pp; English.  
XX  
XX The invention describes an isolated nucleic acid molecule (I) encoding a  
CC novel central nervous system protein. (I) and polypeptides (III) encoded  
CC by (I), are used to treat a medical conditions and in diagnosis of a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and  
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
CC adenocarcinomas and irritable bowel syndrome, reproductive system  
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
CC leukaemia, disorders involving neovascularisation e.g. malignancies,  
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
CC acute kidney failure and blood related disorders e.g. myocardial  
CC infarction. The polypeptides can also be used to aid wound healing and  
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to

CC maintain organs before transplantation, for supporting cell culture of  
CC primary tissues, to regenerate tissues and in chemoraxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities, fat content, lipid, protein,  
Query Match 41.8%; Score 761; DB 22; Length 175;  
Best Local Similarity 96.1%; Pred. No. 4.6e-77;  
Matches 148; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 197 KALLMLEICIGFVPEILMGVCYFITARTMKMKNISRLPLVLTIVVFIPTOLPY 256  
:::  
DB 22 ESISMEDICIGFVPEILMGVCYFITERLTKMKNISRLPLVLTIVVFIPTOLPY 81  
QY 257 NIVKRCRAIDIIYSLITSCNMSKMDIAIQVTESTALPHSCINPLIVYMGASFRNYVMK 316  
82 NIVKRCRAIDIIYSLITSCNMSKMDIAIQVTESTALPHSCINPLIVYMGASFRNYVMK 141  
DB 317 VAKKYGSRORQSVSEFPFDESEPTSTFSI 350  
142 VAKKYGSRORQSVSEFPFDESEPTSTFSI 175  
Db  
RESULT 24  
AAM9976  
ID AAM9976 standard; Protein; 175 AA.  
XX  
AC AAM9976;  
XX  
DT 04-JAN-2002 (first entry)  
XX  
DE Human expressed polypeptide SEQ ID NO 100.  
XX  
KW Human; nootropic; neuroprotective; cytosolic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnereary;  
KW antiparkinsonian; antispasmodic; antianemic; antirheumatic; cancer;  
KW antitubercular; hepatoprotective; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antitumor; anticomvulsant; antifungal;  
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN WO20015387-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01310.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
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PR 11-JUL-2000; 2000US-0217487.  
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PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
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PR 23-AUG-2000; 2000US-0227009.  
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PR 01-SEP-2000; 2000US-0228287.  
PR 01-SEP-2000; 2000US-0229343.  
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PR 01-SEP-2000; 2000US-0229345.  
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PR 08-SEP-2000; 2000US-0231245.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
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PR 14-SEP-2000; 2000US-0232397.  
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PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
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PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
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PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
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PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
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PR 20-OCT-2000; 2000US-0241826.  
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PR 08-NOV-2000; 2000US-0246474.  
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08-NOV-2000; 2000US-0246528.  
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 PR 08-NOV-2000; 2000US-0246609.  
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 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
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 PR 06-DEC-2000; 2000US-0256719.  
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 PR 05-JAN-2001; 2000US-0259678.  
 (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 WPI, 2001-465573/50.  
 DR N-PSDB; AAI99588.  
 DR  
 XX  
 PT Isolated digestive system associated polypeptide for treating,  
 PT preventing and/or prognosing disorders related to the digestive system  
 PT including digestive system cancers and also for testing and detection  
 PT e.g. diagnosis -  
 PS  
 XX Claim 11; SEQ ID NO 100; 509pp + Sequence Listing; English.  
 XX  
 CC The invention relates to novel genes (AAI99548-AAI99604) and proteins  
 CC (AAI99936-AAI99984) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, diabetes mellitus, Crohn's  
 CC haemolytic anaemia, autoimmune thyroiditis, allergies, autoimmune  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasitic infections.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX Sequence 175 AA;  
 SQ

Query Match 41.8%; Score 761; DB 22; Length 175;  
 Best Local Similarity 96.1%; Pred. No. 4,6e-77;  
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 Db 22 ESIDSMLEICIGFVVPFLIMGVCYITERTLMKPNKIKISRPKVLTVVIVITOLPY 81  
 QY 257 NIVKFCRAIDITYSLITSCNNSKMDIAIQVTESIALFHSCLNPILYVFMGASFGNYWK 316  
 Db 82 NIVKFCRAIDITYSLITSCNNSKMDIAIQVTESIALFHSCLNPILYVFMGASFGNYWK 141  
 QY 317 VAKKYSWRRQRQSVSEEPFDESGPTSTPSI 350  
 Db 142 VAKKYSWRRQRQSVSEEPFDESGPTSTPSI 175  
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 AC ABB10276;  
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 DE Human CDNA SEQ ID NO: 584.  
 XX  
 KW Human; gene therapy; neural disorder; immune system disorder;  
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
 KW pulmonary disorder; cardiovascular disorder; renal disorder;  
 KW proliferative disorder; inflammation.  
 OS Homo sapiens.  
 XX  
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 XX 02-AUG-2001.  
 PF 17-JAN-2001; 2001WO-US01349.  
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DT 21-NOV-2001 (first entry)  
XX  
DE Novel human uterine motility-association polypeptide #22.  
XX Human; uterine motility-association disorder; uterus; pregnancy;  
KW labour; menstrual cycle; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FN WO200155201-A1.  
PD  
XX 02-AUG-2001.  
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PF 17-JAN-2001; 2001WO-US01317.  
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PR 05-JAN-2001; 2001US-0259678.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX WPI; 2001-451936/48.  
 DR N-PSDB; AAG29590.  
 XX  
 PT Isolated polypeptide for treating, preventing and/or prognosing  
 PT disorders of the endocrine system such as reproductive disorders,  
 PT endocrine cancers and also for testing and detection e.g. diagnosis -  
 XX  
 PS Claim 11; SEQ ID NO 316; 604pp; English.  
 XX  
 CC Sequences AAU18669-AAU18670 represent endocrine polypeptides of the  
 CC invention. Endocrine polypeptides and their associated polynucleotides  
 CC are useful in the diagnosis, treatment and prevention of various types of  
 CC disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
 CC chickens or sheep. A pathological condition can be determined by  
 CC determining the presence or absence of a mutation in an endocrine  
 CC polynucleotide. The treatable disorders include autoimmune diseases such  
 CC as rheumatoid arthritis, hyperproliferative disorders such as cardiac arrest,  
 CC of the breast or liver, cardiovascular disorders such as nervous system  
 CC cerebrovascular disorders such as cerebral ischaemia, nervous system  
 CC disorders such as Alzheimer's disease, infections caused by bacteria,  
 CC viruses and fungi, ocular disorders such as corneal infection, endocrine  
 CC disorders such as Crohn's disease, renal disorders such as  
 CC glomerulonephritis and respiratory disorders such as asthma. The  
 CC polypeptides can also be used to aid wound healing, to prevent skin aging  
 CC due to sunburn, to maintain organs before transplantation, to regenerate  
 CC tissues and in chemotaxis. The polypeptides can also be used as a food  
 CC additive or preservative to increase or decrease storage capabilities.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

Query Match 41.8%; Score 761; DB 22; Length 175;  
 Best Local Similarity 96.1%; Pred. No. 4,6e-77;  
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QY 197 KALIQMLEICIGFVPLNGVCYFTTARTLMKMPKIKSRPKVLLTVIVIVTQLPY 256  
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 DB 22 ESIDSMLEICIGFVPLNGVCYFTTERTLMKMPKIKSRPKVLLTVIVIVTQLPY 81

QY 257 NIYKFCRAIDIIYSLITSCNMSKRMIDIAIOVTSIALFSGCLNPIIYVFMGASFKKYVWK 316  
 |||  
 DB 82 NIYKFCRAIDIIYSLITSCNMSKRMIDIAIOVTSIALFSGCLNPIIYVFMGASFKKYVWK 141

QY 317 VAKKYGSMRRQROSVBEFPDSEGPTEPTSTFSI 350  
 |||  
 DB 142 VAKKYGSMRRQROSVBEFPDSEGPTEPTSTFSI 175

RESULT 28  
 AAU18669  
 ID AAU18669 standard; Protein; 175 AA.  
 XX  
 AC AAU18669;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 XX Renal and cardiovascular-associated protein, Seq ID 108.  
 DE  
 XX  
 KW Human; antiinflammatory; neuroprotective; immunomodulatory; vulnery;  
 KW cardiovascular; cytosolic; nephroprotective; antianemic; nephritis;  
 KW immunosuppressive; kidney disorder; renal failure; hypertension;  
 KW cardiovascular disorder; myocardial infarction; blood disorder; anaemia;  
 KW blood coagulation disorder; electrolyte imbalance disorder; cancer;  
 KW hypotension; hyperkalaemia; neoplastic disease; nephroma;  
 KW autoimmune disease; inflammatory disease; reproductive system disorder;  
 KW endocrine disorder; neural activity; neurological disorder;

KW	wound healing; respiratory disorder.	PR	25-SEP-2000; 2000US-0234998.
XX		PR	26-SEP-2000; 2000US-0235484.
OS	Homo sapiens.	PR	27-SEP-2000; 2000US-0235834.
XX		PR	27-SEP-2000; 2000US-0235836.
PN	WO200155328-A2.	PR	29-SEP-2000; 2000US-0236327.
XX		PR	29-SEP-2000; 2000US-0236367.
PD	02-AUG-2001.	PR	29-SEP-2000; 2000US-0236368.
XX		PR	29-SEP-2000; 2000US-0236369.
PF	17-JAN-2001; 2001WO-US01359.	PR	29-SEP-2000; 2000US-0236370.
XX		PR	02-OCT-2000; 2000US-0237037.
XX		PR	02-OCT-2000; 2000US-0237038.
PR	31-JAN-2000; 2000US-0179065.	PR	02-OCT-2000; 2000US-0237039.
PR	04-FEB-2000; 2000US-0180628.	PR	02-OCT-2000; 2000US-0237040.
PR	24-FEB-2000; 2000US-0184664.	PR	13-OCT-2000; 2000US-0239935.
PR	02-MAR-2000; 2000US-0186350.	PR	13-OCT-2000; 2000US-0239937.
PR	16-MAR-2000; 2000US-0189874.	PR	20-OCT-2000; 2000US-0240960.
PR	17-MAR-2000; 2000US-0190076.	PR	20-OCT-2000; 2000US-0241221.
PR	18-APR-2000; 2000US-0198123.	PR	20-OCT-2000; 2000US-0241785.
PR	19-MAY-2000; 2000US-0205515.	PR	20-OCT-2000; 2000US-0241786.
PR	07-JUN-2000; 2000US-0209467.	PR	20-OCT-2000; 2000US-0241787.
PR	28-JUN-2000; 2000US-0214886.	PR	20-OCT-2000; 2000US-0241809.
PR	30-JUN-2000; 2000US-0215135.	PR	20-OCT-2000; 2000US-0241826.
PR	07-JUL-2000; 2000US-0216647.	PR	01-NOV-2000; 2000US-0244617.
PR	07-JUL-2000; 2000US-0216880.	PR	08-NOV-2000; 2000US-0246474.
PR	11-JUL-2000; 2000US-0217487.	PR	08-NOV-2000; 2000US-0246475.
PR	11-JUL-2000; 2000US-0217496.	PR	08-NOV-2000; 2000US-0246476.
PR	14-JUL-2000; 2000US-0218290.	PR	08-NOV-2000; 2000US-0246477.
PR	26-JUL-2000; 2000US-0220963.	PR	08-NOV-2000; 2000US-0246524.
PR	26-JUL-2000; 2000US-0220964.	PR	08-NOV-2000; 2000US-0246525.
PR	14-AUG-2000; 2000US-0224518.	PR	08-NOV-2000; 2000US-0246526.
PR	14-AUG-2000; 2000US-0224519.	PR	08-NOV-2000; 2000US-0246527.
PR	14-AUG-2000; 2000US-0225213.	PR	08-NOV-2000; 2000US-0246528.
PR	14-AUG-2000; 2000US-0225214.	PR	08-NOV-2000; 2000US-0246532.
PR	14-AUG-2000; 2000US-0225215.	PR	08-NOV-2000; 2000US-0246609.
PR	14-AUG-2000; 2000US-0225216.	PR	08-NOV-2000; 2000US-0246610.
PR	14-AUG-2000; 2000US-0225217.	PR	08-NOV-2000; 2000US-0246611.
PR	14-AUG-2000; 2000US-0225268.	PR	17-NOV-2000; 2000US-0249217.
PR	14-AUG-2000; 2000US-0225270.	PR	17-NOV-2000; 2000US-0249218.
PR	14-AUG-2000; 2000US-0225447.	PR	17-NOV-2000; 2000US-0249219.
PR	14-AUG-2000; 2000US-0225757.	PR	17-NOV-2000; 2000US-0249220.
PR	14-AUG-2000; 2000US-0225758.	PR	17-NOV-2000; 2000US-0249221.
PR	14-AUG-2000; 2000US-0225759.	PR	17-NOV-2000; 2000US-0249221.
PR	18-AUG-2000; 2000US-0226279.	PR	17-NOV-2000; 2000US-0249221.
PR	22-AUG-2000; 2000US-0226681.	PR	17-NOV-2000; 2000US-0249221.
PR	22-AUG-2000; 2000US-0226688.	PR	17-NOV-2000; 2000US-0249221.
PR	22-AUG-2000; 2000US-0226868.	PR	17-NOV-2000; 2000US-0249221.
PR	22-AUG-2000; 2000US-0227182.	PR	17-NOV-2000; 2000US-0249221.
PR	23-AUG-2000; 2000US-0227009.	PR	17-NOV-2000; 2000US-0249221.
PR	30-AUG-2000; 2000US-0228924.	PR	17-NOV-2000; 2000US-0249221.
PR	01-SEP-2000; 2000US-0229287.	PR	17-NOV-2000; 2000US-0249221.
PR	01-SEP-2000; 2000US-0229293.	PR	17-NOV-2000; 2000US-0249221.
PR	01-SEP-2000; 2000US-0229344.	PR	17-NOV-2000; 2000US-0249221.
PR	01-SEP-2000; 2000US-0229345.	PR	17-NOV-2000; 2000US-0249221.
PR	05-SEP-2000; 2000US-0229509.	PR	17-NOV-2000; 2000US-0249221.
PR	05-SEP-2000; 2000US-0229513.	PR	17-NOV-2000; 2000US-0249221.
PR	06-SEP-2000; 2000US-0230437.	PR	17-NOV-2000; 2000US-0249221.
PR	06-SEP-2000; 2000US-0230438.	PR	17-NOV-2000; 2000US-0249221.
PR	06-SEP-2000; 2000US-0231242.	PR	17-NOV-2000; 2000US-0249221.
PR	08-SEP-2000; 2000US-0231243.	PR	17-NOV-2000; 2000US-0249221.
PR	08-SEP-2000; 2000US-0231244.	PR	17-NOV-2000; 2000US-0249221.
PR	08-SEP-2000; 2000US-0231244.	PR	17-NOV-2000; 2000US-0249221.
PR	08-SEP-2000; 2000US-0231413.	PR	17-NOV-2000; 2000US-0249221.
PR	08-SEP-2000; 2000US-0231414.	PR	17-NOV-2000; 2000US-0249221.
PR	08-SEP-2000; 2000US-0232060.	PR	17-NOV-2000; 2000US-0249221.
PR	08-SEP-2000; 2000US-0232081.	PR	17-NOV-2000; 2000US-0249221.
PR	12-SEP-2000; 2000US-0231968.	PR	01-DEC-2000; 2000US-0250160.
PR	14-SEP-2000; 2000US-0232397.	PR	01-DEC-2000; 2000US-0250391.
PR	14-SEP-2000; 2000US-0232398.	PR	05-DEC-2000; 2000US-0251030.
PR	14-SEP-2000; 2000US-0232399.	PR	05-DEC-2000; 2000US-0251988.
PR	14-SEP-2000; 2000US-0232400.	PR	05-DEC-2000; 2000US-0256719.
PR	14-SEP-2000; 2000US-0232401.	PR	06-DEC-2000; 2000US-0251479.
PR	14-SEP-2000; 2000US-0233063.	PR	08-DEC-2000; 2000US-0251856.
PR	14-SEP-2000; 2000US-0233064.	PR	08-DEC-2000; 2000US-0251868.
PR	14-SEP-2000; 2000US-0233065.	PR	08-DEC-2000; 2000US-0251869.
PR	21-SEP-2000; 2000US-0234223.	PR	08-DEC-2000; 2000US-0251989.
PR	21-SEP-2000; 2000US-0234274.	PR	11-DEC-2000; 2000US-0254097.
PR	25-SEP-2000; 2000US-0234997.	PR	05-JAN-2001; 2001US-0259678.



XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI: 2001-488787/53.  
XX N-ESDB: AAS30190.  
XX  
XX New polynucleotides and polypeptides, useful for diagnosing, treating,  
XX preventing or prognosing e.g. kidney, cardiovascular, blood,  
XX electrolyte imbalance or neoplastic disorders, autoimmune diseases,  
XX cancers -  
XX  
XX Claim 1; SEQ ID No 108; 506bp; English.  
XX  
XX The invention relates to novel nucleic acids and polypeptides useful for  
XX diagnosing, treating, preventing and/or prognosing disorders related to  
XX these polypeptides. The polynucleotides are especially useful in the  
XX diagnosis, prognosis, prevention and/or treatment of diseases which  
XX include kidney disorders (e.g. renal failure or nephritis),  
XX cardiovascular disorders (e.g. hypertension or myocardial infarction),  
XX blood disorders (e.g. anaemia or blood coagulation disorders),  
XX electrolyte imbalance disorders (e.g. hyponatraemia or hyperkalaemia),  
XX neoplastic disorders (e.g. nephroma or renal cell cancer), autoimmune  
XX diseases, cancers, inflammatory diseases, reproductive system  
XX disorders, endocrine disorders, neural activity and neurological  
XX disorders, wound healing and respiratory disorders. AAU18644-AAU18715  
XX represent the novel human renal and cardiovascular-associated amino  
XX acid sequences of the invention. Note: The sequence data for this patent  
XX did not form part of the printed specification, but was obtained in  
XX electronic format directly from WIPO at:  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 175 AA:  
SQ  
Query Match 41.8%; Score 761; DB 22; Length 175;  
Best Local Similarity 96.1%; Pred. No. 4.6e-77;  
Matches 148; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 197 KALIMLEICIFVVPFLIMGVCYFITTARTLMKMNKISRLKLLTVVIVITOLPY 256  
DB 22 ESIDSLTEICIGFVVPFLIMGVCYFITTERTLMKMNKISRLKLLTVVIVITOLPY 81  
QY 257 NIVKPCRAIDIIYSLITSCNMSKMDIAIQVTSIALPHSCNPLIYYFMGASFGNYVMK 316  
DB 82 NIVKPCRAIDIIYSLITSCNMSKMDIAIQVTSIALPHSCNPLIYYFMGASFGNYVMK 141  
QY 317 VAKKYGWROROSVSEFPFDESGPTEPTSTFSI 350  
DB 142 VAKKYGWROROSVSEFPFDESGPTEPTSTFSI 175  
RESULT 29  
AAU21655  
ID AAU21655 standard; Protein; 175 AA.  
XX  
XX AAU21655;  
XX  
XX 06-DEC-2001 (first entry)  
XX  
XX Novel human neoplastic disease associated polypeptide #88.  
XX  
XX Human; neoplastic disease associated polypeptide; cancer;  
XX hyperproliferative disorder; neural disorder; immune system disorder;  
XX muscular disorder; reproductive disorder; gastrointestinal disorder;  
XX pulmonary disorder; cardiovascular disorder; renal disorder;  
XX neuroprotective; cytostatic; anti inflammatory; vasotropic.  
XX  
XX Homo sapiens.  
XX  
XX WO200155163-A1.  
XX  
XX 02-AUG-2001.  
PD

XX  
PF 17-JAN-2001; 2001WO-US01358.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
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PR 14-JUL-2000; 2000US-0218290.  
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PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226688.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231343.  
PR 08-SEP-2000; 2000US-0231444.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.

PR	29-SEP-2000	2000US-0263369
PR	29-SEP-2000	2000US-0263710
PR	02-OCT-2000	2000US-0236802
PR	02-OCT-2000	2000US-0237037
PR	02-OCT-2000	2000US-0237038
PR	02-OCT-2000	2000US-0237040
PR	02-OCT-2000	2000US-0237049
PR	13-OCT-2000	2000US-0239935
PR	13-OCT-2000	2000US-0239937
PR	20-OCT-2000	2000US-0240960
PR	20-OCT-2000	2000US-0241021
PR	20-OCT-2000	2000US-0241122
PR	20-OCT-2000	2000US-0241785
PR	20-OCT-2000	2000US-0241786
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PR	08-NOV-2000	2000US-0246524
PR	08-NOV-2000	2000US-0246525
PR	08-NOV-2000	2000US-0246526
PR	08-NOV-2000	2000US-0246527
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PR	08-NOV-2000	2000US-0246609
PR	08-NOV-2000	2000US-0246610
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PR	17-NOV-2000	2000US-0249207
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PR	17-NOV-2000	2000US-0249244
PR	17-NOV-2000	2000US-0249245
PR	17-NOV-2000	2000US-0249254
PR	17-NOV-2000	2000US-0249255
PR	17-NOV-2000	2000US-0249257
PR	17-NOV-2000	2000US-0249259
PR	17-NOV-2000	2000US-0249300
PR	01-DEC-2000	2000US-0250160
PR	01-DEC-2000	2000US-0250391
PR	05-DEC-2000	2000US-0251030
PR	05-DEC-2000	2000US-0251988
PR	05-DEC-2000	2000US-0251988
PR	06-DEC-2000	2000US-0256179
PR	08-DEC-2000	2000US-0251856
PR	08-DEC-2000	2000US-0251856
PR	08-DEC-2000	2000US-0251869
PR	08-DEC-2000	2000US-0251989
PR	08-DEC-2000	2000US-0251990
PR	11-DEC-2000	2000US-0254097
PR	05-JAN-2001	2001US-0256978
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX	Rosen CA, Bairash SC, Ruben SM	
XX	WPI, 2001-465558/50,	
PR	N-PSDB, AAS34851.	

XX Novel polypeptides and polynucleotides useful as diagnostic reagents to  
PT diagnose diseases or disorders associated with aberrant expression or  
PT activity of polypeptides, and for treating cancers, Rheumatoid  
PT arthritis -  
XX  
XX  
PS Claim 11; SEQ ID No 382; 687bp; English.

XX  
CC The present invention relates to the isolation of novel human neoplastic  
CC disease associated polypeptides, and cDNA (AA334767-AA35050) and DNA  
CC sequences encoding for these polypeptides. The sequences of the  
CC invention are useful in the diagnosis, treatment, prevention of and/or  
CC prognosis of disorders involving neoplastic disease such as  
CC hyperproliferative disorders (e.g. leukemia, bone cancer, bladder  
CC cancer, brain stem glioma, adult liver cancer, childhood cerebellar  
CC astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may  
CC also be useful for treating other disorders such as neural disorders,  
CC immune system disorders, muscular disorders, reproductive disorders,  
CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders  
CC and renal disorders. The polynucleotide sequences of the invention are  
CC also useful in gene therapy. AAU21566-AAU21851 represent the novel human  
CC neoplastic disease associated polypeptides of the invention.

CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp.wipo.int/pubid/published\\_pct\\_sequences](http://wipo.int/pubid/published_pct_sequences).

XX  
XX  
XX Sequence 175 AA;

	Query Match	41.8%	Score 761	DB 22	Length 175
	Best Local Similarity	96.1%	Pred. No. 4.6e-77		
	Matches 146	Conservative	3	Mismatches 3	Indels 0
				Gaps	0
Qy	197	KALLQMLEICGVVVFPELLMGVCYFETARTLMPKNIKISRPKLVTLLVIVFIVTLPY	256		
	:::				
Db	22	ESIDSMLEICGVVVFPELLMGVCYFETERTLMPKNIKISRPKLVTLLVIVFIVTLPY	81		
Qy	257	NIYFECRAIDIIYSLITSCNMSKRMIDAIQVTESTIALPHSCINDIIVYFGASFKNYVMK	316		
Db	82	NIYFECRAIDIIYSLITSCNMSKRMIDAIQVTESTIALPHSCINDIIVYFGASFKNYVMK	141		
Qy	317	VAKYGSWRKQROSVEEFPDSEGTPELTSTFSI	350		
Db	142	VAKYGSWRKQROSVEEFPDSEGTPELTSTFSI	175		

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RESULT 30
AAR53745
ID AAR53745 standard; Protein; 358 AA.
XX
XX AAR53745;
AC
XX
DT 02-FEB-1995 (first entry)
XX
DE Partial sequence of seven transmembrane receptor (V31) .
XX
KW Primer; seven transmembrane receptor; receptor; amplification; PCR
KM polymerase chain reaction.
XX
XX Homo sapiens.
OS
XX
XX MO9412635-A.
PN
XX
XX 09-JUN-1994.
PD
XX
XX 17-NOV-1993; 93WO-US1153.
PF
XX
XX 17-NOV-1992; 92US-0977452.
PR
XX
XX (ICOS-) ICOS CORP.
PA
XX
PI Godiska R, Gray PW, Schweickart VL;
XX
XX WPI; 1994-200264/24.
XX

```

DR N-PSDB; AA066162.

XX DNA encoding seven transmembrane receptors - used to develop  
PT prods. for use as therapeutic or diagnostic agents for conditions  
PT involving the receptors.

PS Example 3; Page 56-57; 100pp; English.

XX Two primers (AA066148, AA066149) were used to amplify human genomic DNA  
CC purified from leukocytes. Approximately 1000 clones were isolated  
CC after the initial amplification reaction and probed with sequences  
CC specific for seven transmembrane receptors IL8R1, A2R and R20.

CC Clones which did not hybridize were then chosen for sequence  
CC analysis. Three new clones were identified that appeared to encode  
CC seven transmembrane receptor segments. Two more primers (AA066151,  
CC AA066152) were used to isolate a full length version of one of these  
CC clones designated V31 (See AA066153). This is the sequence encoded  
CC by exon 3 of the V31 genomic clone

XX Sequence 358 AA;

Query Match 36.2%; Score 659; DB 15; Length 358;

Best Local Similarity 38.7%; Pred. No. 3.3e-65;  
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MAFENOSTDYVENEMNGTYDYSQYELICIKEDVREFAKVLPVLTIVFVIGLAGNS 60

DB 1 VCLCODEVTDDYIGDNT---TVDYTLFESLSCKVDNRNFKAMFLPIMYSIICFVGGLGNG 57

QY 61 MVVAIYAYYKORTKTDVYILNLAVADLLFLTPFMAVNAVHGVGLKIMCKITSALYT 120

DB 58 LVVLTYIFKRLKMTDYLNLAVADLLFLTLTPFMAVSAKSWVFGVHCKLIFAIYK 117

QY 121 INFVSGMQLACISIDRYAVATKVP---QSGVGKPCWIIICFCVMAAIIISIPOLVFY 176

DB 118 MSFSSGMLLILCISIDRYVAIVQAVSAHRARVLLISKSCVGMILATVLSIPELLYS 177

QY 177 TVNDNA-----RCIPFPRYLGTSMKALIQMLEICIGFVPLINGVCYFTARTLMKP 231

DB 178 DIORSSSEQAMRCSLITEH---VEAFITIOVAQWIGFVPLILAMSCYLVIRITLQAR 234

QY 232 NIKISRPKLVLTVYIVFYTQLPYNIYKFCRAIDIIYSLTSCNMSKRMIDIAIOVTESEI 291

DB 235 NFERKAIKVIIVAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIAVDVYSL 294

QY 292 ALFHSCLNPLIYVEMGASFKNYVMKAKKYG-----SW-----RRORQSVBERFPD 337

DB 295 ACVRCCVNPFLIYAFIGVKFRNDLFKLFKDLGCLSQEQLRQWSSCRHRRSSMSVE----- 349

QY 338 SEGPTPEPTSTFS 349

DB 350 ----AETTTTFS 357

RESULT 31

ID AAB21689 standard; Protein; 358 AA.

AC AAB21689;

DT 26-JAN-2001 (first entry)

DE Human 7TM receptor V31-B cDNA clone exon 1 protein.

XX Seven transmembrane receptor; 7TM; heptahelical; serpentine;

KW G-protein-coupled; V28; V31; V112; R20; R2; R12; R3; gene therapy;

XX cancer.

OS Homo sapiens.

XX US6107475-A.

XX PD 22-AUG-2000.

XX 26-APR-1999; 99US-0299843.

XX 17-MAY-1994; 94US-0245242.

PR 01-JUN-1998; 98US-0088337.

PR 17-NOV-1992; 92US-0977452.

PR 17-NOV-1993; 93US-0153848.

XX (ICOS-) ICOS CORP.

PI Schneickart VL, Gray PW, Godiska R;

DR WPI; 2000-571335/53.

DR N-PSDB; AAA91709.

XX Polynucleotide encoding seven transmembrane receptors, antibody

PT specific to the receptor, agonist and antagonist of the receptor useful

PT for treating inflammation in a mammal

XX Example 3; Columns 49-52; 61pp; English.

XX The present sequence is a novel seven transmembrane (7TM) receptors

CC (also known as heptahelical, serpentine or G-protein-coupled receptors).

CC The coding sequence for the present sequence may be used for gene

CC therapy for diseases such as cancer.

XX Sequence 358 AA;

Query Match 36.2%; Score 659; DB 21; Length 358;

Best Local Similarity 38.7%; Pred. No. 3.3e-65;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MAFENOSTDYVENEMNGTYDYSQYELICIKEDVREFAKVLPVLTIVFVIGLAGNS 60

DB 1 VCLCODEVTDDYIGDNT---TVDYTLFESLSCKVDNRNFKAMFLPIMYSIICFVGGLGNG 57

QY 61 MVVAIYAYYKORTKTDVYILNLAVADLLFLTPFMAVNAVHGVGLKIMCKITSALYT 120

DB 58 LVVLTYIFKRLKMTDYLNLAVADLLFLTLTPFMAVSAKSWVFGVHCKLIFAIYK 117

QY 121 INFVSGMQLACISIDRYAVATKVP---QSGVGKPCWIIICFCVMAAIIISIPOLVFY 176

DB 118 MSFSSGMLLILCISIDRYVAIVQAVSAHRARVLLISKSCVGMILATVLSIPELLYS 177

QY 177 TVNDNA-----RCIPFPRYLGTSMKALIQMLEICIGFVPLINGVCYFTARTLMKP 231

DB 178 DIORSSSEQAMRCSLITEH---VEAFITIOVAQWIGFVPLILAMSCYLVIRITLQAR 234

QY 232 NIKISRPKLVLTVYIVFYTQLPYNIYKFCRAIDIIYSLTSCNMSKRMIDIAIOVTESEI 291

DB 235 NFERKAIKVIIVAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIAVDVYSL 294

QY 292 ALFHSCLNPLIYVEMGASFKNYVMKAKKYG-----SW-----RRORQSVBERFPD 337

DB 295 ACVRCCVNPFLIYAFIGVKFRNDLFKLFKDLGCLSQEQLRQWSSCRHRRSSMSVE----- 349

QY 338 SEGPTPEPTSTFS 349

DB 350 ----AETTTTFS 357

RESULT 32

ID AAU91231 standard; Protein; 358 AA.

AC AAU91231;

DT 18-JUN-2002 (first entry)

DE Human 7 transmembrane domain receptor V31 exon 3 protein.

XX Human; 7 transmembrane domain receptor; 7TM;

KW antiinflammatory; immunomodulatory; immunological disease; inflammation;

KM	familial breast cancer; von Hippel-Lindau syndrome;
KM	thyroid hormone resistance; small cell cancer of the lung;
KX	pseudo-Zellweger syndrome; hypoproteinaemia; dysproteinaemia.
OS	Homo sapiens.
PN	US6348574-B1.
PD	19-FEB-2002.
XX	
PF	01-JUN-1998; 98US-0088337.
XX	
PR	17-MAY-1994; 94US-0245242.
PR	17-NOV-1993; 93US-0153848.
XX	
PR	17-NOV-1992; 92US-0977452.
XX	
PA	(ICOS-) ICOS CORP.
PI	Godiska R, Gray PW, Schweickart VL;
DR	WPI, 2002-266543/31.
DR	N-PsDB; ABRK54238.
XX	
PT	New seven transmembrane receptor polypeptide R2, useful for producing antibodies capable of modulating ligand/receptor binding reactions involved in vivo immunological and/or inflammatory events -
PS	Example 3; Column 49-52; 61pp; English.
XX	
CC	The invention relates to a purified and isolated R2 seven transmembrane (7TM) receptor. Also included are an anti-R2 antibody, a hybridoma producing the antibody, antigenic peptide fragments of R2, an antiserum produced by immunising a mammal with a composition comprising R2 or its fragment, where the fragment comprises at least one R2 extracellular or intracellular domain, and obtaining antiserum from the mammal after the immunising step, where the antiserum contains antibodies that bind to the R2 7TM receptor, a polynucleotide encoding 7TM receptor R2 and a host cell stably transformed or transfected with the polynucleotide allowing the expression of R2 in the host cell. The antibody is useful for modulating ligand/antiligand binding of a R2 7TM receptor, especially those ligand/receptor binding reactions involved in immunological and/or inflammatory events in vivo. R2 is useful for producing antibodies. The antibody is useful for immunisation to generate anti-idiotypic antibodies, for purifying R2 polypeptides, for identifying cells producing the polypeptides on their surfaces and for the detection and quantification of 7TM receptors on cell surfaces and in fluids. The polynucleotide is useful in DNA/RNA hybridisation assays to detect the capacity of cells to synthesise a 7TM receptor. The host cell is useful for large scale production of 7TM receptors, and in assays for identifying antagonist or agonists of 7TM receptor binding. Other 7TM receptors isolated in this study include V31 (located on chromosome 17q12-21.2, associated with familial breast cancer), V28 (Chromosome 3p21-ter, associated with von Hippel-Lindau syndrome, thyroid hormone resistance, small cell cancer of the lung and pseudo-Zellweger syndrome), R20 (chromosome 11 p11-p13 associated with hypoproteinaemia and dysproteinaemia), V112 and R12. The present sequence is a 7TM receptor of the invention.
SQ	Sequence 358 AA.
Query Match	36.2%; Score 659; DB 23; Length 358;
Best Local Similarity	38.7%; Pred. No. 3.e-65;
Matches 144; Conservative	66; Mismatches 124; Indels 38; Gaps 7;
Db	1 MALBONOSTDYVEENEMNGYDSGYELCTKEDEBFAKFLPLPLTVIVIGLAGNS 60 .: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : 1 VCLCODEVTDDITGNT--TWDTYLFEELCSKRDVRNFRKFWFLPTMYIILCFVGGLGG 57
Oy	61 MVVAITYAAKKORTKDVIILNLAVADLLLFPLFPWANVANGWLGMCKMTSALTAT 120 .: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : Db 58 LVVLVLYIFKRKTMTDYLNLAVADIILFLLTPRWASAKSWRGVHFCKLTALTRK 117 121 LNFVSQMQLACISIDRYAVATKVDS--QGSGVKPKCMIICFCWMAAILISIPOLVY 176

Db	118	MFPSGMLLICISIDRYALVQVSHRRRAVLLSKLSCGVITATVLSIPBLIS	177
Qy	177	TVNDNA-----RCIPFPERLYGTSMKALLQMLEICIGFVVPFLIMGVCYFITARTLMKP	231
Db	178	DIQRSSSEQAMRCSLITEH--VEAFPTIQVQMVGIFLVPFLMASFCLVIRTLQAR	234
Qy	232	NKISRPLKVLITVIVPIYVTCQLEPYNVYKRCAMIDIIYLSLTSQNNKXMDIAIQVTSI	291
Db	233	NERRKAIKVLIAVVVFVIFQLPYNQSVLAQIVANFNNTSSTCELSKOLNIAVDVTSL	294
Qy	292	ALFHSCINPILIVPMGASFKNYVWKVAKKYG-----SW-----PROROSVEEPED	337
Db	295	ACVRCVAVPFLYAFIVGVFRNDLPKLFKDGLGCSQRLQWSSCRHIRRSSMSV-----	349
Qy	338	SEGPTPTSTFS	349
Db	350	---AETTTFS	357
RESULT	33		
AA#48724			
ID	AA#48724	standard; Protein; 378 AA.	
AC	AA#48724;		
XX			
XX			
DT	25-SEP-1998	(first entry)	
XX			
DE		Human V31 seven transmembrane receptor.	
XX			
KW	V28; p1acenter; seven transmembrane receptor; 77M; signal transduction,		
KW	immunology; inflammation; V31.		
XX			
OS	Homo sapiens.		
XX			
XX			
FH	Key	Location/Qualifiers	
FH	Domain	58..86	
FT		/note= "Transmembrane domain 1"	
FT	Domain	96..119	
FT		/note= "Transmembrane domain 2"	
FT	Domain	131..152	
FT		/note= "Transmembrane domain 3"	
FT	Domain	171..196	
FT		/note= "Transmembrane domain 4"	
FT	Domain	219..247	
FT		/note= "Transmembrane domain 5"	
FT	Domain	264..285	
FT		/note= "Transmembrane domain 6"	
FT	Domain	306..331	
FT		/note= "Transmembrane domain 7"	
XX			
PN	US5759804-A.		
XX			
PD	02-JUN-1998.		
XX			
PF	17-NOV-1993;	93US-0153848.	
XX			
PR	17-NOV-1992;	92US-0977452.	
XX			
PA	(ICOS-) ICOS CORP.		
XX			
PI	Godiska R, Gray PW, Schweickart VL;		
XX			
DR	WPI: 1998-332132/29.		
DR	N-PSDB; AAVI8347.		
XX			
XX			
PT	DNA encoding V28 seven transmembrane receptor polypeptide - useful		
PT	for producing recombinant polypeptide and anti-V28 antibodies, and		
PT	in screening assays for V28 agonists and antagonists		
XX			
XX			
XX	Example 3; Columns 39-42; 56pp; English.		
CC	The present sequence represents the V31 seven transmembrane (77M)		

CC receptor encoded by the V31 cDNA (AAV18347). The invention claims for  
 CC a full length V28 genomic DNA (AAV18343) and the V28 protein it  
 CC encodes (AAV48722). V28 and V31 proteins are 7TM receptors which  
 CC are probably involved in signal transduction. The invention also  
 CC claims that cells transfected with V28 DNA can be used to produce the  
 CC recombinant polypeptide, to produce anti-V28 antibodies or in screening  
 CC assays for V28 agonists or antagonists. The antibodies, agonists and  
 CC antagonists could then be used to modulate V28 receptor-ligand binding,  
 CC for e.g. in immunological and/or inflammatory events in vivo.

XX Sequence 378 AA;

XX Query Match 36.2%; Score 659; DB 19; Length 378;

XX Best Local Similarity 38.7%; Pred. No. 3,66-65;  
 XX Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALKONOSTDYEEENMGTYDYSQYELICTKEDREPAKFLPFLTVFVIGLAGNS 60  
 DB 21 VCLCODEVTDDYIGDNT--TVDYTLFESLCSKQDVNFKAFLEPMYSIIICFVGLGNG 77  
 QY 61 MVVAIYAYYKQRTKTDVYIINLAADLLLFLLPFMAVNAVHGVGLKIMCKITSALYT 120  
 DB 78 LVVLTYYFKRLKTKTDYIINLAADLLLFLLPFMAVSAKSVGFVGHFCKLIYALYK 137  
 QY 121 LNFVSGMOFLACISIDRYVAATKVP---QSGVGKPCWIIICFCVMAAIIISIFOLVY 176  
 DB 138 MSFSSGMILLICISIDRYVAIVQAVSAHRHARVLLISKSCVGIWILATVLSIBELLYS 197  
 QY 177 TVNDNA-----RCIPFPFYLGTSKMAIIOMLEICIGFVVPFLMGVCYFRTATLMKP 231  
 DB 198 DLORSSSEQAMRCSLTEH--VEAFITIQVAMVIGFLVPLAMSFCYLIIRTLLOAR 254  
 QY 232 NIKISRPLKVLTVVIVFVITOLPYNIVKFCRAIDIYSLTSCMSKRMIDIAIOVTESI 291  
 DB 255 NPERKAKIVIIAVVVFVIFOLPFGVLAQTVANFNITSTCELSKQINIAIDVYSL 314  
 QY 292 ALFHSCLNPILYVFMGASFKNYVMKAKYK-----SW-----RRORSVEEPPFD 337  
 DB 315 ACVRCVNPFLYAFIGVGRNDLFLFKDLGCLSOEOLRQMSCHIRRSMSV----- 369  
 QY 338 SEGTEPTSTPS 349  
 DB 370 ---AETTTTFS 377

RESULT 34

AAAB21688  
 ID AAB21688 standard; Protein; 378 AA.

XX AAB21688;

XX 26-JAN-2001 (first entry)

XX Human 7TM receptor V31-B cDNA clone protein.

XX Seven transmembrane receptor; 7TM; heptahelical; serpentine;  
 XX G-protein-coupled; V28; V31; V112; R20; R2; R12; R3; gene therapy;  
 XX cancer.

XX Homo sapiens.

XX OS

XX US6107475-A.

XX 22-AUG-2000.

XX 26-APR-1999; 99US-0299843.

XX 17-MAY-1994; 94US-0245242.

XX 01-JUN-1998; 98US-0088337.

XX 17-NOV-1992; 92US-0977452.

XX 17-NOV-1993; 93US-0153846.

XX (ICOS-) ICOS CORP.

XX PI Schweickart VL, Gray PW, Godiska R;  
 XX DR WPI; 2000-571335/53.  
 XX N-PDB; AAA91707.

XX PT polynucleotide encoding seven transmembrane receptors, antibody  
 XX specific to the receptor, agonist and antagonist of the receptor useful  
 XX for treating inflammation in a mammal

XX Example 3; Columns 41-44; 61pp; English.

XX The present sequence is a novel seven transmembrane (7TM) receptors  
 XX (also known as heptahelical, serpentine or G-protein-coupled receptors).

XX The coding sequence for the present sequence may be used for gene  
 XX therapy for diseases such as cancer.

XX Sequence 378 AA;

XX Query Match 36.2%; Score 659; DB 21; Length 378;

XX Best Local Similarity 38.7%; Pred. No. 3,66-65;  
 XX Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALKONOSTDYEEENMGTYDYSQYELICTKEDREPAKFLPFLTVFVIGLAGNS 60  
 DB 21 VCLCODEVTDDYIGDNT--TVDYTLFESLCSKQDVNFKAFLEPMYSIIICFVGLGNG 77  
 QY 61 MVVAIYAYYKQRTKTDVYIINLAADLLLFLLPFMAVNAVHGVGLKIMCKITSALYT 120  
 DB 78 LVVLTYYFKRLKTKTDYIINLAADLLLFLLPFMAVSAKSVGFVGHFCKLIYALYK 137  
 QY 121 LNFVSGMOFLACISIDRYVAATKVP---QSGVGKPCWIIICFCVMAAIIISIFOLVY 176  
 DB 138 MSFSSGMILLICISIDRYVAIVQAVSAHRHARVLLISKSCVGIWILATVLSIBELLYS 197  
 QY 177 TVNDNA-----RCIPFPFYLGTSKMAIIOMLEICIGFVVPFLMGVCYFRTATLMKP 231  
 DB 198 DLORSSSEQAMRCSLTEH--VEAFITIQVAMVIGFLVPLAMSFCYLIIRTLLOAR 254  
 QY 232 NIKISRPLKVLTVVIVFVITOLPYNIVKFCRAIDIYSLTSCMSKRMIDIAIOVTESI 291  
 DB 255 NPERKAKIVIIAVVVFVIFOLPFGVLAQTVANFNITSTCELSKQINIAIDVYSL 314  
 QY 292 ALFHSCLNPILYVFMGASFKNYVMKAKYK-----SW-----RRORSVEEPPFD 337  
 DB 315 ACVRCVNPFLYAFIGVGRNDLFLFKDLGCLSOEOLRQMSCHIRRSMSV----- 369  
 QY 338 SEGTEPTSTPS 349  
 DB 370 ---AETTTTFS 377

RESULT 35

AAAG80114  
 ID AAG80114 standard; Protein; 378 AA.

XX AAG80114;

XX 17-JAN-2002 (first entry)

XX Human CCR7 protein.

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;  
 XX inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;  
 XX chronic bowel inflammation; rheumatoid arthritis; cystostatic;  
 XX antiinflammatory; antiasthmatic; immunosuppressive; dermatological;  
 XX antiinflammatory; antiarthritic.

XX Homo sapiens.

XX OS

XX WO200172830-A2.

XX 04-OCT-2001.





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DR N-PSDB; AA066153.
XX
XX DNA encoding seven transmembrane receptors - used to develop
PT prods. for use as therapeutic or diagnostic agents for conditions
XX involving the receptors.
XX
XX Example 2; Page 46-48; 100bp; English.
PS
CC Two primers (AA066148, AA066149) were used to amplify human genomic DNA
CC purified from leukocytes. Approximately 1000 clones were isolated
CC after the initial amplification reaction and probed with sequences
CC specific for seven transmembrane receptors IL8R1, A2R and R20.
CC Clones which did not hybridise were then chosen for sequence
CC analysis. Three new clones were identified that appeared to encode
CC seven transmembrane receptor segments. Two more primers (AA066151,
CC AA066152) were used to isolate a full length version of one of these
CC clones, one of which was designated V31 and encoded this
CC polypeptide.
XX
SQ Sequence 410 AA;
Query Match 36.2%; Score 659; DB 15; Length 410;
Best Local Similarity 38.7%; Pred. No. 4e-65;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 MALRQNSTDYVYEEENMGTYDSQYELICIKEDVREFAKVPFLPVLTIVFVIGLAGNS 60
DB 53 VCLQDEVTDDYIGDNT---IVDYTLFESLCSKQDVNFKMFIPIMYSIIICFVGLGNG 109
QY 61 MVVAIYAYKKQRTDYIINLAVALDLLFTLPFMAVNAVHGVLGKIMCKITSALYT 120
DB 110 LVVLTYIYFKRLKMTDTYLLNLAVADILFLLTPFMAVSAKSVGVHCFKLIIFAITYK 169
QY 121 INFVSGMOFLACISIDRVAAATKVP-----OSGVKPCWIIICFVMAAILLSIPQVVFY 176
DB 170 MSFSGMILLICISIDRVAAVQAASHRRARVLLISKSCGIVLWATVLSIPELLYS 229
QY 177 TVNDNA-----RCIPIFPRYLGTSMKALIOMLEICIGFVVPFLMGVCYFITARITMKMP 231
DB 230 DLQRSSSEQAMRCSLITEH---VEAFITIQVAGWVIGFLVPLAMSCYIVIRTLQAR 286
QY 232 NIKISRPKLVLTIVIVFVITQLPYNTVPCRAIDIIYSLTSCNMRMDIAIQVTEST 291
DB 287 NFERNKAIKVIIAVAVVFIVFQLPYNGVLAQIVANFNITSTCELSKQINIAVDVYSL 346
QY 292 ALFHSCNPIIYVFMGASFKNYVVKVAKY-----SW-----RRQROSVSEPPFD 337
DB 347 ACVRCVNPFLYAFIVGVFNRDLFKLFDGCLSQEQLRQSSCRHIRSSMSVE----- 401
QY 338 SEGPTPTSTPS 349
DB 402 ----AETTTTFS 409
RESULT 39
AAW48723
ID AAW48723 standard; Protein; 410 AA.
XX
XX AAW48723;
AC
OS Homo sapiens.
XX
XX US5759804-A.
XX
XX 02-JUN-1998.
XX

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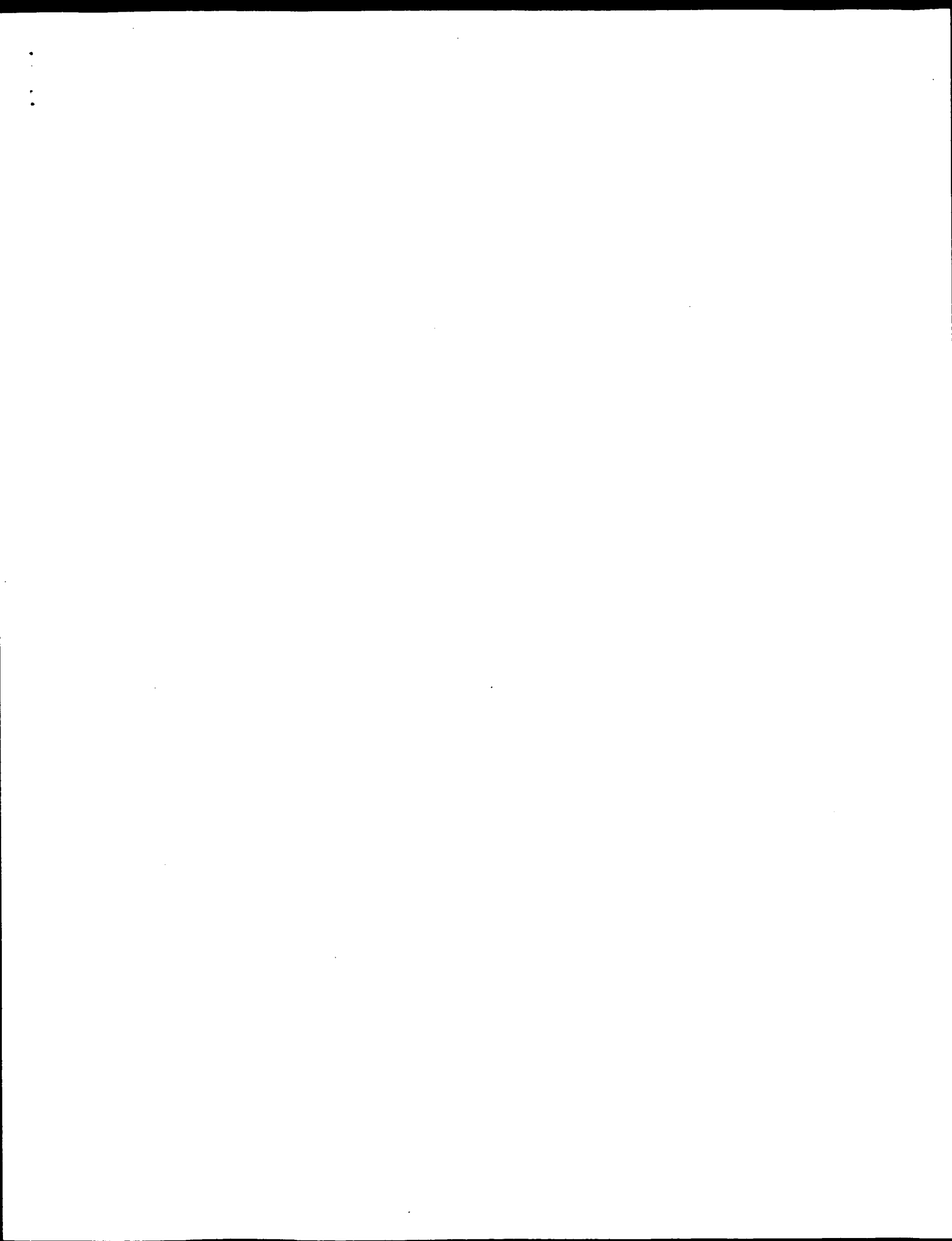
PF 17-NOV-1993; 93US-0153848.
XX
XX 17-NOV-1992; 92US-0977452.
XX
XX (ICOS-) ICOS CORP.
XX
XX Godiska R, Gray PW, Schweickart VL;
XX
XX WPT. 1998-332132/29.
XX
XX N-PSDB; AAV18345.
DR
XX DNA encoding V28 seven transmembrane receptor polypeptide - useful
PT for producing recombinant polypeptide and anti-V28 antibodies, and
XX in screening assays for V28 agonists and antagonists
XX
XX Example 2; Columns 31-34; 56bp; English.
XX
XX The present sequence represents the deduced polypeptide sequence encoded
CC by the V31 genomic DNA (AAV18345) which was isolated from a human
CC placenta genomic library. The invention claims for a full length V28
CC genomic DNA (AAV18343) and the V28 (AAW48722) protein it encodes. V28
CC and V31 (AAW48723) proteins are seven transmembrane (7TM) receptors which
CC are probably involved in signal transduction. The invention also claims
CC that cells transfected with V28 DNA can be used to produce the
CC recombinant polypeptide, to produce anti-V28 antibodies or in screening
CC assays for V28 agonists or antagonists. The antibodies, agonists and
CC antagonists could then be used to modulate V28 receptor-ligand binding,
CC for e.g. in immunological and/or inflammatory events in vivo.
XX
SQ Sequence 410 AA;
Query Match 36.2%; Score 659; DB 19; Length 410;
Best Local Similarity 38.7%; Pred. No. 4e-65;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 MALRQNSTDYVYEEENMGTYDSQYELICIKEDVREFAKVPFLPVLTIVFVIGLAGNS 60
DB 53 VCLQDEVTDDYIGDNT---IVDYTLFESLCSKQDVNFKMFIPIMYSIIICFVGLGNG 109
QY 61 MVVAIYAYKKQRTDYIINLAVALDLLFTLPFMAVNAVHGVLGKIMCKITSALYT 120
DB 110 LVVLTYIYFKRLKMTDTYLLNLAVADILFLLTPFMAVSAKSVGVHCFKLIIFAITYK 169
QY 121 INFVSGMOFLACISIDRVAAATKVP-----OSGVKPCWIIICFVMAAILLSIPQVVFY 176
DB 170 MSFSGMILLICISIDRVAAVQAASHRRARVLLISKSCGIVLWATVLSIPELLYS 229
QY 177 TVNDNA-----RCIPIFPRYLGTSMKALIOMLEICIGFVVPFLMGVCYFITARITMKMP 231
DB 230 DLQRSSSEQAMRCSLITEH---VEAFITIQVAGWVIGFLVPLAMSCYIVIRTLQAR 286
QY 232 NIKISRPKLVLTIVIVFVITQLPYNTVPCRAIDIIYSLTSCNMRMDIAIQVTEST 291
DB 287 NFERNKAIKVIIAVAVVFIVFQLPYNGVLAQIVANFNITSTCELSKQINIAVDVYSL 346
QY 292 ALFHSCNPIIYVFMGASFKNYVVKVAKY-----SW-----RRQROSVSEPPFD 337
DB 347 ACVRCVNPFLYAFIVGVFNRDLFKLFDGCLSQEQLRQSSCRHIRSSMSVE----- 401
QY 338 SEGPTPTSTPS 349
DB 402 ----AETTTTFS 409
RESULT 40
AAB21687
ID AAB21687 standard; Protein; 410 AA.
XX
XX AAB21687;
AC
XX 26-JAN-2001 (first entry)
XX
XX Genomic clone of 7TM receptor V31 protein.
XX

```



[illegible]

Search completed: March 17, 2003, 16:26:44  
Job time : 44 secs



GenCore version 5.1.4 p5\_4578  
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## OM protein - protein search, using sw model

Run on: March 17, 2003, 16:18:55 ; Search time 11 Seconds  
(without alignments)  
1319.701 Million cell updates/sec

Title: US-09-721-495b-2  
Perfect score: 1819  
Sequence: 1 MALEQNGSDYYEENEMNG.....VEEPFDSGTEPTSTFSI 350

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 135 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1819	100.0	350	1	Q9npb9 homo sapien
2	1620	89.1	350	1	CKRB_BOVIN
3	659	36.2	378	1	CKR7_HUMAN
4	650	35.7	378	1	CKR7_MOUSE
5	639	35.1	369	1	CKR9_MOUSE
6	637	35.0	357	1	CKR9_HUMAN
7	605	33.3	367	1	CKR6_MOUSE
8	583	32.1	374	1	CKR6_HUMAN
9	581	31.9	342	1	CKR6_CERAE
10	571	31.4	343	1	CKR6_MACMU
11	569	31.3	342	1	CKR6_MACNE
12	560	30.8	342	1	CKR6_HUMAN
13	537.5	29.5	360	1	CKR4_HUMAN
14	534.5	29.4	360	1	IL8B_HUMAN
15	529.5	29.1	353	1	IL8B_PANTR
16	527	29.0	384	1	CKD6_HUMAN
17	525	28.9	362	1	CKRA_HUMAN
18	524	28.8	354	1	CKX1_RAT
19	522.5	28.7	353	1	IL8B_GORGO
20	522.5	28.7	355	1	CKX1_HUMAN
21	522.5	28.7	360	1	CKR4_MOUSE
22	521.5	28.7	353	1	IL8B_MACMU
23	520.5	28.6	362	1	CKRA_MOUSE
24	512	28.1	356	1	IL8B_CANPA
25	511	28.1	354	1	CKX1_MOUSE
26	511	28.1	358	1	IL8B_RABIT
27	504	27.7	360	1	CKR2_MACMU
28	501.5	27.6	355	1	IL8A_RABIT
29	501.5	27.6	358	1	CKR3_CAVBO
30	500.5	27.5	352	1	CKR4_HUMAN
31	499.5	27.5	353	1	CKR4_BOVIN
32	499.5	27.5	360	1	IL8B_BOVIN
33	498.5	27.4	352	1	CKR4_PAPAN

34	498.5	27.4	352	1	CKR5_CERTO	O62743 cercocebus
35	498.5	27.4	353	1	CKR4_FELCA	P56498 felis silve
36	497.5	27.4	350	1	IL8A_GORGO	P55919 gorilla gor
37	495.5	27.2	352	1	CKR5_CERAE	P56493 cercopithec
38	494.5	27.2	352	1	CKR4_CERTO	O62747 cercocebus
39	493.5	27.1	352	1	CKR4_MACFA	O28474 macaca fasc
40	493.5	27.1	352	1	CKR4_MACMU	P79394 macaca mula
41	492.5	27.1	359	1	CKR3_RAT	O54814 rattus norv
42	492.5	27.1	359	1	IL8B_RAT	P35407 rattus norv
43	491.5	27.0	352	1	CKR5_PAPHA	P56441 papio hamad
44	491.5	27.0	352	1	CKR5_PYGBI	O97880 pygathrix b
45	490.5	27.0	352	1	CKR5_MACMU	P79436 macaca mula
46	490.5	27.0	352	1	CKR5_MOUSE	P49682 homo sapien
47	490	26.9	354	1	CKR3_HUMAN	P51682 mus musculu
48	489.5	26.9	352	1	CKR5_MOUSE	P56439 gorilla gor
49	489.5	26.9	352	1	CKR5_GORGO	O97882 pygathrix n
50	489.5	26.9	352	1	CKR5_PYGBE	O97878 trachypithe
51	488.5	26.9	352	1	CKR5_TRAFR	O97879 trachypithe
52	488.5	26.9	352	1	CKR5_MOUSE	P56484 mus musculu
53	488.5	26.9	354	1	CKR5_RAT	O08556 rattus norv
54	488.5	26.9	352	1	CKR6_RAT	O09027 rattus norv
55	487.5	26.8	352	1	CKR5_PONPY	O97881 pongo pygma
56	486.5	26.7	349	1	CKR4_RAT	P25024 homo sapien
57	486.5	26.7	350	1	IL8A_HUMAN	P55920 pan troglod
58	486	26.7	350	1	IL8A_PANTR	P51685 homo sapien
59	486	26.7	355	1	CKR8_HUMAN	P56440 pan troglod
60	485	26.7	352	1	CKR5_PANTR	P51681 homo sapien
61	484.5	26.6	352	1	CKR5_HUMAN	O97883 hylobates 1
62	484.5	26.6	352	1	CKR5_HYLE	P35343 mus musculu
63	483.5	26.6	349	1	IL8B_MOUSE	P70612 rattus norv
64	483	26.6	349	1	IL8B_RAT	O55193 rattus norv
65	482.5	26.5	373	1	CKR2_RAT	P51675 mus musculu
66	482	26.5	355	1	CKR1_MOUSE	P70658 m c-x-c che
67	482	26.5	359	1	CKR4_MOUSE	P41597 homo sapien
68	482	26.5	374	1	CKR2_HUMAN	P51683 mus musculu
69	480	26.4	373	1	CKR2_MOUSE	P51678 mus musculu
70	479.5	26.4	359	1	CKD6_MOUSE	O08707 mus musculu
71	478	26.3	378	1	CKR6_MOUSE	O97665 macaca mula
72	475.5	26.1	367	1	CKR8_MACMU	O88410 mus musculu
73	475.5	26.1	367	1	CKR3_MOUSE	P32446 homo sapien
74	474	26.1	355	1	CKR1_HUMAN	P56492 cercopithec
75	470	25.8	355	1	CKR3_CERAE	P51677 homo sapien
76	464.5	25.5	355	1	CKR3_HUMAN	P43240 canis famli
77	455.5	25.0	359	1	AG2R_HUMAN	P30556 homo sapien
78	452.5	24.9	359	1	AG2R_HUMAN	P25095 rattus norv
79	452.5	24.9	359	1	AG2R_RAT	P56482 macaca mula
80	451.5	24.8	355	1	CKR1_MACMU	O9wv26 cavia porce
81	450.5	24.8	359	1	AG2R_CAVPO	P25104 bos taurus
82	450	24.7	359	1	AG2R_BOVIN	P34997 rattus norv
83	450	24.7	374	1	CKR5_RAT	P56483 macaca mula
84	449.5	24.7	355	1	CKR3_MACMU	O35210 meriones un
85	447.5	24.6	359	1	AG2R_MERTUN	P34976 oryctolagus
86	446.5	24.5	359	1	AG2R_RABIT	P51676 mus musculu
87	445.5	24.5	356	1	CKRV_MOUSE	P30555 sus scrofa
88	445	24.5	359	1	AG2R_PIG	O75990 ovis aries
89	445	24.4	359	1	AG2R_SHEEP	O89039 rattus norv
90	443	24.4	362	1	RDCL_RAT	P32302 homo sapien
91	442.5	24.3	372	1	CKR5_HUMAN	O04683 mus musculu
92	442.5	24.3	374	1	CKR5_MOUSE	P33303 xenopus lae
93	441	24.2	362	1	AG2R_XENLA	P29754 mus musculu
94	439	24.1	359	1	AG2R_MOUSE	P25106 homo sapien
95	438.5	24.1	359	1	AG2R_MOUSE	P56485 mus musculu
96	438.5	24.1	362	1	RDCL_HUMAN	P29755 mus musculu
97	435.5	23.9	362	1	AG2S_MOUSE	P35373 xenopus lae
98	435	23.9	359	1	AG2S_MOUSE	O13725 homo sapien
99	432.5	23.8	363	1	AG2S_XENLA	P15163 canis famli
100	428.5	23.6	359	1	AG2S_HUMAN	P79785 gallus gall
101	428.5	23.6	362	1	RDCL_CANPA	P33396 melaeagris g
102	428	23.5	359	1	AG2R_CHICK	P35351 rattus norv
103	428	23.5	359	1	AG2R_MELGA	O92026 meriones un
104	411.5	22.6	363	1	AG22_RAT	P35374 mus musculu
105	410.5	22.6	363	1	AG22_MERUN	
106	408.5	22.5	363	1	AG22_MOUSE	

107	405.5	22.3	363	1	AG22_HUMAN
108	394	21.7	391	1	BRE2_HUMAN
109	392.5	21.6	353	1	LAR_XENLA
110	392.5	21.6	354	1	US2B_HCIVA
111	380	20.9	322	1	CXC1_MOUSE
112	380	20.9	372	1	BRE2_CAVPO
113	376	20.7	370	1	VK02_SPVKA
114	374.5	20.6	333	1	BRE2_RAT
115	373	20.5	333	1	CXC1_HUMAN
116	365	20.1	364	1	EMR_MOUSE
117	365	20.1	367	1	BRE2_MOUSE
118	364	20.0	367	1	BRE2_PIG
119	362	19.9	351	1	FML1_HUMAN
120	360.5	19.8	359	1	GPI5_MACFA
121	358.5	19.7	348	1	FML1_PANTR
122	358.5	19.7	371	1	CML1_MOUSE
123	357	19.6	360	1	GPI5_HUDAN
124	356.5	19.6	373	1	CML1_HUDAN
125	354.5	19.5	343	1	FML1_HUMAN
126	353.5	19.4	348	1	FML1_GORGO
127	353.5	19.4	371	1	CML1_RAT
128	353	19.4	360	1	GPI5_MACMU
129	352.5	19.4	346	1	FMLR_MACMU
130	352.5	19.4	346	1	FMLR_PONPY
131	351	19.3	308	1	P2Y8_XENLA
132	351	19.3	537	1	P2Y8_XENLA
133	350	19.2	360	1	GPI5_MACNE
134	349.5	19.2	392	1	BRE2_MOUSE
135	348.5	19.2	352	1	FMLE_RABIT

RESULT 2  
CCKR BOVIN  
ID CCKR BOVIN STANDARD; PRT; 350 AA.  
AC P35350;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE C-C chemokine receptor type 11 (C-C CCR-11) (CCR-11)  
DE (Possible guanine receptor type B) (PPR1 protein).  
GN CCR11.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Tongue; PubMed=8392843;  
RX MEDLINE=93326166; PubMed=8392843;  
RA Matsuda I., Mori T., Aoki J., Sato T., Kurihara K.;  
RT "Identification of novel members of G-protein coupled receptor  
superfamily expressed in bovine taste tissue."  
RT Biochem. Biophys. Res. Commun. 194:504-511(1993).  
CC -1- FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4.  
CC -1- FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN CIRCUMVALLATE AND FUNGIFORM  
PAPILLAE, OLFACTORY EPITHELIUM AND LUNG. LOWER EXPRESSION IN  
LIVER, KIDNEY AND TONGUE EPITHELIUM BEARING NO TASTE PAPILLAE.  
CC VERY LOW EXPRESSION IN THE CEREBRAL CORTEX OF THE BRAIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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CC EMBL, S63848; AAB27547.1; -.  
CC PIR: J06621; J06621.  
DR HSP: P02699; 1BO1.  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR Pfam: PF00001; 7tm1.1.  
DR PRINTS: PR00237; GPCR\_Rhodopsn.  
DR PROSITE: PS00237; G PROTEIN RECP F1.1; 1.  
DR PROSITE: PS50262; G PROTEIN RECP F1.2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
KW Phosphorylation.  
KW DOMAIN 1  
FT TRANSMEM 42 41  
FT TRANSMEM 67 66  
FT TRANSMEM 79 79  
FT TRANSMEM 80 99  
FT TRANSMEM 100 113  
FT TRANSMEM 114 135  
FT TRANSMEM 136 153  
FT TRANSMEM 154 175  
FT TRANSMEM 176 199  
FT TRANSMEM 200 222  
FT TRANSMEM 223 241  
FT TRANSMEM 242 265  
FT TRANSMEM 266 283  
FT TRANSMEM 284 306  
FT TRANSMEM 307 350  
FT DOMAIN 307 350  
FT CARBOHYD 6 6  
FT CARBOHYD 19 19  
FT DISULFID 112 184  
SQ SEQUENCE 350 AA; 40008 MW; E46BF942F319C82 CRC64;  
Query Match 89.1%; Score 1620; DB 1; Length 350;  
Best Local Similarity 86.0%; Pred. No. 1.2e-91;  
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALBNOSTDYEEENMGTYDSQYELI CIKEDVREFAKFLFVPLTIVFGIAGNS 60  
Db 1 MAEYNOSTDYEEENMGTHDYSQYEVICIKEDVREFAKFLFAPFTIAFIAGNS 60  
QY 61 MVAIYAYVKKORTKTYIINLAVALDLLFTLPFAVNAVHGVNLKIMKITSALYT 120  
Db 61 TVVAIYAYVKKORTKTYIINLAVALDLLFTLPFAVNAVHGVNLKIMKITSALYT 120  
QY 121 LNFVSGMOPACISIDRYAVYAKVPSGSGVGRPCWICFCWMAAILISIPOLVYTVND 180  
Db 121 VNFVSGMOPACISIDRYAVYAKVPSGSGVGRPCWICFCWMAAILISIPOLVYTVNH 180  
QY 181 NARCIPFPRIYIGTSKAKALIQMLEICIGFVPEPLMGVCYFTAPTLKMPNIKISPLK 240  
Db 181 KARCVPFPRIYIGTSKAKALIQMLEICIGFVPEPLMGVCYFTAPTLKMPNIKISPLK 240  
QY 241 VLTIVIVFIVTQLPYNYKFCRAIDIIYSLTSCMSKRMIDAIQVESIALFSCINLP 300  
Db 241 VLTIVIVFIVTQLPYNYKFCRAIDIIYSLTSCMSKRMIDAIQVESIALFSCINLP 300  
QY 301 ILVYFNGASPKYVVMVAKKYGSMRQROSVREFPDSGPTPEPTSTFSI 350  
Db 301 ILVYFNGASPKYVVMVAKKYGSMRQROSVREFPDSGPTPEPTSTFSI 350

RESULT 3  
CCKR7 HUMAN  
ID CCKR7 HUMAN STANDARD; PRT; 378 AA.  
AC P32248;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE C-C chemokine receptor type 7 precursor (C-C CCR-7) (CCR-7)  
DE (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)  
DE (EBI1) (BHR7) OR EBI1 OR EVI1.  
GN CCR7 OR CCKR7 OR EBI1 OR EVI1.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9318173; PubMed=839238;  
RA Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,  
RA Kleif E.;  
RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G  
protein-coupled peptide receptors";  
RT J. Virol. 67:2209-2220(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=95154835; PubMed=7851893;  
RA Schewickart V.L., Raport C.U., Godiska R., Byers M.G., Eddy R.L. Jr.,  
RA Shows T.B., Gray P.W.;  
RT "Cloning of human and mouse EBI1, a lymphoid-specific  
G-protein-coupled receptor encoded on human chromosome 17q12-q21.2";  
RT Genomics 23:643-650(1994).  
CC -1- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR  
OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOID TISSUES AND  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS LYMPHOID TISSUES AND  
CC ACTIVATED B AND T LYMPHOCYTES, STRONGLY UPREGULATED IN B CELLS  
CC INFECTED WITH EBSTEIN-BARR VIRUS AND T CELLS INFECTED WITH  
CC HERPESVIRUS 6 OR 7.  
CC -1- INDUCTION: BY EBV.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; L08176; AAA58615.1; -  
DR EMBL; L31584; AAA74230.1; -  
DR EMBL; L31582; AAA74230.1; JOINED.  
DR EMBL; L31583; AAA74230.1; JOINED.  
DR EMBL; L31581; AAA74231.1; -  
DR PIR; A45680; A45680.  
DR HSSP; P34996; 1DD.  
DR Genew; HGNC:1608; CCR7.  
DR MIM; 600242; -  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_HODOPS.  
DR PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECP\_F1\_2; 1.  
KM G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 24  
FT CHAIN 1 24  
FT DOMAIN 25 378  
FT TRANSSEM 25 59  
FT TRANSSEM 60 86  
FT DOMAIN 87 95  
FT TRANSSEM 96 116  
FT DOMAIN 117 130  
FT TRANSSEM 131 152  
FT DOMAIN 153 170  
FT TRANSSEM 171 191  
FT DOMAIN 192 219  
FT TRANSSEM 220 247  
FT DOMAIN 248 263  
FT TRANSSEM 264 289  
FT DOMAIN 290 313  
FT TRANSSEM 314 331  
FT DOMAIN 332 378  
FT CARBOHYD 36 36  
FT DISULFID 129 210  
FT CONFLICT 182 183  
FT CONFLICT 337 337  
SQ SEQUENCE 378 AA; 42874 MW; D4CB4213841A1BD4 CRC64;

Query Match 36.2%; Score 659; DB 1; Length 378;  
Best Local Similarity 38.7%; Pred. No. 1,7e-33;  
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEONOSTDYIEENMGTYDYSQYELICIKEDVREFAKVLPEVLTIVFVIGLAGNS 60  
DB 21 VCLCQDEVTDDYIGDNT---TVDYTLFESLCSKDVRFNFRAMFLPIMSGILCVGLGNG 77  
QY 61 MVAIAIAYKKQRTKTDVTLNLAADLLFLTFWAVNAVHGVLSKIMCKITSAVLT 120  
DB 78 LVVLTLYFRLKLTMDTYLNLAVADILFLTLPEWVSAASWVGVHFCFLFAIK 137  
QY 121 LNFVSGMPLACISIDRYAVATKVP-----OSGVKPCMICGCVMAAILISIPQVRY 176  
DB 138 MSFSGMLLCLSIDRYAIVAVSAHRRRAVLLISKLSGVGILTLVLSIPELLS 197  
QY 177 TVNDNA-----RCIPLEPRYLGTSKALIQMLEICIGFVVPPLINGVCYFIARTLMKP 231  
DB 198 DLRSSSEQAMRCSLITEH---VEAFITIQAVQWVIGFVPLPMSFCVLVIRTLQAR 254  
QY 232 NIKISRLVLTIVTQVPIVTFQVPIVAFCAIDIIYLSLSCMSKMDIAIQVTSI 291  
DB 255 NEERNFAIVIIAAVVFVIFQVPIVGVVLAQTVANFNITSSICLSKQNLNAVTVYSL 314  
QY 292 ALFHSCLNPLVVFMGASPKNYVMKAKYK-----SW-----RRQSQVEPFDP 337  
DB 315 ACVRCVNFVIAFIVGVRKNDLFLKLDGLCSQEQLFQMSCHIRRSSMSVE----- 369  
QY 338 SSGPTEPTSTFS 349  
DB 370 ---AETTTFS 377

## RESULT 4

ID CKR7\_MOUSE STANDARD; PRT; 378 AA.

AC P47774;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE C-C Chemokine receptor type 7 precursor (C-C CKR-7) (CC-CKR-7) (CCR-7)  
DE (MIP-3 beta receptor) (EBV-induced G-protein-coupled receptor 1)  
DE (EBI1).  
GN CCR7 OR CKR7 OR EBI1 OR EBIH.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;  
RX MEDLINE=95154835; PubMed=7851893;  
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,  
RT Shows T.B., Gray P.W.;  
RT "Cloning of human and mouse EBI1, a lymphoid-specific  
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2";  
RL Genomics 23:643-650(1994).  
CC -! FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR  
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.  
CC -! SUBCELLULAR LOCATION: Integral membrane protein.  
CC -! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

QY 5 QNOSTDYIEENMGTYDYSQYELICIKEDVREFAKVLPEVLTIVFVIGLAGNSMVA 64  
Best Local Similarity 35.7%; Score 650; DB 1; Length 378;  
Matches 140; Conservative 67; Mismatches 125; Indels 34; Gaps 8;

Db 25 QDEVTDDYIGENT---TVDTYLVESVCFKDVNFKMFLPLMYSVLCFVGLLNGVLIL 81

Qy 65 IYAYKKORTKIDVYIILNLAVALDILLFTLPFAVANAHCWLGKMTKTSALTLYLNEY 124

Db 82 TYIYFKLKTMTDTYLLNLNLAVALDILLFTLPFAVANAHCWLGKMTKTSALTLYLNEY 141

Qy 125 SGMOPLACISIDRYVAATKPSOSG-----VGKPCMIICFCVMAAAILSLPOLVFTY 177

Db 142 SGMLLCISIDRYVAATKPSOSG-----VGKPCMIICFCVMAAAILSLPOLVFTY 198

Qy 178 VNDNA-----RCIPFPRYLGTSKML--IQMLEICIGFVVPFLMGVCYFTARTLMK 230

Db 199 LQKNSGEBTLRC-----SLVSAQVEALITIQVAGVGFVLPMLAMGFCYLIIRTLQA 253

Qy 231 PNKISRPLKVLTLVYIYVITQLPYNIIVKFCRAIDIIYSLTSCNMSKMDIALQYTES 290

Db 254 RNFERNKAIKVIYAVVVFYFQLPYNGVVLQVAVNFNITNSCETSCKDLNIAVDYTS 313

Qy 291 IALHSCINPLIYVEMGASFKNYMKVAKKYSWROR-----QSVFEPFDESGPTE 343

Db 314 LASVRCVNPFLYAFIVGVKFRSDLPKLPKLDIGLCSQERLHMSSCRIVRASVSM--AE 371

Qy 344 PTSTFS 349

Db 372 TTTTFS 377

RESULT 5

CKR9\_MOUSE STANDARD; PRT; 369 AA.

ID CKR9\_MOUSE

AC 09MUT7:

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE C-C chemokine receptor type 9 (C-C CKR-9) (CC-CKR-9) (CCR-9)

DE (Chemokine C-C receptor 10).

GN CKR9 OR CCKBR10.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

OX [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Thymus;

RX MEDLINE=99248139; PubMed=10229797;

RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;

RA "Cutting edge: Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the receptor for the chemokine TECK";

RT J. Immunol. 162:5671-5675 (1999).

RN [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=20069400; PubMed=10602049;

RA Wutbel M.A., Philippe J.M., Nguyen C., Victorero G., Freeman T.,

RA Wooding P., Mazek A., Matel M.G., Malissen M., Jordan B.R.,

RA Malissen B., Carrier A., Naquet P.;

RA "The chemokine TECK is expressed by thymic and intestinal epithelial cells and attracts double- and single-positive thymocytes expressing the TECK receptor CCR9.";

RT Eur. J. Immunol. 30:262-271 (2000).

RT [1]

CC -1- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN LYMPH NODES AND SPLEEN.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL: AJ132336; CAB43480.1; -

DR EMBL: AJ13357; CAB66136.2; -

DR MGI: MGI:1341902; Cckbr10.

DR InterPro: IPR004069; CC\_chemkine9.

DR InterPro: IPR00276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm\_1; 1.

DR PRINTS: PRO1531; CHEMOKINER9.

DR PRINTS: PRO0237; GPCR\_RHODOPSN.

DR PROSITE: PS00262; G-PROTEIN RECEPTOR\_F1\_1; 1.

DR PROSITE: PS00237; G-PROTEIN RECEPTOR\_F2\_1; 1.

DR PROSITE: PS00262; G-PROTEIN RECEPTOR\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 49

FT TRANSMEM 50 76

FT DOMAIN 77 85

FT TRANSMEM 86 106

FT DOMAIN 107 120

FT TRANSMEM 121 142

FT DOMAIN 143 160

FT TRANSMEM 161 181

FT DOMAIN 182 210

FT TRANSMEM 211 238

FT DOMAIN 239 254

FT TRANSMEM 255 280

FT DOMAIN 281 304

FT TRANSMEM 305 322

FT DOMAIN 323 369

FT CARBOHYD 32 32

FT DISULFID 119 198

FT SEQUENCE 369 AA; 41913 MW; 6971F76F0A24B4AE CRC64;

Query Match 35.1%; Score 639; DB 1; Length 369;

Best Local Similarity 36.0%; Pred. No. 2.7e-32;

Matches 118; Conservative 77; Mismatches 111; Indels 22; Gaps 5;

Qy 10 DYVEENENMGTY---DYGVELICKEDYREPAKFLVFLVITVYVIGLAGNSMVAIY 66

Db 16 DFSYDASTADDYDMMNIFSSF--FCKANNVQPSHFPLPVLYVIVIGLNSGLIYVY 73

Qy 67 AYYKKORTKIDVYIILNLAVALDILLFTLPFAVANAHCWLGKMTKTSALTLYLNEY 126

Db 74 WYCRVKTMTDMLNLAVALDILLFTLPFAVANAHCWLGKMTKTSALTLYLNEY 133

Qy 127 MGPLACISIDRYVAATKPSOSGSGVGRPCW-----IICFCVMAAAILSLPOLVFTY 177

Db 134 VLLMCISSVRYIAIYQ-----AMKQVWRQKRLYSKWCITIIWMAAVLCTPBLIYQ 188

Qy 178 VNDN---ARCIPFPRYLGTSKML--IQMLEICIGFVVPFLMGVCYFTARTLMKPNIK 234

Db 189 VSGSGIATCTMYPPKDKNAKLSAVIILKVTIGFLPFWVMAFCYIIHITLVQAKSS 248

Qy 235 ISRPKLKVLTLVYIYVITQLPYNIIVKFCRAIDIIYSLTSCNMSKMDIALQYTESALT 294

Db 249 KHKRLKLTITLVYIYVITQLPYNIIVKFCRAIDIIYSLTSCNMSKMDIALQYTESALT 308

Qy 295 HSCINPLIYVEMGASFKNYMKVAKKYG 322

Db 309 HSCINPLIYVEMGASFKNYMKVAKKYG 336

RESULT 6

CKR9\_HUMAN STANDARD; PRT; 357 AA.

ID CKR9\_HUMAN

AC P51686;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE C-C chemokine receptor type 9 (C-C CKR-9) (CC-CKR-9) (CCR-9) (GPR-9-6).

GN CKR9 OR CCKBR9.

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RA SEQUENCE FROM N.A.  
 RA Lactens L.L., Tiffany H.L., Gao J.-L., Modi W., Murphy P.M.,  
 RA Bonner T.I.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN  
 RP CHARACTERIZATION.  
 RX MEDLINE=9248139; PubMed=10229797;  
 RA Zaballo A., Gutierrez J., Varona R., Ardavin C., Marquez G.,  
 RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the  
 RT receptor for the chemokine TECK."  
 RL J. Immunol. 162:5671-5675(1999).  
 CC -1- FUNCTION: Receptor for chemokine SCYA25/TECK. Subsequently  
 CC transduces a signal by increasing the intracellular calcium ions  
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN  
 CC LYMPH NODES AND SPLEEN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC  
 CC EMBL; U45982; AAA9319.1; -.  
 CC Genew; HGNC:1610; CCR9.  
 DR MIM; 604738; -.  
 DR InterPro; IPR004069; CC chemkines.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1.1.  
 DR PRINTS; PRO1531; CHEMOKINER9.  
 DR PRINTS; PRO0237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KM G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 37  
 FT TRANSMEM 38 64  
 FT DOMAIN 65 73  
 FT TRANSMEM 74 94  
 FT DOMAIN 95 108  
 FT TRANSMEM 109 130  
 FT DOMAIN 131 148  
 FT TRANSMEM 149 169  
 FT DOMAIN 170 198  
 FT TRANSMEM 199 226  
 FT DOMAIN 227 242  
 FT TRANSMEM 243 268  
 FT DOMAIN 269 292  
 FT TRANSMEM 293 310  
 FT DOMAIN 311 357  
 FT CAROXYD 20 20  
 FT DISULFID 197 186  
 SQ SEQUENCE 357 AA; 40713 MW; 96982E0B922FEB31 CRC64;  
 Query Match 35.0%; Score 637; DB 1; Length 357;  
 Best Local Similarity 36.5%; Pred. No. 3,4e-32;  
 Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps 4;  
 QY 10 DYVYEE-NEMNGYDYVSOYELICIKEDVREFAKFLPVLFTLVFVIGLAGNSVVAIYAY 68  
 DB 4 DVGSESTSMEDYVNNFNFDYCEKKNVQAFSHPLPLYLWLVFVIGLAGNSLVLVWY 63  
 QY 69 YKQRTKTVYVILNLAVALDLFLTPPEVAVAVAGWVLGKIMCKITTSALYTLNFSQMG 128  
 DB 64 CTRVKTMDMFLNLAIALDLFLVTLPLFWAIAADQMKQTFMCKVNSMYMNFYSCVL 123  
 QY 129 FLACISIDRYVAVTVPKSGVSGKPCW-----IICFCVMAAILLSIPQLVFTYV 179

DB 124 LWCISVDKRTIAQ-----AMRAHTREKRLLYSKMCFTIWWAALCIPELVSQIK 178  
 QY 180 DN---ARCIPEPRYLGSMKALIQMLEICIGFVVPFLMGVCYFTRITMKPNKIS 236  
 DB 179 EESGALCTMWPESDESTLKSAVLTKVLIGFLPLFVMAACVYIIHTLLQAKSKS 238  
 QY 237 RELKULTVYVYITVQLPYNIVKCEGDAIDIIYLSITSCNMSKMDAIQVETSLAFHS 296  
 DB 239 KALKRTITVLTVFVLSOPFCILLVQTDVAVMFISNCAVSTNIDICFOVTQRTAFPHS 298  
 QY 297 CLNPLIYVFMGASFKNYVAKKYYG 322  
 DB 299 CLNPLVLYVFGFRFRDLVKTLKING 324  
 RESULT 7  
 CCR6\_MOUSE  
 ID CCR6\_MOUSE STANDARD; PRT; 367 AA.  
 AC 054689;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 6 (C-C CCR-6) (CC-CCR-6) (CCR-6) (KY411).  
 GN CCR6 OR CCR6B6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yanagihara S., Komura E., Yamaguchi Y.;  
 RT "Mouse G-protein-coupled receptor KY411."  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99077268; PubMed=9862452;  
 RA Varona R., Zaballo A., Gutierrez J., Martin P., Roncal F.,  
 RA Albar J.P., Ardavin C., Marquez G.,  
 RT "Molecular cloning, functional characterization and mRNA expression  
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand  
 RT MIP-3alpha."  
 RL FEBS Lett. 440:188-194 (1998).  
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-  
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE  
 CC INTRACELLULAR CALCIUM IONS LEVEL.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC  
 CC EMBL; AB009369; BAA23776.1; -.  
 DR EMBL; AJ222714; CAA10956.1; -.  
 DR MGD; MG1133797; Cmkbr6.  
 DR InterPro; IPR004067; CC\_chemkines.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1.1.  
 DR PRINTS; PRO1529; CHEMOKINER6.  
 DR PRINTS; PRO0237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KM G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 39  
 FT TRANSMEM 40 66  
 FT DOMAIN 67 75  
 FT TRANSMEM 76 96  
 FT DOMAIN 97 111  
 EXTRACELLULAR (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).



Query Match	Best Local Similarity	Matches 129; Conservative	33.3%; Pred. 37.9%;	Score 605; DB 1; Length 367;
FT TRANSMEM	112	133	3 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT DOMAIN	134	151	4 (POTENTIAL).	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	152	172	5 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	173	203	6 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	204	230	7 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	231	246	8 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	247	271	9 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	272	295	10 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	296	313	11 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	314	367	12 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	315	367	13 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	316	367	14 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	317	367	15 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	318	367	16 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	319	367	17 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	320	367	18 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	321	367	19 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	322	367	20 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	323	367	21 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	324	367	22 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	325	367	23 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	326	367	24 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	327	367	25 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	328	367	26 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	329	367	27 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	330	367	28 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	331	367	29 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	332	367	30 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	333	367	31 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	334	367	32 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	335	367	33 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	336	367	34 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	337	367	35 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	338	367	36 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	339	367	37 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	340	367	38 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	341	367	39 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	342	367	40 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	343	367	41 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	344	367	42 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	345	367	43 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	346	367	44 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	347	367	45 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	348	367	46 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	349	367	47 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	350	367	48 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	351	367	49 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	352	367	50 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	353	367	51 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	354	367	52 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	355	367	53 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	356	367	54 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	357	367	55 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	358	367	56 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	359	367	57 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	360	367	58 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	361	367	59 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	362	367	60 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	363	367	61 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	364	367	62 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	365	367	63 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	366	367	64 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	367	367	65 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	368	367	66 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	369	367	67 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	370	367	68 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	371	367	69 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	372	367	70 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	373	367	71 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	374	367	72 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	375	367	73 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	376	367	74 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	377	367	75 (POTENTIAL).	CYTOPLASMIC (POTENTIAL).

RA	ZBELLINO 97040707; PubMed=886020;
RX	Medline=9724503; PubMed=9070937;
RT	Liio F., Lee H.-H., Fairer J.M.,
RT	"Cloning of STR122, a new human gene encoding a G-protein-coupled
RT	receptor related to chemokine receptors and located on chromosome
RT	6q27.";
RL	Genomics 40:175-180(1997).
RL	SEQUENCE FROM N.A.
CC	-1 FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC	ALPHA/LIAC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC	INTRACELLULAR CALCIUM IONS LEVEL.
CC	-1 SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1 TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
CC	LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC	-1 INDUCTION: BY INTERLEUKIN-2.
CC	-1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC	-1 CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; U45984; AAB62714.1; -;
DR	EMBL; Z79784; CAB02144.1; ALT_INIT.
DR	EMBL; U60030; AAB06949.1; -;
DR	EMBL; U68030; AAC51124.1; -;
DR	EMBL; U68032; AAC51125.1; -;
DR	HSSP; P34996; 1DD.
DR	Genew; HGNC:1607; CCR6.
DR	MTM; G01835;
DR	InterPro; IPR000020; Anaphylatoxin.
DR	InterPro; IPR004067; CC_Chemokine6.
DR	InterPro; IPR000276; GPCR_Rhodopsn.
DR	Pfam; PFO0001; 7tm 1, 1.
DR	PRINTS; PR01529; CHEMOKINER6.
DR	PRINTS; PR00237; GPCR_RHODOPSIN.
DR	SMART; SM00104; ANATO_1.
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.
KW	DOMAIN
FT	DOMAIN 1 47
FT	TRANSMEM 48 74
FT	DOMAIN 75 83
FT	TRANSMEM 84 104
FT	DOMAIN 105 119
FT	TRANSMEM 120 141
FT	DOMAIN 142 159
FT	TRANSMEM 160 180
FT	DOMAIN 181 211
FT	TRANSMEM 212 238
FT	DOMAIN 239 254
FT	TRANSMEM 255 279
FT	DOMAIN 280 303
FT	TRANSMEM 304 321
FT	DOMAIN 322 374
FT	DISULFID 118 197
FT	CARBOHYD 7 7
FT	CARBOHYD 23 23
FT	CONFLICT 60 60
FT	G -> A (IN REF. 4).

CC	EMBL: AF007859; AAB64225.1; --
DR	InterPro; IPR000276; GPCR_Rnodbns.
DR	Pfam; PF00001; 7tm_1, 1.
DR	PRINTS; PR000237; GPCRRHODSPN.
DR	PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
DR	PROSITE; PS00262; G PROTEIN RECP FL 2; 1.
KM	G-protein coupled receptor; Transmembrane; glycoprotein.
FT	DOMAIN 1 32
FT	TRANSMEM 33 59
FT	DOMAIN 60 68
FT	TRANSMEM 69 89
FT	DOMAIN 90 103
FT	TRANSMEM 104 125
FT	DOMAIN 126 143
FT	TRANSMEM 144 164
FT	DOMAIN 165 187
FT	TRANSMEM 188 215
FT	DOMAIN 216 231
FT	TRANSMEM 232 259
FT	DOMAIN 260 275
FT	TRANSMEM 276 293
FT	DOMAIN 294 342
FT	DISELFD 102 180
FT	CAROHWD 16 16
SQ	SEQUENCE 342 AA; 39226 MW; 6CBFE389C6E5919E CRC64;
Query Match	31.9%; Score 581; DB 1; Length 342;
Best Local Similarity	34.2%; Pred. No. 8.1e-29;
Matches 121; Conservative 71; Mismatches 130; Indels 32; Gaps	
OY	12 YYEENEMNGTYVYSQYELICIKEDYREAFKVLPEFLTIVFVIGLAGNSMVVAIYAAYKK 71
Db	6 HYEDNGFNFSNDSSGE---HQDFLGSKSVLPFCMYLVVFVCGLVGMSLVLVISFIHK 61
OY	72 QRTKDVIYLINAVALDLLFLTPFWAANAHVAGWLGKIMCKITSAALTLANVSGNOFLA 131
Db	62 LQSLDVFPLVNLPLDLFVCTLPFWAAVAGIHWEIFGVGMCTLLGIITYINFYSMLILT 121
OY	132 CISIDRYAVATVPSS--OSGVAKPCW--ICECVMAAILLSIPOLVPTYV--NDNARCI 185
Db	122 CITVDREFIVVATATANYNQAKMTMGVKVICTLIIVISILVSLPDIIGNVFNPKLIC- 180
OY	186 PTFPYRLGTSMKALIQMLEICIGFVVPLINGVCYFITARTLMKNPNIKISRPKLVT 245
Db	181 ----GYHDEISTVLAQTOMTLGFELPLAMIVCSYVIKTLHLHAGQKRSLKIIFLV 236
OY	246 VIVFVLTOFPNIYVFCRAIDIYLSLSCMSKRMDAIDVOTBSIALFHSGIANILVVF 305
Db	237 MAVFLITOTPRVLVLAISTHMEYAMTSFHT-----LIVETAIALAQLACLNVLVAF 290
OY	306 MGASEFKNYVMVAKKYG-----SWRROQSVEEPDPSEGETPTSTFSI 350
Db	291 VSLKRFKNFMVLVKDIGCLPYLGVS HQKSSEDNSK--TFASHNVLEATSNFQL 342
RESULT 10	
ID CCR6_MACMU STANDARD; PRT; 343 AA.	
AC O9XT45;	
DT 16-OCT-2001 (Rel. 40, Created)	
DT 16-OCT-2001 (Rel. 40, Last sequence update)	
DT 15-JUN-2002 (Rel. 41, Last annotation update)	
DE X-C chemokine receptor type 6 (CXCR-6) (G protein-coupled	
receptor bonzo) (G protein-coupled receptor STRL33).	
GN CXCR6 OR BONZO OR STRL33.	
OS Macaca mulatta (Rhesus macaque).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;	
OC Cercopithecinae; Macaca.	
NCBI_taxid=9544;	
NN [1]	
SEQUENCE FROM N.A.	

RX MEDLINE=21354176; PubMed=11461684;  
 RA Margulies B.J., Hauer D.A., Clements J.E.;  
 RT "Identification and comparison of eleven rhesus macaque chemokine  
 RT receptors";  
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).  
 CC - FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A  
 CC CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.  
 CC - SUBCELLULAR LOCATION: Integral membrane protein.  
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL: AF124380; AAD31419.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.  
 DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 CC -----  
 FT DOMAIN 1 33  
 FT TRANSSEM 34  
 FT DOMAIN 60  
 FT TRANSSEM 69  
 FT DOMAIN 70 90  
 FT TRANSSEM 91 104  
 FT DOMAIN 105 126  
 FT TRANSSEM 127 144  
 FT DOMAIN 145 165  
 FT TRANSSEM 166 188  
 FT DOMAIN 189 216  
 FT TRANSSEM 217 232  
 FT DOMAIN 233 260  
 FT TRANSSEM 261 276  
 FT DOMAIN 277 294  
 FT TRANSSEM 295 343  
 FT CARBOHYD 17 17  
 FT DISULFID 103 181  
 FT SEQUENCE 343 AA; 39423 MW; 48DB2544949EB83F CRC64;  
 SQ  
 Query Match 31.4%; Score 571; DB 1; Length 343;  
 Best Local Similarity 33.4%; Pred. No. 3.3e-28;  
 Matches 119; Conservative 73; Mismatches 132; Indels 32; Gaps 8;

10 DYVEENENNGTYDYSOVELICIKEDVREFAKFLPVEFLTVFVIGLAGNSMVAIYAY 69  
 5 DHYEDDGLFNSNDSSQEE---HODPLQFRKVPFLPCMYLVFVGVGLVNSLIVISIFY 60  
 70 KQRTKTDVYIINLAVADILLFTLPFMAVNAVHGVLGKIMCKTSLTYLTNPFVSGNQF 129  
 61 HGLQSLDVLVNLPLADLVFVCTLPFMAVAGIHGMVIGQVWCKTLGVYITNFTSMLI 120  
 130 IACISIDRVAAVATKPS--QSGVGKPCW--IICFCVMAAILISIPOLVFVTV--NDNAR 183  
 121 LCTIVYDRIIVVAKTKAVNQAKMTGKVCILTIWISLVSIPQIIYGVFVNLDTLI 180  
 184 CTIPFRYLGTSKMLIOMLEICIGFVFPFLMGVCYFTIARTLMKMPNIKISPLKVL 243  
 181 C-----GYHDEISIVLATLQWTLGFLPLAMIVCYSVYIKTLIHAGGFQKHSILKTIIF 235  
 244 TVYIVETVQLPYNIYKFGRAIDIIYSLTSCMSKMDIALQVNESIALPHSCINPLTY 303  
 236 LVAWAVLLQTFENLVKILRSTHWEYVAMTSFHYT-----LIVTEALAYLRACINPVLY 289  
 304 VFMGASFKYVVMKVAKYG-----SMRROQSVEEFPDSEGPTEPTSFESI 350  
 290 AFVSLKFRKFKVLVDIGCLPILGVSHQWKSSEDSNK--TSASHNVATATSMFQL 343  
 DB

RESULT 11  
 ID\_CCR6\_MACNE STANDARD; PRT; 342 AA.  
 AC 019024;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled  
 DE receptor bonzo).  
 GN CXCR6 OR BONZO.  
 OS Macaca nemestrina (Pig-tailed macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 NCBI\_TaxID=9545;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97373958; PubMed=9230441;  
 RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;  
 RT "Expression cloning of new receptors used by simian and human  
 RT immunodeficiency viruses";  
 RL Nature 388:296-300(1997).  
 CC - FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A  
 CC CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.  
 CC - SUBCELLULAR LOCATION: Integral membrane protein.  
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL: AF007858; AAB64224.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.  
 DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 CC -----  
 FT DOMAIN 1 32  
 FT TRANSSEM 33 59  
 FT DOMAIN 60 88  
 FT TRANSSEM 69 89  
 FT DOMAIN 90 103  
 FT TRANSSEM 104 125  
 FT DOMAIN 126 143  
 FT TRANSSEM 144 164  
 FT DOMAIN 165 187  
 FT TRANSSEM 188 215  
 FT DOMAIN 216 231  
 FT TRANSSEM 232 259  
 FT DOMAIN 260 275  
 FT TRANSSEM 276 293  
 FT DOMAIN 294 342  
 FT DISULFID 102 180  
 FT CARBOHYD 16 16  
 FT SEQUENCE 342 AA; 39297 MW; 55F9F68CB2D2DF5 CRC64;  
 SQ  
 Query Match 31.3%; Score 569; DB 1; Length 342;  
 Best Local Similarity 33.6%; Pred. No. 4.3e-28;  
 Matches 119; Conservative 72; Mismatches 131; Indels 32; Gaps 8;

12 YVEENENNGTYDYSOVELICIKEDVREFAKFLPVEFLTVFVIGLAGNSMVAIYAYKK 71  
 6 YHEDYGLNSNDSSQEE---HODPLQFRKVPFLPCMYLVFVGVGLVNSLIVISIFYK 61  
 72 QRTKTDVYIINLAVADILLFTLPFMAVNAVHGVLGKIMCKTSLTYLTNPFVSGNQFLA 131  
 62 LQSLDVLVNLPLADLVFVCTLPFMAVAGIHGMVIGQVWCKTLGVYITNFTSMLILT 121  
 DB

QY 132 CISIDRYAVATKVPSS--OSGVKPCW--IICFCVMAAILISIPOLVFYVY--NDNARCI 185  
 DB 122 CITVDRFIVVVKATKANKNOQAKMTWKGVTICLLIIVISLVSLEQIIYGVNENIDKILC- 180  
 QY 186 PIFPRYLGTSKAKALIOMLEICIGFVVPFLINGVCYFITAATLMKMPNIKISRLPKVLLTV 245  
 DB 181 ----GYHDEAISTVLAQTOMTLGFFLPLAMIVCYSVIAIKTLHAGGFQKRSIKIIFLV 236  
 QY 246 VIVFLVQLPYNIYVFCRAIDIIISLTSCMSKRMIDAIQVETISALFHSCLNPIIYVF 305  
 DB 237 MAVFLITPFPNLVNLKIFISTHWEYAMTSFHYT-----IMVTEALVYLRACLNPIVLYAF 290  
 QY 306 MGASFKNYVMVAKKYG-----SWRROROSVEEFPDSEGPTEPTSTFSI 350  
 DB 291 VSLKRRKNFVWLVDIGLPLVGVSHQKXSEDSK--TFSASHNVATISMFOU 342

RESULT 12  
 CCR6 HUMAN STANDARD; PRT; 342 AA.  
 ID CCR6\_HUMAN 000574; 000575;  
 AC 000574; 000575;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled  
 DE receptor bonzo) (G protein-coupled receptor STRL33).  
 GN CXCR6 OR BONZO OR STRL33 OR TYMSR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97373958; PubMed=9230441;  
 RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;  
 RT "Expression cloning of new receptors used by simian and human  
 RT immunodeficiency viruses.";  
 RL Nature 388:296-300(1997).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97311099; PubMed=9166430;  
 RA Liao F., Alkhatib G., Peden K.W.C., Sharma G., Berger E.A.,  
 RA Farber J.W.;  
 RT "STRL33, A novel chemokine receptor-like protein, functions as a  
 RT fusion cofactor for both macrophage-tropic and T cell line-tropic  
 RT HIV-1.";  
 RL J. Exp. Med. 185:2015-2023(1997).  
 RL [3]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Blood;  
 MEDLINE=97431687; PubMed=9285716;  
 RA Loetscher M., Amara A., Oberlin E., Brass N., Legler D.F.,  
 RA Loetscher P., D'Amico M., Meese E.U., Rouselet D., Virelizier J.L.,  
 RA Baggiolini M., Arenzana-Seisdedos F., Moser B.;  
 RT "TYMSR, a putative chemokine receptor selectively expressed in  
 RT activated T cells, exhibits HIV-1 coreceptor function.";  
 RL Curr. Biol. 7:652-660(1997).  
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A  
 CC CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID TISSUES AND ACTIVATED T  
 CC CELLS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL, AF007545; AAB64221.1; --

DR EMBL, U73529; AAB61456.1; --  
 DR EMBL, U73531; AAB61457.1; --  
 DR EMBL, U13248; CAA73698.1; --  
 DR MIM, 605163; --  
 DR InterPro; IPR00276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCR\_Rhodopsn.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.  
 FT DOMAIN 1 32  
 FT TRANSMMEM 33 59  
 FT DOMAIN 60 68  
 FT TRANSMMEM 69 89  
 FT DOMAIN 90 103  
 FT TRANSMMEM 104 125  
 FT DOMAIN 126 143  
 FT TRANSMMEM 144 164  
 FT DOMAIN 165 187  
 FT TRANSMMEM 188 215  
 FT DOMAIN 216 231  
 FT TRANSMMEM 232 259  
 FT DOMAIN 260 275  
 FT TRANSMMEM 276 293  
 FT DOMAIN 294 342  
 FT DISULFID 102 180  
 FT CARBOHYD 16 16  
 FT VARIANT 25 25  
 FT D -> A (IN STRL33.3).  
 FT N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT FTID=VAR\_003506.  
 SQ SEQUENCE 342 AA; 39280 MW; 9FBC025556D1082E CRC64;

Query Match 30.8%; Score 560; DB 1; Length 342;  
 Best Local Similarity 33.1%; Pred. No. 1.5e-27; Indels 32; Gaps 8;  
 Matches 117; Conservative 75; Mismatches 130;

QY 12 YVENENNGTYDYSQYELICIKEDREPAKFLPFLITVEVIGLAGNSMVAIAYYKK 71  
 DB 6 YHEDYGFSFSDSSQEE---HDFLQSKVFLPCMYLVVFCGLVGNLSLVISIFYHK 61  
 QY 72 QRTKDYIILNLAVALDLLETLPEFNAVNAVHGVNLKIMKITSALTYLTNPFSGMFLA 131  
 DB 62 LQSLTDFVLNPLADLIVFCTLPFNAVAGIHEVFPQVWCKSLGLYITNPFYSMLIT 121  
 QY 132 CISIDRYAVATKVPSS--OSGVKPCW--IICFCVMAAILISIPOLVFYVY--NDNARCI 185  
 DB 122 CITVDRFIVVVKATKANKNOQAKMTWKGVTISLIVISLVSLEQIIYGVNENIDKILC- 180  
 QY 186 PIFPRYLGTSKAKALIOMLEICIGFVVPFLINGVCYFITAATLMKMPNIKISRLPKVLLTV 245  
 DB 181 ----GYHDEAISTVLAQTOMTLGFFLPLAMIVCYSVIAIKTLHAGGFQKRSIKIIFLV 236  
 QY 246 VIVFLVQLPYNIYVFCRAIDIIISLTSCMSKRMIDAIQVETISALFHSCLNPIIYVF 305  
 DB 237 MAVFLITPFPNLVNLKIFISTHWEYAMTSFHYT-----IMVTEALVYLRACLNPIVLYAF 290  
 QY 306 MGASFKNYVMVAKKYG-----SWRROROSVEEFPDSEGPTEPTSTFSI 350  
 DB 291 VSLKRRKNFVWLVDIGLPLVGVSHQKXSEDSK--TFSASHNVATISMFOU 342

RESULT 13  
 CCR4 HUMAN STANDARD; PRT; 360 AA.  
 ID CCR4\_HUMAN 051679; 09UUY6; 09UUY7;  
 AC 051679; 09UUY6; 09UUY7;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-X-C chemokine receptor type 4 (C-CR-4) (CCR-4) (CCR4)  
 DE (K5-5).  
 GN CCR4 OR CMKBR4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

CC NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Spleen;  
RX MEDLINE=95370289; PubMed=7642634;  
RA Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,  
RA Proudfoot A.E.I., Wells T.N.C.;  
RT "Molecular cloning and functional expression of a novel CC chemokine  
RL J. Biol. Chem. 270:19495-19500(1995).  
RN [2]  
RN SEQUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.  
RX MEDLINE=21040311; PubMed=11196669;  
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,  
RA Hirai K., Tokunaga K.;  
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";  
RL Genes Immun. 1:97-104(1999).  
RN [3]  
RN FUNCTION.  
RX MEDLINE=97313486; PubMed=9169480;  
RA Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;  
RT "The T cell-directed CC chemokine TARC is a highly specific  
RL J. Biol. Chem. 272:15036-15042(1997).  
RN [4]  
RN FUNCTION.  
RX MEDLINE=98104168; PubMed=9430724;  
RA Imai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska R.,  
RA Yoshie O., Gray P.W.;  
RT "Macrophage-derived chemokine is a functional ligand for the CC  
RL J. Biol. Chem. 273:1764-1768(1998).  
RN [5]  
RN FUNCTION.  
RX MEDLINE=99393604; PubMed=10466728;  
RA Campbell J.J., Haraldsen G., Pan J., Rotteman J., Qin S., Ponath P.,  
RA Andrew D.P., Wankle R., Ruffing N., Kassam N., Wu L., Butcher E.C.;  
RT "The chemokine receptor CCR4 in vascular recognition by cutaneous but  
RL not intestinal memory T cells.";  
RN Nature 400:776-780(1999).  
RN [6]  
RN FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.  
RP MEDLINE=20219238; PubMed=10754297;  
RX Immingfjorden M., Danaei B., Maghaeechi A.A.;  
RT "Human NK cells express CC chemokine receptors 4 and 8 and respond to  
RL chemokine, and activation-regulated chemokine, macrophage-derived  
RN J. Immunol. 164:4048-4054(2000).  
CC -I- FUNCTION: HIGH AFFINITY RECEPTOR FOR THE C-C TYPE CHEMOKINES  
CC TARC/SCYA17 AND MDC/SCYA22. THE ACTIVITY OF THIS RECEPTOR IS  
CC MEDIATED BY G11 PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITOL-  
CC CALCIUM SECOND MESSENGER SYSTEM. CAN FUNCTION AS A CHEMOATTRACTANT  
CC HOMING RECEPTOR ON CIRCULATING MEMORY LYMPHOCYTES AND AS A  
CC CORECEPTOR FOR SOME PRIMARY HIV-2 ISOLATES. IN THE CNS, COULD  
CC MEDIATE HIPPOCAMPAL-NEURON SURVIVAL.  
CC SUBCELLULAR LOCATION: Integral membrane protein.  
CC -I- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE THYMUS, IN  
CC PERIPHERAL BLOOD LEUKOCYTES, INCLUDING T CELLS, MOSTLY CD4+ CELLS,  
CC AND BASOPHILS, AND IN PLATELETS; AT LOWER LEVELS, IN THE SPLEEN  
CC AND IN MONOCYTES. DETECTED ALSO IN MACROPHAGES, IL-2-ACTIVATED  
CC NATURAL KILLER CELLS AND SKIN-HOMING MEMORY T CELLS, MOSTLY THE  
CC ONES EXPRESSING THE CUTANEOUS LYMPHOCYTE ANTIGEN (CLA). EXPRESSED  
CC IN BRAIN MICROVASCULAR AND CORONARY ARTERY ENDOTHELIAL CELLS.  
CC -I- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES  
CC PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY  
CC BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.  
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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CC	EMBL; X85740; CAAS9743.1; -.
DR	EMBL; AB023888; BAA6965.1; -.
DR	EMBL; AB023889; BAA6966.1; -.
DR	EMBL; AB023890; BAA6967.1; -.
DR	EMBL; AB023891; BAA6968.1; -.
DR	EMBL; AB023892; BAA6969.1; -.
DR	GeneW; HGNC.1605; CCRA.
DR	MIM; 604836; -.
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm.1; 1.
DR	PRINTS; PR00237; GFCCRHOOPSN.
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;
KW	Phosphorylation; Polymorphism.
KM	DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM 40 67 1 (POTENTIAL).
FT	DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM 78 98 2 (POTENTIAL).
FT	DOMAIN 99 111 EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM 112 133 3 (POTENTIAL).
FT	DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM 151 175 4 (POTENTIAL).
FT	DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM 207 226 5 (POTENTIAL).
FT	DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM 243 267 6 (POTENTIAL).
FT	DOMAIN 268 284 EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM 285 308 7 (POTENTIAL).
FT	DOMAIN 309 360 CYTOPLASMIC (POTENTIAL).
FT	CAROHWD 183 183 N-LINKED (GHCNAC. . .) (POTENTIAL).
FT	CAROHWD 194 194 N-LINKED (GHCNAC. . .) (POTENTIAL).
FT	DISULFD 110 187 BY SIMILARITY.
FT	VARIANT 130 L->V.
FT	/FTId=VAR_010669.
FT	C->S.
FT	/FTId=VAR_010670.
SQ	SEQUENCE 360 AA; 41402 MW; 51BBI2NDLFAFABF CRC64;

Query Match	29.5%;	Score 537.5;	DB 1;	Length 360;
Best Local Similarity	35.8%;	Pred. No. 3,6e-26;		
Matches 115;	Conservative 63;	Mismatches 124;	Indels 19;	Gaps 6
Qy	10	DYYEENENGGTYDYSQYBCLCKEVRHSAKVELVFLTIVVIGLAGSMVVAIYAY	69	
Db	8	DTTLDESITSNYLVESIPKPTCKBQIKAFGEFLFLPLYSVLVVFGLGNSVVVLFXK	67	
Qy	70	KKORTTDDYVLIINLAVAADLLLEFTTEPFMAVNAVHGVWLQKIMKITSALYTLNPFVSGMOF	129	
Db	68	KRLRSMSTDVYLLNLALISDLLFVPSLFPMGXYAADQVAVFGIGLCKMISMWLVGFYSGIFF	127	
Qy	130	LACISIDRYAVAYTKV-----PSQSGYCKPCMIIOFCVMAAILISIPOLVF---YTVN	179	
Db	128	VMIAMSIDRYALIAVHAFSLRARTLYGV-----TSLATWSAVAFPSLPPFLSTCYTER	162	
Qy	180	DNARCPIPFPRYLGTSKMAKLIQMLEI-CIGFYVVPFLIMGVCYPTARTMKMENIKISR	238	
Db	183	NHYYCKTKKS--LNSITWKLSSLSEILNIGLVPLGIMLFCYGMIIIRTLCHCKNEKNKA	240	
Qy	239	LKVLVLVVVVFITYTQLPYNIYKFCRAIDITYSLITSCNMSKRMDDIAIQVETSLAFHSC	298	
Db	241	VKNIFVAVVVFLEFQWPNYNVLVLETL--VELAVLODCTFERRYLDYALQATETTLAFVHCL	299	
Qy	299	NPLIYVFMGASPFKNYVMKAVK	319	
Db	300	NPLIYFPLGKFRKRYTLQLFK	320	

ID IL8B HUMAN STANDARD; PRT; 360 AA.  
AC P25025;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (GRO/MGSA receptor) (IL-8 receptor type 2) (CDW128b).  
GN IL8RB OR CXCR2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91368200; PubMed=1891716;  
RA Murphy P.M., Tiffany H.L.;  
RT "Cloning of complementary DNA encoding a functional human interleukin-8 receptor.";  
RL Science 253:1280-1283 (1991).  
RL [2]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RX MEDLINE=93205012; PubMed=8384312;  
RA Certecci D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P., Beckmann M.P.;  
RT "Molecular characterization of receptors for human interleukin-8, GRO/melanoma growth-stimulatory activity and neutrophil activating peptide-2.";  
RL Mol. Immunol. 30:359-367 (1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94209273; PubMed=7512557;  
RA Sprenger H., Lloyd A.R., Lautens L.L., Bonner T.I., Kelvin D.J.;  
RT "Structure, genomic organization, and expression of the human interleukin-8 receptor B gene.";  
RL J. Biol. Chem. 269:11065-11072 (1994).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Placenta;  
RX MEDLINE=95014476; PubMed=7929358;  
RA Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;  
RT "Comparison of the genomic organization and promoter function for human interleukin-8 receptors A and B.";  
RL J. Biol. Chem. 269:26381-26389 (1994).  
RN [5]  
RP CHARACTERIZATION.  
RX MEDLINE=92355587; PubMed=1379593;  
RA Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;  
RT "Characterization of two high affinity human interleukin-8 receptors.";  
RL J. Biol. Chem. 267:16283-16287 (1992).  
CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -1- DATABASE: NAME=PRO; NOTE=CD guide Cdw128b entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw128b.htm".  
CC -----  
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CC -----  
CC EMBL; M73969; AAA83148.1; -  
DR EMBL; M94582; AAA36108.1; -  
DR EMBL; M99412; AAC14460.1; -  
DR EMBL; L19593; AAB59437.1; -  
DR

DR EMBL; U11869; AAB0656.1; -  
DR PIR; A39446; A39446.  
DR PIR; A53611; A53611.  
DR HSSP; P34996; 1DD.  
DR Genew; HGNC:6027; IL8RB.  
DR MIM; 146928; -  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR000832; GPCR\_secretin.  
DR Pfam; PF00001; 7tm1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSN.  
DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS0262; G-PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
KW Chemotaxis.  
FT DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 49 75 1 (POTENTIAL).  
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 85 105 2 (POTENTIAL).  
FT DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 121 142 3 (POTENTIAL).  
FT DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 164 183 4 (POTENTIAL).  
FT DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 209 231 5 (POTENTIAL).  
FT DOMAIN 232 251 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 252 273 6 (POTENTIAL).  
FT DOMAIN 274 294 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 295 315 7 (POTENTIAL).  
FT DOMAIN 316 360 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT DISULFID 119 196 BY SIMILARITY.  
SQ SEQUENCE 360 AA; 40759 MW; 564F04A8BCC0A197 CRC64;  
Query Match 29.4%; Score 534.5; DB 1; Length 360;  
Best Local Similarity 33.2%; Pred. No. 5.5e-26;  
Matches 120; Conservative 75; Mismatches 141; Indels 25; Gaps 8;  
QY 3 LEONOSTDYEEENENGTVDYSQYEI-----CIKEDREFAKVFLPVFLTIVFVIGLA 57  
DB 6 MDSDFEDFWKEDSDNSYSSTLPRLDDAPCEPSEI-EINKYFVYIYALVFLSL 64  
QY 58 GNSMVAIYAYKKORTDYIINLAVADLLFTLPFMAVNAHGVGKIMCKITSA 117  
DB 65 GNSLVMLVILSVGRSVTDVYLLNLALADLLFALTLPIMASKNGMIFGFLCKVSL 124  
QY 118 LYTINLVGMOPLACISIDRYAV---TKVPSQSGVGKPCPIICPCVMAAILLSIQVL 174  
DB 125 LKEVNFYSGILLACISVDYLAIVHATRTLTOKRY--LVKFIQLSIWGLSLALPVL 182  
QY 175 F---YTVNDNARCIPRPVYIG--TSMKALIQMLEICIGFVVPFLIMGVCFITARTL 227  
DB 183 FRTYYSNVSPAC---EDMGNTANWRMLILPOSFFIYPLIMLFCYFTLRTL 238  
QY 228 MKPNIKISRLPKVLLTVIVFIVTQLEPYNIYKFCRAIDIIYSLITSCNMSKMDIAIOV 287  
DB 229 FGAHNGQGHARARVFAVVLFLCMLPYNLVLLADTLMTROVIOECERNRHIDRLDA 298  
QY 288 TESTILFHSCLNPLIYVMGSPKMYVKAUKGSMRQ---RQSVSEFPDSEGTPEP 344  
DB 299 TEILDILHSCLNPLIYVARGFRRGLKILAIHGLSKSLPDSRSPSPFVGSSGHTST 358  
QY 345 T 345  
DB 359 T 359  
RESULT 15  
ID IL8B\_PANTR STANDARD; PRT; 353 AA.  
AC Q28607;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DR

DE High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (Fragment).  
 GN IL8RB OR CXCR2.  
 OS Pan troglodytes (Chimpanzee). Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominoidea; Pan.  
 NC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.  
 NCBI\_TaxId=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96175151; PubMed=9110929;  
 RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,  
 RA Lopez-Iarrea C.;  
 RT "Characterization of interleukin-8 receptors in non-human primates";  
 CC Immunogenetics 43:261-267(1996).  
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL  
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR  
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A  
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND  
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY  
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; X91113; CAA62563.1; -  
 DR HSPB; P34996; 1DD0  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR InterPro; IPR000832; GPCR\_secretin.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL\_1; 1.  
 DR PROSITE; PS50262; G-PROTEIN RECEPTOR FL\_2; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KM Chemotaxis.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 46 72 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 73 81 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 82 102 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 103 117 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 118 139 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 140 160 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 161 180 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 206 228 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 229 248 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 249 270 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 292 312 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 313 353 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 116 193 BY SIMILARITY.  
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 353 353  
 FT SEQUENCE 353 AA; 39998 MW; E745ACD9EC10C1E2 CRC64;  
 Query Match 29.1%; Score 529.5; DB 1; Length 353;  
 Best Local Similarity 33.6%; Pred. No. 1,1e-25;  
 Matches 118; Conservative 74; Mismatches 132; Indels 27; Gaps 8;

DB 122 IKEVNFYSGILLACISVDYRIATVHATRTLTQKRY--LVKFTICISTIGSLALAPVLL 179  
 QY 175 F---YTVNDNARCIPRPRIYLG---TSMKALIQMLFICIGFVVPFLIMGYCYFTARTL 227  
 DB 180 FRRIVYSSVSPACY---EDGKNTTANWRMLRLNLPSPGFYPLDMLCYGFTARTL 235  
 QY 228 MGPENIKISRPILKVLITFVIVFIVTQLPYNIYKFCRAIDIIYSITSCNMSKMDIAIQV 287  
 DB 236 FFAHNGQKHARARVFAVVLFLCMLPYNLYLADLTMRQTVOIETCERRNHIRALDA 295  
 QY 288 TESIALFHSCLNPIIYVMGASFKYVNVKAKYSSMRQGSVEEPFDS 338  
 DB 296 TELIGLHSCINPLIYAFIQGKFRHGLKILAIHG-----LISKSLPDS 341  
 RESULT 16  
 ID CKD6\_HUMAN STANDARD; PRT; 384 AA.  
 AC 000590; 000537; 096A02;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Chemokine binding protein 2 (chemokine-binding protein D6) (C-C  
 DE chemokine receptor D6) (Chemokine receptor CCR-9) (CC-Chemokine  
 DE receptor CCR10).  
 GN CCBR2 OR CMBRK9 OR CCR10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=98030218; PubMed=9364936;  
 RA Bonini J.A., Martin S.K., Dralyuk F., Roe M.W., Philipson L.H.,  
 RA Steiner D.F.;  
 RT "Cloning, expression, and chromosomal mapping of a novel human CC-  
 RT chemokine receptor (CCR10) that displays high-affinity binding for  
 RT MCP-1 and MCP-3.";  
 RL MCP-1 and MCP-3.";  
 RL DNA Cell Biol. 16:1249-1256(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98070370; PubMed=9405404;  
 RA Nibbs R.J.B., Wylie S.M., Yang J., Landau N.R., Graham G.J.;  
 RT "Cloning and characterization of a novel promiscuous human  
 RT beta-chemokine receptor D6.";  
 RL J. Biol. Chem. 272:32078-32083(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=21134058; PubMed=11238036;  
 RA Nibbs R.J.B., Kriebner E., Ponath P.D., Parent D., Qin S.,  
 RA Campbell J.D., Henderson A., Kerjaschki D., Maurer D., Graham G.J.,  
 RA Rot A.;  
 RT "The beta-chemokine receptor D6 is expressed by lymphatic endothelium  
 RT and a subset of vascular tumors.";  
 RL Am. J. Pathol. 158:867-877(2001).  
 CC -1- FUNCTION: RECEPTOR FOR C-C TYPE CHEMOKINES INCLUDING SCYA2/MCP-1,  
 CC SCYA/MIP-1-ALPHA, SCYA5/RANTES AND SCYA7/MCP-3.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE LUNG AND LYMPH NODE.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE LUNG AND LYMPH NODE.  
 CC FOUND IN ENDOTHELIAL CELLS LINING APPARENT LYMPHATICS IN DERMIS  
 CC AND LYMPH NODES. ALSO FOUND IN LYMPH NODES SUBCAPSULAR AND  
 CC MEDULLARY SINUSES, TONSILAR LYMPHATIC SINUSES AND LYMPHATICS IN  
 CC MUCOSA AND SUBMUCOSA OF SMALL AND LARGE INTESTINE AND APPENDIX.  
 CC ALSO FOUND IN SOME MALIGNANT VASCULAR TUMORS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.



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DR EMBL: U94888; AAB97728.1; -;  
 DR EMBL: Y12815; CAA73346.1; -;  
 DR EMBL: BC020558; AAH20558.1; -;  
 DR EMBL: BC011631; AAH11631.1; -;  
 DR EMBL: BC008816; AAH08816.1; -;  
 DR Genew: HGNC:1565; CCBP2.  
 DR MIM: 602648; -;

DR InterPro: IPR000276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm\_1; 1.

DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; FALSE\_NEG.  
 DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 50  
 FT TRANSMEM 51 71  
 FT TRANSMEM 72 92  
 FT TRANSMEM 93 113  
 FT TRANSMEM 114 118  
 FT TRANSMEM 119 140  
 FT TRANSMEM 141 162  
 FT TRANSMEM 163 183  
 FT TRANSMEM 184 217  
 FT TRANSMEM 218 238  
 FT TRANSMEM 239 250  
 FT TRANSMEM 251 271  
 FT TRANSMEM 272 293  
 FT TRANSMEM 294 314  
 FT TRANSMEM 315 384  
 FT CARBOHYD 19 19  
 FT DISULFID 117 195  
 FT CONFLICT 17 17  
 FT CONFLICT 161 161  
 FT CONFLICT 356 356  
 SQ SEQUENCE 384 AA; 43442 MW; 464CS703CIDE9A6A CRC64;

Query Match 29.0%; Score 527; DB 1; Length 384;  
 Best Local Similarity 32.9%; Pred. No. 1.6e-25;  
 Matches 107; Conservative 72; Mismatches 112; Indels 34; Gaps 7;

QY 6 NOSTDYEEENKNGTYDSQYE--LICIKEDVREFAKVLFPVPLTIVPYIGLAGSNMNV 63  
 DB 17 SENSSEFY-----VDYLDVAVFAMLCRDADVVSFGKVELPVEYSLLIFVLGLSGNLLLL 68  
 QY 64 AIAVYKORRTKIDVYLNLAVADLLFLTPFAVAVAVHGWLGKMKCTSAVTNP 123  
 DB 69 MVLIRYPRRRMVEITLNLALISMLFLVLPFGISVANHWVGSFLCMTVSLTYIN 128  
 QY 124 VSGWQFLACISIDRYVAV-----TVYPSQGVGKPCWITICCVMAAAILISPOL 173  
 DB 129 YSGIFPISCMGLKYLEIVAAQPYHARTRAKS-----LLATITVAVSLAVSIPDM 180  
 QY 174 VFTVANDNAR---CIPFRYIGTSKALIQMLEICIGVAVPPLINGVCYFTARTLMK 229  
 DB 181 VFQVQHTENPGVWVNCADFGGH-GTIWKLFRLRQNLGFLPLMLMIFPYSRIGCVLR 239  
 QY 230 MPNIKISRLPKVLLTVIVIVLQVPIVYKFCRAIDIIYSLTSCMSKRMALAOVTE 289  
 DB 240 LRPAGQGRALKIAALVAALVAFVLMFPYNLTLPLHTL-LDLQVNGCEVSOHLDAVLQVTE 298  
 QY 290 SIALFSGCLNPIIYVFWGASFKNV 314  
 DB 299 SIAFLHCCFSPILIYAFSNNFRQYL 323

## RESULT 17

AC CKRA HUMAN STANDARD; PRT; 362 AA.  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 10 (C-C CKR-10) (CC-CKR-10) (CCR-10) (G-  
 DE protein coupled receptor 2).  
 GN CCR10 OR GPR2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RX MEDLINE=20191997; PubMed=10725696;  
 RA Jarmán D.I., Rite W., Bota D., Gerard N.P., Graham G.J.,  
 RA Clark-Lewis I., Gerard C.;  
 RT "Cutting edge: identification of the orphan receptor G-protein-coupled  
 RT receptor 2 as CCR10, a specific receptor for the chemokine ESKine.";  
 RL J. Immunol. 164:3460-3464(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RX MEDLINE=20191998; PubMed=10725697;  
 RA Homey B., Wang W., Soto H., Buchanan M.E., Wiesenborn A., Catron D.,  
 RA Muller A., McClanahan T.K., Dieu-Nosjean M.C., Orozco R., Ruzicka T.,  
 RA Lehmann P., Oldham E., Zlotnik A.;  
 RT "Cutting edge: the orphan chemokine receptor G protein-coupled  
 RT receptor-2 (GPR-2, CCR10) binds the skin-associated chemokine CCL27  
 RT (CTACK/ALP/ILC).";  
 RL J. Immunol. 164:3465-3470(2000).  
 RN [3]  
 RP SEQUENCE OF 9-362 FROM N.A.  
 RX MEDLINE=95154831; PubMed=7851889;  
 RA Marchese A., Docherty J.M., Nguyen T., Heiber M., Cheng R.,  
 RA Heng H.H.Q., Tsai L.-C., Shi X., George S.R., O'Dowd B.P.;  
 RT "Cloning of human genes encoding novel G protein-coupled receptors.";  
 RN Genomics 23:609-618(1994).  
 RN [4]  
 RP LIGAND BINDING, AND TISSUE SPECIFICITY.  
 RX MEDLINE=20357357; PubMed=10781587;  
 RA Wang W., Soto H., Oldham E.R., Buchanan M.E., Homey B., Catron D.,  
 RA Jenkins N., Copeland N.G., Gilbert D.J., Nguyen N., Abrams J.,  
 RA Kershenovich D., Smith K., McClanahan T., Vicari A.P., Zlotnik A.;  
 RT "Identification of a novel chemokine (CCL28), which binds CCR10  
 RT (GPR2).";  
 RL J. Biol. Chem. 275:22313-22323(2000).  
 RN [5]  
 RP LIGAND BINDING.  
 RX MEDLINE=20432268; PubMed=10975800;  
 RA Pan J., Kunkel E.J., Gossard U., Lazarus N., Langdon P., Broadwell K.,  
 RA Vierra M.A., Genovese M.C., Butcher E.C., Soler D.;  
 RT "A novel chemokine ligand for CCR10 and CCR3 expressed by epithelial  
 RT cells in mucosal tissues.";  
 RL J. Immunol. 165:2943-2949(2000).  
 CC -1- FUNCTION: RECEPTOR FOR CHEMOKINES SCYA27 AND SCYA28. SUBSEQUENTLY  
 CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS  
 CC LEVEL AND STIMULATES CHEMOTAXIS IN A PRE-B CELL LINE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT TESTIS,  
 CC SMALL INTESTINE, FETAL LUNG, FETAL KIDNEY. WEAKER EXPRESSION WAS  
 CC OBSERVED IN MANY OTHER ADULT TISSUES INCLUDING SPLEEN, THYMUS,  
 CC LYMPH NODE, PEYER'S PATCHES, COLON, HEART, OVARY, PERIPHERAL BLOOD  
 CC LYMPHOCYTES, THYROID AND SPINAL CORD. ALSO EXPRESSED BY  
 CC MELANOCYTES, DERMAL FIBROBLASTS, DERMAL MICROVASCULAR ENDOTHELIAL  
 CC CELLS. ALSO DETECTED IN T CELLS AND IN SKIN-DERIVED LANGERHANS  
 CC CELLS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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QY 142 TKVPS-----QSGVGKPCWIIICPCWMAAILSLPOLVFTVNDNARCIPFRYIGT 194  
 DB 133 VLAANSNNRRVQHGV-----TISGVMAAILVAVPQMTTKKDN-ECIGDVPVLQOE 186  
 QY 195 SMKALIQMLEICIGFVPEFLMGVCYFTTARTLMKMPNIKISRLPKVLLTVVIVFVITQL 254  
 DB 187 IMPVLNSENVAIIGFVLLPLILMSFCYFRIVRTLFSCRRKARARILLLVAVVVFPLFWT 246  
 QY 255 PYNIVKFCRAIDIIYSLTSCNMSKMDIAIOVTESTALFHSCLNPLIYVPMGASFKNV 314  
 DB 247 PYNIVFETETK-FYNFPSCGMKRDLMALSTETVAFSHCCLNPLIYAPAGEKFRRL 305  
 QY 315 MKVAKK 320  
 DB 306 RHLVVK 311

RESULT 19  
 IL8B GORGO STANDARD; PRT; 353 AA.  
 AC 028423;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE High affinity Interleukin-8 receptor B (IL-8R B) (CXCR-2) (Fragment).  
 OS IL8RB OR CXCR2.  
 GN Gorilla gorilla gorilla (lowland gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.  
 OC NCBI\_TaxID=9595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9617515; PubMed=9110929;  
 RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,  
 Lopez-Larrea C.,  
 RT "Characterization of interleukin-8 receptors in non-human primates";  
 RL Immunogenetics 43:261-267(1996).  
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL  
 NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR  
 CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A  
 G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND  
 MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY  
 AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X91114; CA62564.1; -.  
 DR HSSP; P34996; 1DDU.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR000832; GPCR\_secretin.  
 DR Pfam: PF00001; 7tm\_1, 1.1.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL\_1, 1.  
 DR PROSITE; PS50262; G-PROTEIN RECEPTOR FL\_2, 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KM Chemotaxis.  
 FT NON\_TER 1 1  
 FT DOMAIN <1 45  
 FT TRANSMEM 46 72  
 FT DOMAIN 73 81  
 FT TRANSMEM 82 102  
 FT DOMAIN 103 117  
 FT TRANSMEM 118 139  
 FT DOMAIN 140 160  
 FT TRANSMEM 161 180  
 FT DOMAIN 181 205  
 EXTRACELLULAR (POTENTIAL).  
 1 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 2 (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 3 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 4 (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 206 228 5 (POTENTIAL).  
 FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 249 270 6 (POTENTIAL).  
 FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 292 312 7 (POTENTIAL).  
 FT DOMAIN 313 353 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 116 193 BY SIMILARITY.  
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 353 353  
 SQ SEQUENCE 353 AA; 39919 MW; 1PF04E31A7B825E4 CRC64;  
 Query Match 28.7%; Score 522.5; DB 1; Length 353;  
 Best Local Similarity 33.1%; Pred. No. 2.9e-25;  
 Matches 115; Conservative 74; Mismatches 139; Indels 19; Gaps 6;  
 QY 3 LEONOSTDYIYENENMGTYDSQYEI-----CKEVDREPAKFLPVLFTIYFVIGLA 57  
 DB 3 MESDSFEDFWKGEDLSYSSALPPFLIDASPCEPESL-EINKYFVVIYALVFLSL 61  
 QY 58 GNSMVAIYAYKKQRTQTDVYILNLAVADLLLETPFMVAVNAGVGLKINCKITSA 117  
 DB 62 GNSLVILVILSRVRSVTDYLLNLADLLFALTLPIMASKVNGHIFGTFLCKVSL 121  
 QY 118 LYTLPVSGMOFLACISIDRYAV--TKVPSQSGVGKPCWIIICPCWMAAILSLPOLV 174  
 DB 122 LKEVNFYSGIILLACISDRYALIVHATRTLTQKRY-LYKFCISIGSLALLALPVLL 179  
 QY 175 FTYVDNARCIFIPRYIG--TSKALIQMLEICIGFVPEFLMGVCYFTTARTLMKMP 231  
 DB 180 FRRTIYPSVSPVCYEDGNMTANMLRLIPQSGFIVPLILMLFCYGTPLTLFVQAH 239  
 QY 232 NIKISRLPKVLLTVVIVFVITQLPYNIVKFCRAIDIIYSLTSCNMSKMDIAIOVTESEI 291  
 DB 240 MGQKRAKRVIVAVVILFLCMLPYNVLLADTLMRQTIVGTETGERNHINQALDATEIL 299  
 QY 292 ALFHSCLNPLIYVPMGASFKNVYMKVAKKSGMRRQSVSEPPPS 338  
 DB 300 GILHSCNPLIYAFIGQFCGLKILAIHG-----LISKSLPDS 341

RESULT 20  
 C3X1\_HUMAN STANDARD; PRT; 355 AA.  
 AC P49238;  
 ID C3X1\_HUMAN  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE CX3C chemokine receptor 1 (C-X3-C CR-1) (CX3CR1) (Fractalkine  
 DE receptor) (GPR13) (V28) (beta chemokine receptor-like 1) (CMK-BRL-1)  
 DE (CMKBLR1).  
 GN CX3CR1 OR GPR13.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96011651; PubMed=7590284;  
 RA Raport C.J., Schweickart V.L., Eddy R.L., Jr., Shows T.B., Gray P.W.,  
 RT "The orphan G-protein-coupled receptor-encoding gene V28 is closely  
 RT related to genes for chemokine receptors and is expressed in lymphoid  
 RT and neural tissues";  
 RL Gene 163:295-299(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95374679; PubMed=7646814;  
 RA Combadere C., Ahuja S.K., Murphy P.M.,  
 RT "Cloning, chromosomal localization, and RNA expression of a human  
 RT beta chemokine receptor-like gene";  
 RL DNA Cell Biol. 14:673-680(1995).  
 RN [3]  
 RP CHARACTERIZATION.  
 RX MEDLINE=98050927; PubMed=9390561;

RA Imai T., Hieshima K., Haskell C., Baba M., Nagira M., Nishimura M.,  
 RA Kakizaki M., Takagi S., Nomiyama H., Schall T.J., Yoshie O.;  
 RT "Identification and molecular characterization of fractalkine receptor  
 RT CX3CR1, which mediates both leukocyte migration and adhesion.";  
 RL Cell 91:521-530(1997).  
 RN [4]  
 RP CHARACTERIZATION.  
 RX MEDLINE=98395093; PubMed=9726990;  
 RA Combadiere C., Salzwedel K., Smith E.D., Tiffany H.L., Berger E.A.,  
 RA Murphy P.M.;  
 RT "Identification of CX3CR1, A chemotactic receptor for the human CX3C  
 RT chemokine fractalkine and a fusion coreceptor for HIV-1.";  
 RL J. Biol. Chem. 273:23799-23804(1998).  
 RN [5]  
 RP VARIANTS ALA-57, ILE-122, ILE-249 AND MET-280.  
 RX MEDLINE=20196025; PubMed=10731151;  
 RA Faure S., Meyer L., Costagliola D., Vaneesberghe C., Genin E.,  
 RA Auriant B., Delfraissy J.-F., McDermott D.H., Murphy P.M., Debre P.,  
 RA Theodorou I., Combadiere C.;  
 RT "Rapid progression to AIDS in HIV+ individuals with a structural  
 RT variant of the chemokine receptor CX3CR1.";  
 RL Science 287:2274-2277(2000).  
 CC -1- FUNCTION: RECEPTOR FOR THE CX3C CHEMOKINE FRACTALKINE AND MEDIATES  
 CC BOTH ITS ADHESIVE AND MIGRATORY FUNCTIONS. ACTS AS CO-RECEPTOR  
 CC WITH CD4 FOR HIV-1 VIRUS ENVELOPE PROTEIN (IN VITRO).  
 CC -1- SUBCELLULAR LOCATION: EXPRESSED IN LYMPHOID AND NEURAL TISSUES.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID AND RAPID  
 CC PROGRESSION TO AIDS ARE ASSOCIATED WITH THE 1-249/M-280 HAPLOTYPE.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL; U20350; AAA91783.1; -;  
 DR EMBL; U28934; AAA87032.1; -;  
 DR Genew; HGNC:2558; CX3CR1.  
 DR MIM: 601470; -;  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1  
 DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECPT\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECPT\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Polymorphism.  
 FT DOMAIN 1 31  
 FT TRANSMEM 32 59  
 FT DOMAIN 60 69  
 FT TRANSMEM 70 90  
 FT DOMAIN 91 103  
 FT TRANSMEM 104 125  
 FT DOMAIN 126 142  
 FT TRANSMEM 143 167  
 FT DOMAIN 168 195  
 FT TRANSMEM 196 215  
 FT DOMAIN 216 231  
 FT TRANSMEM 232 256  
 FT DOMAIN 257 273  
 FT TRANSMEM 274 297  
 FT DOMAIN 298 355  
 FT DISULFID 102 175  
 FT VARIANT 57 57  
 FT VARIANT 122 122  
 FT VARIANT 249 249  
 FT VARIANT 280 280

FT FT POPULATION).  
 FT /FTID=VAR\_010044;  
 SQ SEQUENCE 355 AA; 40396 MW; C59DC5F4C4312F22 CRC64;  
 Query Match 28.7%; Score 522.5; DB 1; Length 355;  
 Best Local Similarity 36.4%; Pred. No. 2.9e-25;  
 Matches 112; Conservative 57; Mismatches 122; Indels 17; Gaps 5;  
 QY 22 YDSQYELICIKEDYREPAKVELPVELTIVFVIGLANSMTVAIYAYKKORTKTDVTL 81  
 DB 12 FEYDILAEACVYIGDVLVGQVFLSIFYSVIFAGVGNLIVFALTNKSKPSVDIVYL 71  
 QY 82 NLAVALDLILFLPFWANVAHGWLGIMCKITSAKTINPVSGMOFLACISIDRYAV 141  
 DB 72 NLAISDLFLVATLPFWTHYLINKEGHNAMCKFTTAPFFPGSIFITVVISIDRYALI 131  
 QY 142 TVPVS-----OSGVGRKWCIFCVMMAALISLPOLVFVTVDNARCIPFPRYUGT 194  
 DB 132 VLAANSNNRTYQHG-----TISLGWAAALIVAPQPMFKOKEN-ECIGDYDEVLOE 185  
 QY 195 SMKALIQMLEICIGFVPEPLMGVCYFITARTLMKPNIKSRPLKULTTVIVFIVQL 254  
 DB 186 IMPVLANVTENFLGFLPLILMSYCFRIQTLFSCKNHKKAKAIKLILVIVFLEWT 245  
 QY 255 PNIYVFCALDIYISLITSCMSKRMDAIQVTSIALFHSCLNPLIVFPGASFKNYV 314  
 DB 246 PYVMIFLETLK-LYDFPSCDMRDLRLASVETVAFSHCCNPLIYAFAGEFRRL 304  
 QY 315 MKVAKKYG 322  
 DB 305 YHL---YG 309  
 RESULT 21  
 ID CKR4\_MOUSE STANDARD; PRT; 360 AA.  
 AC P51680;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 4 (C-C-CR-4) (CC-CR-4) (CCR4).  
 GN CCR4 OR CMKBR4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;  
 RX MEDLINE=96136324; PubMed=8573157;  
 RA Hoogewerf A.J., Black D., Proudfoot A.B.I., Wells T.N.C., Power C.A.;  
 RT "Molecular cloning of murine CC CR-4 and high affinity binding of  
 RT chemokines to murine and human CC CR-4.";  
 RL Biochem. Biophys. Res. Commun. 218:337-343(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Cytotoxic T-cell;  
 RX MEDLINE=97335974; PubMed=9192769;  
 RA Youn B.-S., Kim S.-H., Lyu M.S., Kozak C.A., Taub D.D., Kwon B.S.;  
 RT "Molecular cloning and characterization of a cDNA, CHER1, encoding a  
 RT chemokine receptor with a homology to the human C-C chemokine  
 RT receptor, CCR-4.";  
 RL Blood 89:4448-4460(1997).  
 RN [3]  
 RP FUNCTION.  
 RX MEDLINE=20273981; PubMed=10811868;  
 RA Buser R., Conquet F., Proudfoot A.E.I., Wells T.N.C., Power C.A.;  
 RT "A key role for CC chemokine receptor 4 in lipopolysaccharide-induced  
 RT endotoxic shock.";  
 RL J. Exp. Med. 191:1755-1764(2000).  
 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR THE C-C TYPE CHEMOKINES  
 CC TARC/SCYA17 AND MDC/SCYA22. THE ACTIVITY OF THIS RECEPTOR IS  
 CC MEDIATED BY G(I) PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITOL-

CC CALCIUM SECOND MESSENGER SYSTEM. COULD PLAY A ROLE IN  
 CC LIPOPOLYSACCHARIDE (LPS)-INDUCED ENDOTOXIC SHOCK. IN THE CNS,  
 CC COULD MEDIATE HIPPOCAMPAL-NEURON SURVIVAL.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE THYMUS, MACROPHAGES AND T-  
 CC AND B-CELLS.  
 CC -1- DEVELOPMENTAL STAGE: LOW EXPRESSION AT 7.5 DPC AND 12.5 DPC IN THE  
 CC YOLK SAC.  
 CC -1- PM: IN NATURAL KILLER CELLS, SCY22 BINDING INDICES  
 CC PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY  
 CC BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2 (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL: X90862; CAA62372.1; -  
 DR EMBL: U15208; AAA92582.1; -  
 DR MGI: 107824; Cmkb14.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHOPOPSN.  
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.  
 DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Phosphorylation.  
 FT DOMAIN 1 39  
 FT TRANSMEM 67  
 FT DOMAIN 68 77  
 FT TRANSMEM 78 98  
 FT DOMAIN 99 111  
 FT TRANSMEM 112 133  
 FT DOMAIN 134 150  
 FT TRANSMEM 151 175  
 FT DOMAIN 176 206  
 FT TRANSMEM 207 226  
 FT DOMAIN 227 242  
 FT TRANSMEM 243 267  
 FT DOMAIN 268 284  
 FT TRANSMEM 285 308  
 FT DOMAIN 309 360  
 FT TRANSMEM 343 346  
 FT CARBOHYD 2 2  
 FT CARBOHYD 183 183  
 FT CARBOHYD 194 194  
 FT DISULFID 110 187  
 FT CONFLICT 4 4  
 FT CONFLICT 145 145  
 FT CONFLICT 181 181  
 FT CONFLICT 205 205  
 FT CONFLICT 221 221  
 FT CONFLICT 241 241  
 FT CONFLICT 246 246  
 FT CONFLICT 293 293  
 FT CONFLICT 311 311  
 SO SEQUENCE 360 AA; 41462 MW; 97BDB8C6D539AE3 CRC64;  
 Query Match 28.7%; Score 522.5; DB 1; Length 360;  
 Best Local Similarity 33.7%; Pred. No. 2,9e-25;  
 Matches 110; Conservative 69; Mismatches 128; Indels 19; Gaps 6;

QY 123 FVSGMQLACISIDRVAVTKV-----PSOSGVKPCWIIICFWMAAILLSPOLVF 175  
 DB 121 FVSGIFPIMMSIDRYLAVHAFSLKARTLTGV-----ITSLTWASVAFASLPGLIF 175  
 QY 176 ---YVNDNARCIPIPRYIGTSMKALIQMLEI-CIGFVPLINGVCYIFARILMKMP 231  
 DB 176 STCYTEHNHTCYKQYS--VNSTWVKVLSLEINVLGILFGLIFWYSMIRLQK 233  
 QY 232 NITISPLKVLTVVIVFIVTQLPNIVKECAIDIIYSLTSCNMSKMDIAIQVTESI 291  
 DB 234 NEKKNVAMMIGVAVLVFGFWTPYNAVVLFEETL-VELEVLQDCTLERYLDVAIQATELT 292  
 QY 292 ALFHSCLNPLVYFNGASFKNYVMKV 317  
 DB 293 GFHHCNPLVYIFFGKFRKXITQTL 318  
 RESULT 22  
 IL8R MACMU  
 ID IL8R MACMU STANDARD; PRT; 353 AA.  
 AC Q28519;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (Fragment).  
 GN IL8RB OR CXCR2.  
 OS Macaca mulatta (rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OC NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96175151; PubMed=9110929;  
 RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,  
 RA Lopez-Larrea C.;  
 RT "Characterization of interleukin-8 receptors in non-human primates";  
 RL Immunogenetics 43:261-267(1996).  
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL  
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR  
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A  
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND  
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY  
 CC AND TO GBO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL: X91116; CAA62565.1; -  
 DR HSSP: P34996; IDDD.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR InterPro: IPR000832; GPCR\_secretin.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.  
 DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Chemotaxis.  
 FT NON TER 1 1  
 FT DOMAIN 1 1  
 FT TRANSMEM 46 72  
 FT DOMAIN 73 81  
 FT TRANSMEM 82 102  
 FT DOMAIN 103 117  
 FT TRANSMEM 118 139  
 FT DOMAIN 140 160  
 EXTRACELLULAR (POTENTIAL).  
 1 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 2 (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 3 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 161 180 4 (POTENTIAL).
FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 228 5 (POTENTIAL).
FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON TER 353
SQ SEQUENCE 353 AA; 39947 MW; EC8B38130657C713 CRC64;

Query Match 28.7%; Score 521.5; DB 1; Length 353;
Best Local Similarity 33.2%; Pred. No. 3.3e-25;
Matches 117; Conservative 74; Mismatches 132; Indels 29; Gaps 8;

QY 3 LEONQSDIYYEENMGTYDSQ-----YELICIKEDYREFAKVPFLPIVIVIGL 56
DB 3 MESDSEFDLMKGEDEFSN--YSISDLPSPSPDVAPCRPSLEINKYVITVAVLVLSTL 60
QY 57 AGNSMVAIYVYKQKRTKTDVTLNLAVADLLFTLPFAVANAHHGVLGKIMKITS 116
DB 61 LGNSLWMLVILYSVGRSVTDVYTLNLADLLFALFLPIWASKVNGWIFGFLCKVVS 120
QY 117 ALVTLNFSVGMQFLACISIDRYAV--TKVPSGVGKPCWITICFVWMAAILISPOL 173
DB 121 LKKEVNFSGILLACISVDRYLAIVHATRLTLQRY--LVKFLCISWGLSLALPVL 178
QY 174 VF---YVUNNARCIPFPFHYLG--TSMKALIQMLEICIGFVVPPLINGVCYFIART 226
DB 179 LFRRTVSSNVSPACY---EDMGNTNANMMLRLIPQSGFVPLILMFCVGFILRT 234
QY 227 LMKMENIKISPLKVLTLTVLTVLTVLPVNIYKFCRAIDITLYLITSCNMSKMDIAIQ 286
DB 235 LFKAMGQKHAMRVIFAVVLIFLLCWLPSYSLVLTADTLMTQVIOETCERNHIDRALD 294
QY 287 VTESIALFHSCLNPLIYVFMGASPKNYVMKAKKYSRRORSVEEPFDS 338
DB 295 ATEIIGLHSCNPLIYAFIQGKFRHGLKTLAIHG---LISKDSLPRDS 341

RESULT 23
CRA MOUSE STANDARD; PRT; 362 AA.
ID CRA MOUSE STANDARD; PRT; 362 AA.
AC Q9JL21; Q9JL20; Q9JL19;
PT 16-OCT-2001 (Rel. 40, Created)
PT 16-OCT-2001 (Rel. 40, Last sequence update)
PT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 10 (C-C CKR-10) (CCR-10)
GN (Chemokine C-C receptor 9) (G-protein coupled receptor 2).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=BALB/c; TISSUE=Peyer's patch;
RX MEDLINE=20191997; PubMed=10725696;
RA Jamin D.I., Rits M., Bots D., Gerard N.P., Graham G.J.,
RA Clark-Lewis I., Gerard C.;
RT "Cutting edge: Identification of the orphan receptor G-protein-coupled
RT receptor 2 as CCR10, a specific receptor for the chemokine ESKine.";
RT J. Immunol. 164:3460-3464(2000).
RN [2]
RN SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND LIGAND BINDING.
RP TISSUE=Thymocytes;
RC MEDLINE=20357357; PubMed=10781587;
RX Wang W., Soto H., Oldham E.R., Buchanan M.E., Homey B., Catron D.,
RX Jenkins N., Copeland N.G., Gilbert D.J., Nguyen N., Abrams J.,
RX Kerstenovich D., Smith K., McClanahan T., Vicari A.P., Zlotnik A.;
RT "Identification of a novel chemokine (CCL28), which binds CCR10

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RT (GPR2).";
RL J. Biol. Chem. 275:22313-22323(2000).
CC -1- FUNCTION: RECEPTOR FOR CHEMOKINES SCYA27 AND SCYA28. SUBSEQUENTLY
CC TRANSDUCE A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
CC LEVEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN SMALL INTESTINE,
CC COLON, LYMPH NODES, PEYER'S PATCHES AND AT LOWER LEVELS IN THYMUS,
CC LUNG, AND SPLEEN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL, AF215982; AAF63710.1; -.
DR EMBL, AF215983; AAF63711.1; -.
DR EMBL, AF208238; AAF72872.1; -.
DR MGD, MGI:1096320; Cmkbr9.
DR InterPro, IPR000276; GPCR_Rhodpsn.
DR Pfam, PF00001; 7cm_1; 1.
DR PRINTS, PR00237; GPCR_RHODOPSIN.
DR PROSITE, PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE, PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 49 69 1 POTENTIAL.
FT DOMAIN 70 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 101 2 POTENTIAL.
FT DOMAIN 102 115 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 116 136 3 POTENTIAL.
FT DOMAIN 137 159 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 160 180 4 POTENTIAL.
FT DOMAIN 181 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 229 5 POTENTIAL.
FT DOMAIN 230 247 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 248 268 6 POTENTIAL.
FT DOMAIN 269 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 POTENTIAL.
FT DOMAIN 313 362 CYTOPLASMIC (POTENTIAL).
FT DISULFID 113 191 BY SIMILARITY.
FT CONFLICT 135 135 N -> S (IN REF. 2).
SQ SEQUENCE 362 AA; 38926 MW; 0FF4EA2005B94E99 CRC64;

Query Match 28.6%; Score 520.5; DB 1; Length 362;
Best Local Similarity 33.9%; Pred. No. 3.8e-25;
Matches 119; Conservative 68; Mismatches 133; Indels 31; Gaps 7;

QY 22 YDSQYEL-----ICIKEDYREFAKVPFLPIVIVIGLANSMVAVIY-AYYKQRTK 75
DB 17 YDEBAYVGGVLPCLCYKADQVARSFAFQPSLWVAVLGIAGGLVATHTLAARRTRSP 76
QY 76 TDVYIILNLAVALDILLFTLPFAVANAHHGVLGKIMKITSALYTLNFSVGMQFLACISI 135
DB 77 TSVHLLQALADLLALTLTPFAAAGALQGMNLSGTCRAISGLYSASFHGLFLACINA 136
QY 136 DRYAVAVK-VPSSGVGKP--CWICFCVWMAAILISIPOLVY--TVNANRCIPFP 189
DB 137 DRYAVAVK-VPSSGVGKP--CWICFCVWMAAILISIPOLVY--TVNANRCIPFP 189
QY 190 RYLQTSKALIQMLEICIGFVVPPLINGVCYFIARTLMKMNKISRPKVLTVIVYV 249
DB 197 ESTLQYVKGASAVAGVVLGFLPLGVAAACVALLGRTLLAARPERRRALRVVAVLVAF 256
QY 250 IVTQLPNIYKFCADITLYLITSCNMSKMDIAIOVESIALFHSCLNPLIYVFMGAS 309
DB 257 VVTLQPSLALLDADTLAARSSSSSKRKDALALVTGTLVRCSLNPLVYAFPLGUR 316
QY 310 FKNYVMKAKKYGSM-----RRORSVEEPFDSGTEPTSTFSI 350

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DR MGD:1333815; Cx3crl.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 DR G-protein coupled receptor; Transmembrane.  
 KW DOMAIN 1 32  
 FT TRANSMEM 33 60  
 FT TRANSMEM 61 70  
 FT TRANSMEM 71 91  
 FT TRANSMEM 92 104  
 FT TRANSMEM 105 126  
 FT TRANSMEM 127 143  
 FT TRANSMEM 144 168  
 FT TRANSMEM 169 196  
 FT TRANSMEM 197 216  
 FT TRANSMEM 217 232  
 FT TRANSMEM 233 257  
 FT TRANSMEM 258 274  
 FT TRANSMEM 275 298  
 FT TRANSMEM 299 354  
 FT DISULFID 103 176  
 SQ SEQUENCE 354 AA; 40266 MW; 12C7458E83755CA9 CRC64;  
 Query Match 28.1%; Score 511; DB 1; Length 354;  
 Best Local Similarity 36.2%; Pred. No. 1.4e-24;  
 Matches 111; Conservative 57; Mismatches 123; Indels 16; Gaps 6;  
 QY 22 YDYGVEYLICIKEDVREFAKFLPFLITVFIYVIGLAGNSWVAIVAYKKRKTQTDVYIL 81  
 DB 13 FEYDSDAEACVIGIDIVAFGLTFISVYALVTFGLVGNLLVLLATNSRRKSTIDTYLL 72  
 QY 82 NLAVADLLFLTPPVAIVAVHGVWLVKIMKITSALYTLNPFVSGMPLACISIDRVAV 141  
 DB 73 NLALSDILFVATLPFWTHYLLISHEGLHNAKCKLTAFPEFGIGFPIYVISIDRYLAI 132  
 QY 142 TKVPS-----QSGVGPCKWICFCVMAAILSLIPOLVFEYVNDNARCIPIPRYIGT 194  
 DB 133 VLAANSNNRNVQVGV-----TISGVMAAILVASPQFMTRKKN-EGIGDYPEVL-Q 165  
 QY 195 SMKALIQMLEI-CIGFVVPFLIMGVCFITARTIMKRNKISPLKYLTVIVIVITQ 253  
 DB 186 EMMFPLARSEVNIIGFALPLLIMSCFYRIQTLFSCNRRKAKAVRLILLVAFELFW 245  
 QY 254 LPYNTVRCRAIDITISLITSCNMSKMDIAIQTESIALHSCINPLTYVEMASFKNY 313  
 DB 246 TPYNIMIFLETIK-FYNFPSCDMKRDRLALSVTEIVAFSHCCINPITYAFGEKFRRY 304  
 QY 314 VMKVAKK 320  
 DB 305 LGHLYRK 311  
 RESULT 26  
 IL8B\_RABIT STANDARD; PRT; 358 AA.  
 AC P35344;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE High affinity interleukin-8 receptor B (IL-8R B) (CKCR-2) (GRO/MSA receptor)  
 GN IL8RB OR CKCR2.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxId=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Albino; TISSUE=Blood;  
 RX MEDLINE=9430294; PUBMED=8175642;  
 RA Prado G.N., Thomas K.M., Suzuki H., Larosa G.J., Wilkinson N.C.,

RA Folco E., Navarro J.;  
 RT "Molecular characterization of a novel rabbit interleukin-8 receptor  
 RT isotype."  
 RL J. Biol. Chem. 269:12391-12394(1994).  
 CC -I- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL  
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR  
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A  
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND  
 CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAF-2 >  
 CC MSA (GRO).  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -I- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEUTROPHILS.  
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL: L24445; AAA1378.1; -.  
 DR PIR: A53752; A53752.  
 DR InterPro: IPR00276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Chemotaxis.  
 KW DOMAIN 1 46  
 FT TRANSMEM 47 73  
 FT TRANSMEM 74 82  
 FT TRANSMEM 83 103  
 FT TRANSMEM 104 118  
 FT TRANSMEM 119 140  
 FT TRANSMEM 141 161  
 FT TRANSMEM 162 181  
 FT TRANSMEM 182 206  
 FT TRANSMEM 207 229  
 FT TRANSMEM 230 249  
 FT TRANSMEM 250 271  
 FT TRANSMEM 272 292  
 FT TRANSMEM 293 313  
 FT TRANSMEM 314 358  
 FT CARBOHYD 8 20  
 FT CARBOHYD 20 194  
 FT DISULFID 117 194  
 SQ SEQUENCE 358 AA; 40632 MW; 6899716944D6126A CRC64;  
 Query Match 28.1%; Score 511; DB 1; Length 358;  
 Best Local Similarity 32.3%; Pred. No. 1.4e-24;  
 Matches 116; Conservative 72; Mismatches 139; Indels 32; Gaps 8;  
 QY 10 DYYEENENGVYDYSQYELI-----CIKEDVREFAKFLPFLITVFIYIGLA 57  
 DB 8 NYSYE--DFRG--DFSNYSYTDLPPTLDSAPCRSESESETNSVYLLIYI-LVFLSL 62  
 QY 58 GNSGVAIVAYKKRKTQTDVYILNLAVDLLFLPPVAIVAVHGVWLVKIMKITS 117  
 DB 63 GNSLVMVLVILSRSTCSVDVYILNLAIDLFPATLLPMAASKHGMFGPIKCVSL 122  
 QY 118 LYTLPFVSGMPLACISIDRVAV-----TKVPSQSGVGPCKWICFCVMAAILSLIPQ 172  
 DB 123 VKENVTFSGLLACISVRYALIVATRTIMQKRLVYK---FICLSMVGSLISLP 178  
 QY 173 LVFYTVNDNARCIPIPRYIGTS---MKALIQMLEICIGFVVPFLIMGVCFITARTIMK 229  
 DB 179 LTFRNALFPNNSPVCEDMGNSTAKRMVRLILPOTFGILPLVLMCCYFTLRLLQ 238  
 QY 230 MPNIKISRLKVLTVIVIVITQLPYNTVRCRAIDITISLITSCNMSKMDIAIQTE 289

Db 239 AHMGQKHAMRYFAVAVLIFLLCMLPYNLVLTDTLMTARTHYIQETCERNRIDALDATE 298  
 QY 290 SIALFHSCLNPLLYFMGASFNKVMYKAKKXGWRQ---RQSYEEPPFSGEPTPT 345  
 Db 299 ILGLHSLNPLIYAFQKFRYGLKILIAHGLISKEFLAKSRPSPVASSGNTSTT 357

RESULT 27

ID	CR2_MACMU	STANDARD	PRT	360 AA
AC	DI8793;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	C-C chemokine receptor type 2 (C-C CR-2) (CC-CR-2) (CCR-2) (CCR2)			
DE	(Monocyte chemoattractant protein 1 receptor) (MCP-1-R) (CCR2).			
GN	CCR2 OR CCR2.			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Macaca.			
OX	NCBI_TaxID=9544;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21354176; PubMed=11461684;			
RA	Margulies B.J., Hauer D.A., Clements J.E.;			
RT	"Identification and comparison of eleven rhesus macaque chemokine			
RT	receptors."			
RL	AIDS Res. Hum. Retroviruses 17:981-986(2001).			
CC	-1- FUNCTION: RECEPTOR FOR THE MCP-1, MCP-3 AND MCP-4 CHEMOKINES.			
CC	-1- TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS			
CC	LEVEL.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE			
CC	PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL: AF013958; AAD1572.1; -			
DR	InterPro: IPR000276; GPCR_Rhodopsin.			
DR	Pfam: PF00001; 7tm_1, 1.			
DR	PRINTS; PR00237; GPCRHHODPSN.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;			
KW	Alternative splicing.			
FT	DOMAIN 1 42			
FT	TRANSMEM 43 70			
FT	DOMAIN 71 80			
FT	TRANSMEM 81 100			
FT	DOMAIN 101 114			
FT	TRANSMEM 115 136			
FT	DOMAIN 137 153			
FT	TRANSMEM 154 178			
FT	DOMAIN 179 206			
FT	TRANSMEM 207 226			
FT	DOMAIN 227 243			
FT	TRANSMEM 244 268			
FT	DOMAIN 269 285			
FT	TRANSMEM 286 309			
FT	DOMAIN 310 360			
FT	CARBOHYD 14 14			
FT	MOD RES 26 26			
FT	DISULFID 113 190			
SO	SEQUENCE 360 AA; 41139 MW; 482552CBCE913FB9F CRC64;			

Query Match 27.7%; Score 504; DB 1; Length 360;  
 Best Local Similarity 33.5%; Pred. No. 3.8e-24;  
 Matches 107; Conservative 66; Mismatches 118; Indels 28; Gaps 8;

QY 17 ENMGTVDSQYELICIKEDVREFAKFLPEVFLTIFVIGLGNSSVAIYAYKKQRTKT 76  
 Db 19 EVTFPFDY-DYAPCHKRPVQKQIGNQLPLPLXSLVFIIFGVNMVLILINCKKLSLT 77  
 QY 77 DVTILNLAVADLLFLTPFMAVNAHGVATGKINCKTSALTYLTVSGMOFLACISID 136  
 Db 78 DVTILNLAVADLLFLTPFMAVNAHGVATGKINCKTSALTYLTVSGMOFLACISID 137  
 QY 137 RYAAVTKV-----PSQSGVGKPCMIICFCVMAAILLSIPQVIFYVNNAR---CIP 186  
 Db 138 RYAAVTKV-----PSQSGVGKPCMIICFCVMAAILLSIPQVIFYVNNAR---CIP 192  
 QY 187 IEPK--YLGTSKALLQMLLEICIGFVVPFLMGVCYFTARTLAKMPN-IKISPLKVL 242  
 Db 193 YPFRGNMNHITMRN-----LGLVPLILMVICSGILKTLRCNKKRRARVLI 245  
 QY 243 LTVIVYFVITQLPNIVKFCRAIDIIYSLITSCKMSKMDIAIOVTESIALFHSCLNPL 302  
 Db 246 FTIMIVYFLFTPNIVILNLTFCFEGFL-SNCESTRQDQATQVETLGMTHCCINPII 304  
 QY 303 YVFMGASFNKVMYKAKKY 321  
 Db 305 YAFVGEKFRYLSMFEPRKI 323

RESULT 28

ID	IL8A_RABIT	STANDARD	PRT	355 AA
AC	P21109;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	High affinity interleukin-8 receptor A (IL-8R A) (CXCR-1).			
GN	IL8RA OR CXCR1.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91378994; PubMed=1898400;			
RA	Beckmann M.P., Munger W.E., Kozlosky C., Vandenbos T., Price V.,			
RA	Lyman S., Gerard N.P., Gerard C., Cerretti D.P.;			
RT	"Molecular characterization of the interleukin-8 receptor.";			
RL	Biochem. Biophys. Res. Commun. 179:784-789(1991).			
CC	[2]			
CC	SEQUENCE FROM N.A.			
CC	STRAIN=Albino; TISSUE=Neutrophils;			
CC	MEDLINE=91056034; PubMed=1700779;			
CC	Thomas K.M., Pynn H.Y., Navarro J.;			
CC	"Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.";			
CC	J. Biol. Chem. 265:20061-20064(1990).			
CC	[3]			
CC	SEQUENCE FROM N.A.			
CC	TISSUE=Neutrophils;			
CC	MEDLINE=92148149; PubMed=1737938;			
CC	Lee J., Kuang W.-J., Rice G.C., Wood W.I.;			
CC	"Characterization of complementary DNA clones encoding the rabbit			
CC	IL-8 receptor.";			
CC	J. Immunol. 148:1261-1264(1992).			
CC	-1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL			
CC	NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR			
CC	CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A			
CC	G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND			
CC	MESSENGER SYSTEM.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: NEUTROPHILS.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			





DB 11 ETEFGTFTVDY-EPAPCFKVSITDLGAQFLPSLFLVIFVGLGNITVIVLTKYQKL 69  
QY 73 RTKDVYVLTINAVDILLFTLPFAVNAH--GVLGKIMCKITTSALTINLPSGQFL 130  
DB 70 KIMNIVYLTINAVDILLFTLPFWTY-YVMNKNVGFHEKCKISGLYYGLSEIFFI 128  
QY 131 ACISIDRYVAATKV-----PSOSGVKPCWIIICFCVMAAIIISLPOLVFTVNNAR 183  
DB 129 ILFTIDRLVLAIVHAFVARTRTVFGI-----ITSVITVLAVALPEPFVYTOGHFE 183  
QY 184 ---CLPIPRVLGISMKALIMLEICIGFVVPFLIMGVCFYTTARTMKPNKISPLK 240  
DB 184 VLFQPSYPERKEHMKRFPALRMNIFGLALPLIMICVYGIKTLRCPSKKKKAIR 243  
QY 241 VLLTVVIFVITQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIAIOTESIALFHSCLNP 300  
DB 244 LIFPIWVFVFPWTFPYNILLFSAFDL--SFLDCCERSKOLDMAKHVEVIAHTHCCLNP 301  
QY 301 ILVYFMGASFKNYV 314  
DB 302 IIVAFVGERFQKYL 315

RESULT 30  
CCR4 HUMAN STANDARD; PRT; 352 AA.  
ID CCR4 HUMAN  
AC P30991; P56438; Q9UKN2; O60835;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE C-X-C chemokine receptor type 4 (CXCR-4) (CXCR-4) (stromal cell-  
derived factor 1 receptor) (SDF-1 receptor) (Fusin) (leukocyte-derived  
seven transmembrane domain receptor) (LESTR) (LCR1) (PB22) (NPYRL,  
HM89) (CD184 antigen).  
GN CXCR4.  
OS Homo sapiens (Human), and  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606, 9598;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC SPECIES=Human; TISSUE=Lung;  
RX MEDLINE=93319629; PubMed=8329116;  
RA Herzog H., Hort Y.J., Shine J., Selbie L.A.;  
RT "Molecular cloning, characterization, and localization of the human  
RT homolog to the reported bovine NPY Y3 receptor: lack of NPY binding  
RT and activation.";  
RL DNA Cell Biol. 12:465-471(1993).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC SPECIES=Human; TISSUE=Fetal brain;  
RX MEDLINE=94052833; PubMed=8234909;  
RA Jazin E.E., Yoo H., Blomqvist A.G., Yee F., Weng G., Walker M.W.,  
RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its  
RT human homologue, confers neither NPY binding sites nor NPY  
RT responsiveness on transfected cells.";  
RL Regul. Pept. 47:247-258(1993).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC SPECIES=Human; TISSUE=Fetal spleen;  
RX MEDLINE=93315164; PubMed=8325644;  
RA Federspiel B., Melhado I.G., Duncan A.M., Delaney A.D.,  
RT Schappert K.T., Clark-Lewis I., Jirik F.R.;  
RT "Molecular cloning of the cDNA and chromosomal localization of the  
RT gene for a putative seven-transmembrane segment (7-TMS) receptor  
RT isolated from human spleen.";  
RL Genomics 16:707-712(1993).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC SPECIES=Human; TISSUE=Monocytes;  
RX MEDLINE=94103215; PubMed=8276799;

RA Loetscher M., Geisler T., O'Reilly T., Zwaahlen R., Baggiolini M.,  
RA Moser B.;  
RT "Cloning of a human seven-transmembrane domain receptor, LESTR, that  
RT is highly expressed in leukocytes.";  
RL J. Biol. Chem. 269:232-237(1994).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC SPECIES=Human; TISSUE=Monocytes;  
RX MEDLINE=94092629; PubMed=7505609;  
RA Nomura H., Nielsen B.W., Matsushima K.;  
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative  
RT leukocyte chemotactic peptide receptors.";  
RL Int. Immunol. 5:1239-1249(1993).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION OF ITS HIV-1  
RP CORRESPONDING FUNCTION.  
RX MEDLINE=96217947; PubMed=8629022;  
RA Feng Y., Broder C.C., Kennedy P.E., Berger E.A.;  
RT "HIV-1 entry cofactor: functional cDNA cloning of a seven-  
RT transmembrane, G protein-coupled receptor.";  
RL Science 272:872-877(1996).  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC SPECIES=Human; TISSUE=Peripheral blood leukocytes;  
RX MEDLINE=98136183; PubMed=9468539;  
RA Wegner S.A., Ehrenberg P.K., Chang G., Dayhoff D.E., Sleeker A.L.,  
RT "Genomic organization and functional characterization of the chemokine  
RT receptor CXCR4, a major entry co-receptor for human immunodeficiency  
RT virus type 1.";  
RL J. Biol. Chem. 273:4754-4760(1998).  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC SPECIES=Human;  
RX MEDLINE=98258970; PubMed=9599023;  
RA Caruz A., Samson M., Alonso J.M., Alcamí J., Baleux F.,  
RT Virelizier J.L., Parmentier M., Arenzana-Seisdedos F.;  
RT "Genomic organization and promoter characterization of human CXCR4  
RT gene.";  
RL FEBS Lett. 426:271-278(1998).  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC SPECIES=Human;  
RX MEDLINE=9408510; PubMed=10480633;  
RA Xiao L., Weiss S.H., Qari S.H., Rudolph D., Zhao C., Denny T.N.,  
RT "Partial resistance to infection by R5X4 primary HIV type 1 isolates  
RT in an exposed-uninfected individual homozygous for CCR5 32-base pair  
RT deletion.";  
RL AIDS Res. Hum. Retroviruses 15:1201-1208(1999).  
RN [10]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC SPECIES=Human; TISSUE=Peripheral blood lymphocytes;  
RX MEDLINE=99095114; PubMed=9879064;  
RA Froid R., Gierschik P., Moepfs B.;  
RT "Genomic organization and expression of the CXCR4 gene in mouse and  
RT man: absence of a splice variant corresponding to mouse CXCR4-B in  
RT human tissues.";  
RL J. Recept. Signal Transduct. Res. 18:321-344(1998).  
RN [11]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC SPECIES=Human; TISSUE=Neutrophils;  
RX MEDLINE=99384048; PubMed=10452968;  
RA Gupta S.K., Pillarsetti K.;  
RT "CXCR4-LD: molecular cloning and functional expression of a novel  
RT human CXCR4 splice variant.";  
RL J. Immunol. 163:2368-2372(1999).  
RN [12]  
RP SEQUENCE FROM N.A.  
RC SPECIES=P. troglodytes;  
RX MEDLINE=98090115; PubMed=9430250;  
RA Pretet J.-L., Zeribb A.C., Girard M., Guillet J.-G., Butor C.;  
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";

RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).  
 RN SULFATION.  
 RC SPECIES=Human;  
 RX MEDLINE=99189752; PubMed=10089882;  
 RA Farzan M., Mirzabekov T., Kojichinsky P., Wyatt R., Cayabyab M.,  
 RT Gerard N.P., Gerard C., Sodroski J., Choe H.;  
 "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1  
 entry.";  
 RL Cell 96:667-676(1999).  
 RN [14]  
 RP FUNCTION.  
 RX MEDLINE=96351077; PubMed=8752280;  
 RA Bleul C.C., Farzan M., Choe H., Parolin C., Clark-Lewis I.,  
 RT Sodroski J., Springer T.A.;  
 "The lymphocyte chemoattractant SDF-1 is a ligand for LESTR/fusin and  
 RT blocks HIV-1 entry.";  
 RL Nature 382:829-833(1996).  
 RN [15]  
 RP FUNCTION.  
 RX MEDLINE=96351078; PubMed=8752281;  
 RA Oberlin E., Amara A., Bachelet F., Bessia C., Virelizier J.-L.,  
 RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,  
 RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;  
 "The CXC chemokine SDF-1 is the ligand for LESTR/fusin and prevents  
 RT infection by T-cell-line-adapted HIV-1.";  
 RL Nature 382:833-835(1996).  
 RN [16]  
 RP ERRATUM.  
 RA Oberlin E., Amara A., Bachelet F., Bessia C., Virelizier J.-L.,  
 RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,  
 RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;  
 Nature 384:288-288(1996).  
 RN [17]  
 RP CHARACTERIZATION OF ITS HIV-1 CORECEPTOR FUNCTION.  
 RX MEDLINE=97002453; PubMed=8849450;  
 RA Lapham C.K., Ouyang J., Chandrasekhar B., Nguyen N.Y., Dimitrov D.S.,  
 RA Golding H.;  
 "Evidence for cell-surface association between fusin and the CD4-gp120  
 RT complex in human cell lines.";  
 RL Science 274:602-605(1996).  
 RN [18]  
 RP CHARACTERIZATION OF ITS HIV-2 RECEPTOR FUNCTION.  
 RX MEDLINE=97083584; PubMed=8929542;  
 RA Endres M.J., Clepham P.R., Marsh M., Anuja M., Turner J.D.,  
 RA McNight A., Thomas J.F., Stoeckenau-Haggarty B., Choe S., Vance P.J.,  
 RA Wells T.N.C., Power C.A., Sutherland S.S., Doms R.W., Landau N.R.,  
 RA Hoxie J.A.;  
 "CD4-independent infection by HIV-2 is mediated by fusin/CXCR4.";  
 RL Cell 87:745-756(1996).  
 RN [19]  
 RP FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A  
 SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
 INVOLVED IN HAEMATOPOIESIS AND IN CARDIAC VENTRICULAR SEPTUM  
 FORMATION. PLAYS ALSO AN ESSENTIAL ROLE IN VASCULARIZATION OF THE  
 GASTROINTESTINAL TRACT, PROBABLY BY REGULATING VASCULAR BRANCHING  
 AND/OR REMODELING PROCESSES IN ENDOTHELIAL CELLS. COULD BE  
 INVOLVED IN CEREBELLAR DEVELOPMENT. IN THE CNS, COULD MEDIATE  
 HIPPOCAMPAL-NEURON SURVIVAL. ACTS AS A PRIMARY RECEPTOR FOR SOME  
 HIV-2 ISOLATES AND AS A CO-RECEPTOR WITH CD4 FOR HIV-1 X4 VIRUSES  
 (LYMPHOCYTE-TROPIC HIV-1 VIRUSES, ALSO CALLED SYNCYTIIUM-INDUCING  
 (SI) STRAINS). PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.  
 CC (SI) STRAINS). PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.  
 CC LYMPHOCYTE-TROPIC HIV-1 VIRUSES, ALSO CALLED SYNCYTIIUM-INDUCING  
 CC (SI) STRAINS). PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.  
 CC SUBCELLULAR LOCATION: Integral membrane protein.  
 CC ALTERNATIVE PRODUCTS: IN HUMANS, AT LEAST 2 ISOFORMS; ISOFORM 1  
 CC (SHOWN HERE) AND ISOFORM 2/CXCR4-LO, ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC TISSUE SPECIFICITY: EXPRESSED IN NUMEROUS TISSUES, SUCH AS  
 CC PERIPHERAL BLOOD LEUKOCYTES, SPLEEN, THYMUS, SPINAL CORD, HEART,  
 CC PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS,  
 CC CEREBELLUM, CEREBRAL CORTEX AND MEDULLA (IN MICROGLIA AS WELL AS  
 CC IN ASTROCYTES), BRAIN MICROVASCULAR CORONARY ARTERY AND UMBILICAL  
 CC CORD ENDOTHELIAL CELLS. THE SHORT ISOFORM IS PREDOMINANT IN ALL  
 CC TISSUES TESTED.  
 CC -1- PTM: SULFATED.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -1- CAUTION: WAS ORIGINALLY (REF.1 AND REF.2) THOUGHT TO BE A RECEPTOR  
 CC FOR NEUROPEPTIDE Y, TYPE 3 (NPY3-R).  
 CC -1- DATABASE: NAME=PROW; NOTE=PROW 2:50-58(2001);  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/192999234\_g.htm".  
 CC -----  
 Query Match 27.5%; Score 500.5; DB 1; Length 352;  
 Best Local Similarity 34.6%; Pred. No. 6.1e-24;  
 Matches 107; Conservative 57; Mismatches 134; Indels 11; Gaps 4;  
 QY 8 STDYEEENKNGYDYSQYELICKEDVREFAKFLPVFLTYVGLAGNSMVVAIYA 67  
 DB 8 TSDNYTEE---MGSGDYDMKBPCEPREENANFNKIPLFTYISILFLGIVANGVLIVMG 64  
 QY 66 YKKRRTKDVYIINLAADLLLEFTLFPMANAVHGVNLKINCKITSAIYTLNPFVSGM 127  
 DB 65 YOKLRSMTDKRLHLSTADLLFVTLTFPMADVANNVFNPFCKAHVITYTNLVSSV 124  
 QY 128 QPLACISIDRYVAVTKVPSQSGVKPC--WIIICVMAAILLSIPOLVFYTV--NDNA 182  
 DB 125 LILAFISIDRYLAIVHATNSQRPRLAEKVYVGVWIPALITLPDPIFANVSEADRY 184  
 QY 183 KCIPIPRYLGTSMKALLQMLEICGFVVPFLMVCVCFITARTLMKMPNLIKSRPLKVL 242  
 DB 185 ICDRFYPNDLWV---VVFQFHIMWGLLPGVILSCYCIILSKSHSGHOKKALKTT 241  
 QY 243 LVIVIVFIVITOLPYNIVKRAIDIIYSILTSCKMSKMDIAIQVTESIALFHSCLANPIL 302  
 DB 242 VVILILFFPCWLPYITGISIDSFILIEIHKOCPEFNVHMKISTTALAFHCLANPIL 301  
 QY 303 YVFMGASFX 311  
 DB 302 YAFLGAKFK 310  
 RESULT 31  
 ID CCR4 BOVIN STANDARD; PRT; 353 AA.  
 AC P25930;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE C-X-C chemokine receptor type 4 (CXCR-4) (CXCR-4) (SDF-1 receptor)  
 DE (Stromal cell-derived factor 1 receptor) (Fusin) (Leukocyte-derived  
 DE seven transmembrane domain receptor) (LESTR) (LCR1).  
 GN CXCR4.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_Taxid=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Locus coeruleus;  
 RX MEDLINE=92100053; PubMed=1661837;  
 RA Rimland J., Xin W., Sweetnam P., Saijoh K., Nestler E.J., Duman R.S.;  
 RT "Sequence and expression of a neuropeptide Y receptor cDNA.";  
 RL Mol. Pharmacol. 40:869-875(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Werling D.;  
 RT "Role of chemokines in respiratory syncytial virus infection.";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBD databases.  
 RN [3]  
 RP SHOWS THAT IT IS NOT A NPY3-R.  
 RX MEDLINE=94052833; PubMed=8234909;  
 RA Jazin E.E., Yoo H., Blomqvist G., Yee F., Meng G., Walker M.W.,  
 RA Salton J., Larhammar D., Wahlestedt C.R.;  
 RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its  
 RT human homologue, confers neither NPY binding sites nor NPY  
 RT responsiveness on transfected cells.";  
 RL Regul. Pept. 47:247-258(1993).

```

CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, HEART, KIDNEY, LUNG AND LIVER.
CC -1- PMM: SULFATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- CAUTION: Was originally (Ref.1) thought to be a receptor for
CC neuropeptide Y type 3 (NPY3-R).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M86739; -; NOT ANNOTATED_CDS.
DR EMBL; AF399642; AAK94452.1; -.
DR PIR; S28787; S28787.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodpsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN RECEPTOR_F2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 40
FT TRANSSEM 41 64
FT DOMAIN 65 80
FT TRANSSEM 81 100
FT DOMAIN 101 111
FT TRANSSEM 112 133
FT DOMAIN 134 155
FT TRANSSEM 156 176
FT DOMAIN 177 201
FT TRANSSEM 202 221
FT DOMAIN 222 241
FT TRANSSEM 242 262
FT DOMAIN 263 286
FT TRANSSEM 287 306
FT DOMAIN 307 353
FT MOD RES 22 22
FT CARBOHYD 11 11
FT DISULFID 110 187
SQ SEQUENCE 353 AA; 39938 MW; 42FE5BC7545505E CRC64;

Query Match 27.5%; Score 499.5; DB 1; Length 353;
Best Local Similarity 34.5%; Pred. No. 7e-24;
Matches 106; Conservative 60; Mismatches 126; Indels 15; Gaps 5;

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RESULT 32
IL8B_BOVIN STANDARD; PRT; 360 AA.
ID IL8B_BOVIN
AC Q28003;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2).
GN IL8B OR CXCR2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Y., Feng J., Templeton J.W.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; U19947; AAA8496.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodpsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN RECEPTOR_F2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 48
FT TRANSSEM 49 75
FT DOMAIN 76 84
FT TRANSSEM 85 105
FT DOMAIN 106 120
FT TRANSSEM 121 142
FT DOMAIN 143 163
FT TRANSSEM 164 183
FT DOMAIN 184 208
FT TRANSSEM 209 231
FT DOMAIN 232 251
FT TRANSSEM 252 273
FT DOMAIN 274 294
FT TRANSSEM 295 315
FT DOMAIN 316 360
FT DISULFID 119 196
FT CARBOHYD 10 10
FT CARBOHYD 24 24
SQ SEQUENCE 360 AA; 40625 MW; 9A7F70C98263201 CRC64;

Query Match 27.5%; Score 499.5; DB 1; Length 360;
Best Local Similarity 33.1%; Pred. No. 7.1e-24;
Matches 118; Conservative 67; Mismatches 130; Indels 41; Gaps 10;

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DR EMBL; AF051902; AAC39830.1; -  
DR EMBL; AF051903; AAC39831.1; -  
DR EMBL; AF051904; AAC39832.1; -  
DR EMBL; AF051905; AAC39833.1; -  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT TRANSSEM 31 58 1 (POTENTIAL).  
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 69 89 2 (POTENTIAL).  
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 103 124 3 (POTENTIAL).  
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 142 166 4 (POTENTIAL).  
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 199 218 5 (POTENTIAL).  
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 236 260 6 (POTENTIAL).  
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 278 301 7 (POTENTIAL).  
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 101 178 BY SIMILARITY.  
FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
FT VARIANT 2 2 D -> E (IN ISOLATE 087).  
FT VARIANT 3 3 Y -> D (IN ISOLATE 087).  
FT VARIANT 25 25 Y -> G (IN ISOLATE 087).  
FT VARIANT 100 100 M -> K (IN ISOLATE 079).  
FT VARIANT 107 107 L -> V (IN ISOLATE 089).  
FT VARIANT 134 134 V -> G (IN ISOLATE 079).  
FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).  
FT VARIANT 340 340 T -> I (IN ISOLATE 079).  
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query March 27.4%; Score 498.5; DB 1; Length 352;  
Best Local Similarity 34.5%; Pred. No. 8e-24;  
Matches 112; Conservative 63; Mismatches 113; Indels 37; Gaps 10;

QY 21 TYDYSQY-ELICIKEDVAREFAKFLPVFLTIVFVIGLNGSMVAIYAYYKORTKTDVY 79  
DB 9 TYDIDYVSEPCOKINVKQIAARLLPLYSVIFGFVGNLIVVLLIINCKRLKSMTDIY 68  
QY 80 ILNTAVADLLFLTPPAVNAVHGVLGKIMCKITSLATLNVSGMOFLACISIDRYV 139  
DB 69 ILNTAISDLFLTLVPEFAHAAQWDFGNTMCOILLGLYFIFGFSGIFILLITIDRYL 128  
QY 140 AVTKV-----PSQSGYKRCWIIICCVMAAILISPOLVF-----TVVNDNR 183  
DB 129 AIVHAPALAKRTVTFG-----VTSVITVWVAVFASIPGILFRSREGLAHT----- 177  
QY 184 CIPFPRYIGTSMKALIQMLEICI-GFVVPFLINGVCFITARTLMQPN-IKISRLKY 241  
DB 178 CSPHFP-YSQGFQPMNPGTLKIVILGLVPLVAVVICYSGILKTLKCRMEKRRHRAVRL 236  
QY 242 LLTVVYFIVTQLPYNVYKFCRAIDIIYSLTSCMSKRDIAIQVETSLAFHSCINPI 301  
DB 237 IFTIMIVFLEWAPYNYVLLNTPQEFFGL-NNCSSNRDQAOVETETLGMTHCINPI 295  
QY 302 LVVFMGASFKNYVM-----KVAKY 321  
DB 296 IYAFVGEKRYNYLVFPOKHAKEP 320

RESULT 35  
CCR4\_FELCA STANDARD; PRT; 353 AA.  
ID CCR4\_FELCA  
AC PS6498; P79172; 002700;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE C-X-C chemokine receptor type 4 (CXCR-4) (SDF-1 receptor)  
DE (Stromal cell-derived factor 1 receptor) (fusin) (LESTRI).  
GN CXCR4.  
OS Feline silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_Taxid=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97404646; PubMed=9261358;  
RA Willett B.J., Picard L., Hosie M.J., Turner J.D., Adema K.,  
RA Clapham P.R.;  
RT "Shared usage of the chemokine receptor CXCR4 by the feline and human  
RT immunodeficiency viruses".  
RT J. Virol. 71:6407-6415(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Willett B.J.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Lerner D.L., Elder J.H.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RX PubMed=10470253;  
RA Kovacs E.M., Baxter G.D., Robinson W.F.;  
RT "Feline peripheral blood mononuclear cells express message for both  
RT CXC and CC type chemokines".  
RL Arch. Virol. 144:273-285(1999).  
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A  
CC -1- SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- PTM: SULFATED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL; U63558; AAC48852.1; -  
DR EMBL; U92795; AAB51765.1; -  
DR EMBL; AJ009816; CAA08839.1; -  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 41 60 1 (POTENTIAL).  
FT DOMAIN 65 84 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 81 100 2 (POTENTIAL).  
FT TRANSSEM 101 111 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 112 133 3 (POTENTIAL).  
FT TRANSSEM 134 155 4 (POTENTIAL).  
FT TRANSSEM 156 176 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 177 201 5 (POTENTIAL).  
FT TRANSSEM 202 221 6 (POTENTIAL).  
FT TRANSSEM 222 241 6 (POTENTIAL).  
FT TRANSSEM 242 262 6 (POTENTIAL).  
FT TRANSSEM 263 286 6 (POTENTIAL).  
FT DOMAIN 286 EXTRACELLULAR (POTENTIAL).

```

FT TRANSMEM 287 306 7 (POTENTIAL).
FT DOMAIN 307 353 CYTOPLASMIC (POTENTIAL).
FT MOD RES 22 22 SUBPATION (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
FT CONFLICT 67 67 Q -> H (IN REF. 3).
FT CONFLICT 263 263 D -> E (IN REF. 3).
SQ SEQUENCE 353 AA; 39935 MW; EA2BD46068A6C05B CRC64;

Query Match 27.4%; Score 498.5; DB 1; Length 353;
Best Local Similarity 34.5%; Pred. No. 8.1e-24;
Matches 105; Conservative 60; Mismatches 130; Indels 9; Gaps 5;

QY 13 YEENMGATDYSGVELICIKEDVREPAKFLPVFLITVFIAGNSMVAIYAYKKQ 72
DB 12 YTEDDL-GSGDIYSMKPCRENAHNRIFLPYVSIITLITVGNGLVIMGQKLL 70
QY 73 RTKIDVYILMAVADLLFTLPMAVNAVHGVLGKIMCKITSLTYLTFVSGQFLAC 132
DB 71 RSMIDKRYLHLSVADLLFVLTLPMAVDAVANVYFGKFLCKAHVITYVNLVSSVLLAF 130
QY 133 ISIDRYAVAKVRSQSGVGPC--WICPCVMAAILISIPOLVFTVND--NAR--CIP 187
DB 131 ISIDRYAVIATNSQRPRLAEKVYGVWIPALLITPDTIFANVREADGRYICDRF 190
QY 188 PPRVLTGSMALQMLEICIGFVVPFLIMGVCFITARTLMKNPKIKISRLVLTVA 247
DB 191 YP--SSMVLVRFQIMVGLIPGIVLSICYIISKLSHGQKRAKLTIVLIL 247
QY 248 VFIYVQLPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTSIALPHSCNPLIYVNG 307
DB 248 AFPAWLPYIIGISIDFILEIKQCEFEFVHKWISITELAFPHCLINILYAFILG 307
QY 308 ASFK 311
DB 308 AKFK 311

RESULT 36
IL8A_GORGO STANDARD; PRT; 350 AA.
AC P55919; P55921;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE High affinity interleukin-8 receptor A (IL-8R A) (IL-8 receptor type 1) (CXCR-1) (CDW128).
GN IL8RA OR CXCR1.
OS Gorilla gorilla (lowland gorilla), and
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OC NCBI_TaxID=9595, 9600;
RN
RP MEDLINE=9617515; Pubmed=9110929;
RA Alvarez V, Coto E, Setien F, Gonzalez S, Gonzalez-Roces S,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
RL Immunogenetics 43:261-267(1996).
CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO WGA (GRO) WITH A LOW AFFINITY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; X91110; CAB37671.1; -.
DR HSSP; P25024; 11LP.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 66 1 (POTENTIAL).
FT DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 76 96 2 (POTENTIAL).
FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 174 4 (POTENTIAL).
FT DOMAIN 175 199 5 (POTENTIAL).
FT TRANSMEM 200 220 5 (POTENTIAL).
FT TRANSMEM 221 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 264 6 (POTENTIAL).
FT DOMAIN 265 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 308 7 (POTENTIAL).
FT TRANSMEM 309 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 350 AA; 39790 MW; DB99591CD6C10757 CRC64;

Query Match 27.4%; Score 497.5; DB 1; Length 350;
Best Local Similarity 34.0%; Pred. No. 9.2e-24;
Matches 105; Conservative 65; Mismatches 120; Indels 19; Gaps 6;

QY 23 DYSGVELICIKEDVREPAKFLPVFLITVFIAGNSMVAIYAYKKQRTKDVYILN 82
DB 26 DYSPQRL-----ETELNKVYVITVYALAFLLSLGNSLWMLVILYSGRGSVDDVYILN 80
QY 83 LAVADLLFTLPMAVNAVHGVLGKIMCKITSLTYLTFVSGQFLACISIRVAVV- 141
DB 81 LAIADLLFTLPMAVNAVHGVLGKIMCKITSLTYLTFVSGQFLACISIRVAVV- 140
QY 142 --TKVPSQSGVGPCMIICFCVMAAILISIPOLV--TYVNDNARCIPIFPRYLG-- 193
DB 141 HARTITQK--RLHYKFPVCLGSGMSLISLPFLFRQAYHPNNS---PVCYVILGNDT 195
QY 194 TSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKNPKIKISRLVLTVA 253
DB 196 AKRBRVRLRLPHTFGFIVDLFVFLFCYGFITLTLFKAHWGQGRAMRVIAFVVLIFLLCW 255
QY 254 LPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTSIALPHSCNPLIYVNGASPNY 313
DB 256 LPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTSIALPHSCNPLIYVNGASPNY 315
QY 314 VMKVAKYK 322
DB 316 FLKILAMHG 324

RESULT 37
CKR5_CERAB STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CR-5) (CCR-5) (CCR5).
GN CKR5 OR CCR5.
OS Cercopithecus aethiops (Green monkey) (Primate).

```



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Cercopithecoidea;  
 OC NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=98001387; PubMed=9343222;  
 RA Kuhlman S.E., Platt E.J., Kozak S.L., Kabat D.;  
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice  
 implicate specific amino acids in infections by simian and human  
 immunodeficiency viruses.";  
 RL J. Virol. 71:8642-8656(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Murayama Y., Matsunaga S., Inoue-Murayama M.;  
 RT "cDNA sequence of African green monkey CCR-5 chemokine receptor  
 gene.";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE  
 IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR  
 DIFFERENTIATION.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL; U83324; AAC51795.1; -;  
 DR EMBL; U83325; AAC51796.1; -;  
 DR EMBL; AB015944; BAA31328.1; -;  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPS.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL\_1; 1.  
 DR PROSITE; PS50262; G-PROTEIN RECEPTOR FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
 KW Polymorphism.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 FT VARIANT 14 14 N -> Y.  
 FT VARIANT 352 352 F -> L.  
 SQ SEQUENCE 352 AA; 40561 MW; 7F52B690C72EC29A CRC64;  
 Query Match 27.2%; Score 495.5; DB 1; Length 352;  
 Best Local Similarity 33.2%; Pred. No. 1.2e-23;  
 Matches 116; Conservative 69; Mismatches 127; Indels 37; Gaps 11;  
 QY 21 TYDYSQY-ELICIKEDVREPAKFLPVFLITVFIQGLAGNSMVAIVAYVKKORTKTDVY 79

DB 9 TYDIDNVTSEPCQKINVAQIARLLPPLYSLVFIFGVGNILVILINCRKLSMTDIY 68  
 QY IINIAADLLFTLPAPAVNAVHGVNGKIMCKITSLATYLNFPSCGQPLACISIDRYV 139  
 DB 69 LNLALISDLLFTLPAPAVNAVHGVNGKIMCKITSLATYLNFPSCGQPLACISIDRYV 128  
 QY 140 AVTKV-----PSQGVGKPCMIICFCWMAAILSLPOLVF-----TYVNDNR 183  
 DB 129 ALVHANFALKATVTFGV-----VTSVITVAVAVASLPRIIFRSQBGALHYT----- 177  
 QY 184 CIPFPRYIGTSMKALLIOMLEICI-GEVVPFLINGVCYFIPARTLMKPN-IKISRLPKV 241  
 DB 178 GSHFP-YQYQFWMKRFOTLKIVILGLVPLVWVICYSGILKTLRCRNRKRRHRAVRL 236  
 QY 242 LITVAVFVITLDPYNYKFCALDIISLTSCMSKRMIDAIQVETSIAPFSCNAPI 301  
 DB 237 IFTIMIVFLFAPYINIVLLNTFOEPFGL-NNCSSNRLLQAMQVITLGHCTCINPI 295  
 QY 302 LVFMGASFKNVVMKAYKGSWRQR-QSVEEPFDESGTEPTSTPS 349  
 DB 296 IYAFVGEKRNVLVFPQKIAKRCCKCSI-----FQGEAPRASSVYT 340  
 RESULT 38  
 ID CCR4\_CERTO STANDARD; PRT; 352 AA.  
 AC 062747;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-X-C chemokine receptor type 4 (CXCR-4) (SDF-1 receptor)  
 DE (Stromal cell-derived factor 1 receptor) (Fusin) (LESTR).  
 GN CXCR4.  
 OS Cercopithecus torquatus alys (Red-crowned mangabey) (Sooty mangabey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Cercopithecoidea;  
 OC NCBI\_TaxID=9531;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98321155; PubMed=9656999;  
 RA Chen Z., Gettie A., Ho D.D., Marx P.A.;  
 RT "Primary SIVM isolates use the CCR5 coreceptor from sooty mangabey  
 RT naturally infected in west Africa: a comparison of coreceptor usage  
 of primary SIVM, HIV-2, and SIVmac.";  
 RL Virology 246:113-124(1998).  
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A  
 SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- PTM: SULFATED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF051906; AAC39834.1; -;  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPS.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL\_1; 1.  
 DR PROSITE; PS50262; G-PROTEIN RECEPTOR FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
 KW Polymorphism.  
 FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 40 63 1 (POTENTIAL).  
 FT DOMAIN 64 79 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 80 99 2 (POTENTIAL).  
 FT DOMAIN 100 110 EXTRACELLULAR (POTENTIAL).







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## OM protein - protein search, using sw model

Run on: March 17, 2003, 16:24:05 ; Search time 32 Seconds

(without alignments)  
2253.640 Million cell updates/sec

Title: US-09-721-495B-2

Perfect score: 1819

Sequence: 1 MALBQNSQSDYYEENEMNG.....VEPPFDSBGPTEPTFSI 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 135 summaries

## Database :

SPTREMBL\_21:\*  
1: sp archaea:\*  
2: sp bacteria:\*  
3: sp fungi:\*  
4: sp human:\*  
5: sp invertebrate:\*  
6: sp mammal:\*  
7: sp mhc:\*  
8: sp organelle:\*  
9: sp phage:\*  
10: sp plant:\*  
11: sp rodent:\*  
12: sp virus:\*  
13: sp vertebrate:\*  
14: sp unclassified:\*  
15: sp\_rv1rus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1596	87.7	350	11 Q92413	Q92413 mus musculus
2	1593	87.6	350	11 Q8Q2W9	Q8Q2W9 mus musculus
3	912	50.1	221	11 Q9ESK1	Q9ESK1 rattus norv
4	643	35.3	369	4 Q9U006	Q9U006 homo sapien
5	611	33.6	367	11 Q9RIW0	Q9RIW0 mus musculus
6	586.5	32.2	368	13 Q42444	Q42444 oncorhynch
7	578	31.8	343	6 Q9N0Z0	Q9N0Z0 cercocobus
8	566.5	31.1	351	11 Q9E016	Q9E016 mus musculus
9	566	31.1	343	6 Q9BDS6	Q9BDS6 macaca fasc
10	561.5	30.9	351	11 Q9ERH5	Q9ERH5 mus musculus
11	560	30.8	342	4 Q9HCAS	Q9HCAS homo sapien
12	559	30.7	342	6 Q9TV16	Q9TV16 pan troglod
13	544	29.9	358	13 Q9PUA0	Q9PUA0 acipenser r
14	534.5	29.4	360	11 Q91ZM4	Q91ZM4 rattus norv
15	529	29.1	361	11 Q8VHP3	Q8VHP3 cavia porce
16	520.5	28.6	358	13 Q9YGC3	Q9YGC3 xenopus lae

17	516	28.4	355	11 Q9J1Y8	Q9J1Y8 rattus norv
18	507.5	27.9	347	6 Q9MZM1	Q9MZM1 eulemur mac
19	507	27.8	357	13 Q42445	Q42445 oncorhynch
20	506.5	27.8	347	6 Q9MZM7	Q9MZM7 callimico g
21	506.5	27.8	347	6 Q9MZM6	Q9MZM6 callimico g
22	503.5	27.7	347	6 Q9MZM0	Q9MZM0 alouatta se
23	503.5	27.7	352	6 Q9TV44	Q9TV44 cercopithec
24	502.5	27.6	347	6 Q9MZP1	Q9MZP1 mandrillus
25	502.5	27.6	347	6 Q9MZM9	Q9MZM9 ateles pani
26	502.5	27.6	347	6 Q9MZM8	Q9MZM8 callithrix
27	502.5	27.6	347	6 Q9MZM5	Q9MZM5 pithecia pi
28	500.5	27.5	347	6 Q9MZP6	Q9MZP6 presbytis j
29	500.5	27.5	347	6 Q9MZM6	Q9MZM6 hylobates c
30	500.5	27.5	347	6 Q9MZM5	Q9MZM5 hylobates h
31	500.5	27.5	347	6 Q9MZM2	Q9MZM2 pongo pygma
32	500.5	27.5	347	6 Q9MZM1	Q9MZM1 gorilla gor
33	500.5	27.5	347	6 Q9TSQ8	Q9TSQ8 cercopithec
34	499.5	27.5	339	6 Q9TUB8	Q9TUB8 cercopithec
35	499.5	27.5	339	6 Q9TUR4	Q9TUR4 mandrillus
36	499.5	27.5	347	6 Q9MZQ3	Q9MZQ3 pygathrix a
37	499.5	27.5	347	6 Q9MZQ2	Q9MZQ2 rhinopithec
38	499.5	27.5	347	6 Q9MZQ1	Q9MZQ1 pygathrix b
39	499.5	27.5	347	6 Q9MZQ0	Q9MZQ0 pygathrix i
40	498.5	27.5	347	6 Q9MZP9	Q9MZP9 nasalis lar
41	498.5	27.5	347	6 Q9MZP8	Q9MZP8 colobus pol
42	498.5	27.5	347	6 Q9MZP5	Q9MZP5 presbytis p
43	498.5	27.5	347	6 Q9MZP4	Q9MZP4 presbytis f
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45	498.5	27.5	347	6 Q9MZP0	Q9MZP0 mandrillus
46	498.5	27.5	347	6 Q9MZP0	Q9MZP0 macaca assa
47	498.5	27.5	347	6 Q9MZP9	Q9MZP9 macaca arct
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49	498.5	27.5	347	6 Q9MZN7	Q9MZN7 macaca neme
50	498.5	27.5	347	6 Q9MZN4	Q9MZN4 hylobates i
51	499.5	27.5	347	6 Q9MZN3	Q9MZN3 hylobates s
52	499.5	27.5	352	6 Q9J1Y8	Q9J1Y8 cercocobus
53	498.5	27.4	347	6 Q9MZP7	Q9MZP7 presbytis s
54	498.5	27.4	352	4 Q9BXA0	Q9BXA0 homo sapien
55	498.5	27.4	352	6 Q9J1Y8	Q9J1Y8 cercopithec
56	497.5	27.4	347	6 Q9MZM0	Q9MZM0 perodicticu
57	497.5	27.4	352	6 Q9BGN5	Q9BGN5 cercopithec
58	497.5	27.4	367	11 Q9J1Y8	Q9J1Y8 rattus norv
59	497	27.3	334	6 Q9N1P2	Q9N1P2 saginus oe
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62	497	27.3	346	6 Q9MZM2	Q9MZM2 nycticebus
63	496	27.3	334	6 Q9N130	Q9N130 saimiri bol
64	496	27.3	353	13 Q9J247	Q9J247 cyrtinus ca
65	495.5	27.2	339	6 Q9TUV0	Q9TUV0 aotus triui
66	495.5	27.2	339	6 Q9TUN3	Q9TUN3 macaca fasc
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69	495.5	27.2	352	6 Q9XT14	Q9XT14 colobus que
70	495.5	27.2	352	6 Q9SENE1	Q9SENE1 cercocobus
71	494.5	27.2	339	6 Q9TUR9	Q9TUR9 saginus sp
72	494.5	27.2	339	6 Q9TUR7	Q9TUR7 cercopithec
73	494.5	27.2	339	6 Q9TUR8	Q9TUR8 cercopithec
74	494.5	27.2	339	6 Q9TUR6	Q9TUR6 erythrocedu
75	494.5	27.2	339	6 Q9TOX3	Q9TOX3 mandrillus
76	494.5	27.2	339	6 Q9TOX6	Q9TOX6 cercopithec
77	494.5	27.2	339	6 Q9TOX5	Q9TOX5 cercopithec
78	494.5	27.2	352	6 Q9TQU4	Q9TQU4 cercopithec
79	494.5	27.2	352	6 Q9TQU1	Q9TQU1 cercopithec
80	494.5	27.2	352	6 Q9TV48	Q9TV48 cercopithec
81	494.5	27.2	352	6 Q9TV47	Q9TV47 cercopithec
82	494.5	27.2	352	6 Q9TSO7	Q9TSO7 cercopithec
83	494.5	27.2	352	6 Q9SENE8	Q9SENE8 cercopithec
84	494.5	27.2	352	6 Q9SENE2	Q9SENE2 mandrillus
85	494.5	27.2	352	6 Q9SENE1	Q9SENE1 mandrillus
86	494	27.2	334	6 Q9N1P3	Q9N1P3 hylobates i
87	494	27.2	360	13 Q9TUV8	Q9TUV8 brachydanio
88	493.5	27.1	339	6 Q9TUV1	Q9TUV1 macaca mula
89	493.5	27.1	339	6 Q9TSQ2	Q9TSQ2 cercopithec

90 493.5 27.1 339 6 09T0U7 09T0U7 cercopithec  
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94 493.5 27.1 352 6 09SNC4 09SNC4 atelae geot  
95 492.5 27.1 339 6 09TSN2 09TSN2 macaca fasc  
96 492.5 27.1 339 6 09TUT6 09TUT6 macaca neme  
97 492.5 27.1 339 6 09TUS5 09TUS5 papio cynoc  
98 492.5 27.1 351 6 09T0V6 09T0V6 colobus gue  
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101 492.5 27.1 352 6 09BDS5 09BDS5 macaca fasc  
102 492.5 27.1 352 6 09SNC8 09SNC8 colobus pol  
103 492.5 27.1 353 13 08OPR5 08OPR5 xenopus lae  
104 492 27.0 334 6 09N1P4 09N1P4 cercopithec  
105 492 27.0 353 13 09PTF7 09PTF7 brachydanto  
106 491.5 27.0 339 6 09TSQ4 09TSQ4 cercopithec  
107 491.5 27.0 339 6 09TUS6 09TUS6 alouatta ca  
108 491.5 27.0 339 6 09T0X2 09T0X2 erythrocebu  
109 491.5 27.0 339 6 09T0V3 09T0V3 cercopithec  
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111 491.5 27.0 352 6 09TV43 09TV43 cercopithec  
112 491.5 27.0 352 6 09SND0 09SND0 erythrocebu  
113 491 27.0 352 6 09MZA1 09MZA1 lagotrix 1  
114 490.5 27.0 334 6 097724 097724 felis silve  
115 490.5 27.0 339 6 09TUT9 09TUT9 cercopithec  
116 490.5 27.0 339 6 09TUT7 09TUT7 macaca fusc  
117 490.5 27.0 339 6 09TUT9 09TUT9 macaca mula  
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131 490.5 27.0 352 6 097975 097975 macaca arc  
132 490 26.9 339 6 09TUT5 09TUT5 pan troglod  
133 490 26.9 339 6 09TUT4 09TUT4 callitrix  
134 490 26.9 355 6 09MYJ8 09MYJ8 callitrix  
135 489.5 26.9 339 6 09TUT8 09TUT8 gorilla gor

## ALIGNMENTS

RESULT 1  
092413 PRELIMINARY; PRT; 350 AA.  
AC 092413;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Chemokine receptor CCR1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RA MDLJNE=20519697; PubMed=11063828;  
RA Dorf M.E., Berman M.A., Tanabe S., Heesen M., Luo Y.;  
RT "Astrocytes express functional chemokine receptors."; J.  
RT J. Neuroimmunol. 111:109-121(2000).  
DR EMBL; AF306532; AAK81712.1;  
DR InterPro; IPR000276; GPCR\_Rhodospn.  
DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PRO1557; CHEMOKINER10.  
DR PRINTS; PRO1558; CHEMOKINER11.  
DR PRINTS; PRO1559; DUF9ANTIGEN.  
DR PROSITE; PS00237; G\_PROTEIN\_REC\_P1\_1; UNKNOWN\_1.  
DR PROSITE; PS00262; G\_PROTEIN\_REC\_P1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 350 AA; 39530 MW; C5F7D9DC49CECCF CRC64;

Query Match 87.7%; Score 1596; DB 11; Length 350;  
Best Local Similarity 85.4%; Pred. No. 4e-137;  
Matches 299; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

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DB 1 MALELNQSAEYEEENKTYHDYSQYEVICKEVRQFAKFLPAFTVAFTVIGLAGNS 60  
QY 61 MVVAIYAYKKORTKTDVYIINLAVADLLITLTPFMAVNAVHGVILKINCKITSALT 120  
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DB 121 VNVSGMOFLACISIDRYAAVTKVPSQSGVKPCWIIICCVMAAILISTPOLVFTVNO 180  
QY 181 NARCTPIFPFVYGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLAKMNIKISRLK 240  
DB 181 NARCTPIFPFHHIGTSLKSIQMLEIGIGFVVPFLMGVCYSTARALIKMNIKISRLR 240  
QY 241 VLVTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIQTESIALFHSCLNP 300  
DB 241 VLVAVVVFIVTQLPYNNVVKFCQAIIDAIYLLITSCDMSKRMIDIAIQTESIALFHSCLNP 300  
QY 301 IIVFVGASFKYVWKVAKKYSMROROSVEEPFDESGPEPTSTSI 350  
DB 301 IIVFVGASFKYVWKVAKKYSMROROSVEEPFDESGPEPTSTSI 350

RESULT 2  
08QZM9 PRELIMINARY; PRT; 350 AA.  
AC 08QZM9;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Chemokine receptor CCX CKR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SV;  
RA Townson J.R., Nibbs R.J.;  
RT "Characterization of mouse CCX CKR, a receptor for the lymphocyte-  
RT attracting chemokines TECK (CCL25), SLK (CCL21) and MIP-3beta (CCL19):  
RT comparison to human CCX CKR.";  
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY072796; AAL68400.1;  
DR EMBL; AY072938; AAL68962.1;  
KW Receptor.  
SQ SEQUENCE 350 AA; 39544 MW; D017CC29749CECD5 CRC64;

Query Match 87.6%; Score 1593; DB 11; Length 350;  
Best Local Similarity 85.1%; Pred. No. 7.5e-137;  
Matches 298; Conservative 27; Mismatches 25; Indels 0; Gaps 0;  
QY 1 MALEQNSTDYDYENENGTVDYQYELICKEVREFAKFLPVFLTVFVIGLAGNS 60  
DB 1 MALELNQSAEYEEENKTYHDYSQYEVICKEVRQFAKFLPAFTVAFTVIGLAGNS 60  
QY 61 MVVAIYAYKKORTKTDVYIINLAVADLLITLTPFMAVNAVHGVILKINCKITSALT 120  
DB 61 VVVAIYAYKKORTKTDVYIINLAVADLLITLTPFMAVNAVHGVILKINCKITSALT 120

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QY 121 LNFVSGMOFLACISIDRYAVATKVPSSQGVKPCWIIICFCVMAAILLSPOLVFTYND 180
DB 121 VNFVSGMOFLACISIDRYAVATKVPSSQGVKPCWIIICFCVMAAILLSPOLVFTYND 180
QY 181 NARCIPFPFRLTSGMSKALIQMLEICIGFVFPPLINGVCYFARTLTKMKNIKSRPK 240
DB 181 NARCIPFPFRLTSGMSKALIQMLEICIGFVFPPLINGVCYFARTLTKMKNIKSRPK 240
QY 241 VLLTVVIVFIVTOLPYNIVKFCRAIDIIYSLTSCMSKMDIAIQVTESIALFHSCLNP 300
DB 241 VLLTVVIVFIVTOLPYNIVKFCRAIDIIYSLTSCMSKMDIAIQVTESIALFHSCLNP 300
QY 301 ILVFMGASFRNIVKAKYKGGVSROROSVEEPFSEPTSTPSI 350
DB 301 ILVFMGASFRNIVKAKYKGGVSROROSVEEPFSEPTSTPSI 350

RESULT 3
Q9ESK1 PRELIMINARY; PRT; 221 AA.
AC Q9ESK1;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Putative G-protein coupled receptor GPCR14 (Fragment).
GN GPCR14.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=HARLAN SPRAGUE-DAWLEY;
RA Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;
RT "Identification and characterization of novel G-protein coupled
RT receptors expressed in regeneration peripheral nerve."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090348; AAG24470.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01557; CHEMOKINER10.
DR PROSITE; PS00237; GPCR_RHODOPSIN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR KEGG; K01101; G_PROTEIN_RECEP_F1_2; 1.
KM Receptor.
FT NON_TER 1
FT NON_TER 221
SQ SEQUENCE 221 AA; 24342 MW; 5622DD6073738A6C CRC64;

Query Match 50.1%; Score 912; DB 11; Length 221;
Best Local Similarity 83.3%; Pred. No. 4e-75; Indels 0; Gaps 0;
Matches 169; Conservative 19; Mismatches 15;

QY 96 FMVAVAVHGVWLGKIMKITSALYTLNFVSGMOFLACISIDRYAVATKVPSSQGVKPCW 155
DB 19 FMVAVAVHGVWLGKIMKITSALYTLNFVSGMOFLACISIDRYAVATKVPSSQGVKPCW 78
QY 156 IICFCVMAAILLSPOLVFTYNDNACIPFPFRLTSGMSKALIQMLEICIGVFPPLI 215
DB 79 IICFCVMAAILLSPOLVFTYNDNACIPFPFRLTSGMSKALIQMLEICIGVFPPLI 138
QY 216 MGVCYFARTLTKMKNIKSRPKVLLTVVIVFIVTOLPYNIVKFCRAIDIIYSLTSC 275
DB 139 MGVCYFARTLTKMKNIKSRPKVLLTVVIVFIVTOLPYNIVKFCRAIDIIYSLTSC 198
QY 276 NMSKMDIAIQVTESIALFHSCL 298
DB 199 NMSKMDIAIQVTESIALFHSCL 221

RESULT 4
Q9UQ06

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ID Q9UQ06 PRELIMINARY; PRT; 369 AA.
AC Q9UQ06;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chemokine receptor CCR9 (CC chemokine receptor 9A).
GN CCR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99248139; PubMed=10229797;
RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
RT receptor for the chemokine TECK."
RL J. Immunol. 162:5671-5675(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Yu C.-R., Peden K.W.C., Farber J.M.;
RT "CCR9A and CCR9B, Two Receptors for the Chemokine CCL25 (TECK/Ckdelta-
RT 15)."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132337; CAB43477.1; -
DR EMBL; AF145439; AAF66699.1; -
DR InterPro; IPR004069; CC_chemokine9.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01558; CHEMOKINER11.
DR PRINTS; PR01551; CHEMOKINER9.
DR PROSITE; PS00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM Receptor.
SQ SEQUENCE 369 AA; 42015 MW; F27CEA0CFB66B44C CRC64;

Query Match 35.3%; Score 643; DB 4; Length 369;
Best Local Similarity 36.4%; Pred. No. 1.9e-50; Indels 18; Gaps 4;
Matches 120; Conservative 75; Mismatches 117;

QY 6 NOSTDYVEE-NENNGVYVSEYELICIKEDVREPAKVFLLPFLTIVFVIGLAGSMVVA 64
DB 12 NMAADDGSESTSMEDYVNFNTDYCEKANNKQPSHPLPFLYVLVPLVIGLAGSMVVL 71
QY 65 IYAYYKQRTKTDVYTLNLAVALDLLFTLPPWAVAVHGVWLGKIMKITSALYTLNFV 124
DB 72 VYMYCTRVKTMDFMLNLAIDLFLVTLFPWALAADQWKFQFMCKVVMYKMFY 131
QY 125 SGMQFLACISIDRYAVATKVPSSQGVKPCW-----IICFCVMAAILLSPOLV 175
DB 132 SCVLLIMCISVRYIAIDQ-----AMRAHTREKRLVSKVWCFTIWLVAALCIPETLY 186
QY 176 YTNNDN---ARCIPFRLTSGMSKALIQMLEICIGFVFPPLINGVCYFARTLTKMKN 232
DB 187 SQKESGALICMWPVSPSESTKLSAVTLKVLIGFLPFPVMAACCTIIHTLIQAKK 246
QY 233 IKISRLKVLTVVIVFIVTOLPYNIVKFCRAIDIIYSLTSCMSKMDIAIQVTESIA 292
DB 247 SSKHAKLKTIVLTVFVLSQFPYNCILLVGTIDAVAMFISNCAVSTNIDICFOYVOTIA 306
QY 293 LPHSCINPLIYVFMGASFRNIVKAKYKGG 322
DB 307 FPHSCINPLIYVFMGASFRNIVKAKYKGG 336

RESULT 5
Q9RIVO PRELIMINARY; PRT; 367 AA.
AC Q9RIVO;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

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DE	CC chemokine LARC specific receptor.
DN	CCKBR6 OR MCCR6.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCB1_taxid=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Tanaka Y.;
RT	"Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor
RT	for CC Chemokine LARC,";
RL	Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AB016031; BAA82443.1; .
DR	HSSP; P34996; 1DD.
DR	MGD; MGI:133797; Cckbr6.
DR	InterPro; IPR004067; CC_chemkine6.
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm.1; 1._Rhodpsn.
DR	PRINTS; PR01529; CHEMOKINER6.
DR	PRINTS; PR00237; GPCRHODPSN.
DR	PROSITE; PS00237; G_PROTEIN_RECPT_P1.1; UNKNOWN_1.
DR	PROSITE; PS50262; G_PROTEIN_RECCE_FT_2; 1.
KW	Receptor.
SQ	SEQUENCE 367 AA; 42082 MW; 207FDP9B2F7A6DD3 CRC64;
Query Match	33.6%; Score 611; DB 11; Length 367;
Best Local Similarity	38.2%; Pred. NO.1.6e-47;
Matches 130; Conservative	60; Mismatches 124; Indels 26; Gaps
Qy	8 STDYEEENEMNGVYDSQVELI-----CIKEDREFAKFLPVLTIVFVIGLAGNSM 61
Dz	3 STESFGIDD----YDNEYYSIPDHGPCGLEEVRFYTFVPFIANSLSLCVGLGNIM 58
Qy	62 VVAIYAAYKKORTKTDTYVILNLAVADLLFTLPFMV-NAVHGWLGIKMKITSLALT 120
Dz	59 VMTEFAFYKKARSMTDVYLIMATITDLFPVLTPFMVATHATMTWPSDALCKLMKGTYA 118
Qy	121 INFPSGMQFLACISIDRVAVNTKYPSPSGVGKPCW----IIICCVMAAILSLIPQLVF 175
Dz	119 VFNFQGMILLACISMDRIAYIAVOATKSFRVRSRITLTHSKVICAAMWFISLIISPFFIFN 178
Qy	176 --YYNDVARCPIYFPRLGTS---WKALIOMLEICGVVPEFLINGVCYFITARTLTK 229
Dz	179 KYEIQBDNVDC--EPKRSVSSEITWTKLGLGLETFPGFTPLFEVWFCYLETIKTLVQ 235
Qy	230 MPNIKISPKLVLTLYVIVFLVTQPYNIYFKCAIIDIIISLTSCMSKRMIDIAQYTE 289
Dz	236 AONSRRHAIIRVIADVLFVLAQCIDPHMWLVLTAVA-TGVKVASSTETKVLAFTNVAE 294
Qy	290 SIALFHSGCLNPILVFNMGASRKNTVMKVAKYGSWRQRQ 329
Dz	295 VLAFHSCLNPFVLYAFVIGQKRNYFMKIMDWCMCRKNK 334
RESULT 6	
O42444	PRELIMINARY; PRT; 368 AA.
A042444	
AC O42444;	
DT 01-JAN-1998 (TREMBlrel. 05, Created)	
DT 01-JUN-1998 (TREMBlrel. 05, Last sequence update)	
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)	
DE Chemokine receptor.	
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Actinopterygii; Neopterygii; Teleostei; Vertebrate; Euteleostei;	
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.	
OX NCBI_TaxID=8022;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=99260342; Pubmed=1031499;	
RA Daniels G.D., Zou J., Charlemagne J., Partula S., Cunningham C.,	
RA Seemings C.J.;	
RT "Cloning of two chemokine receptor homologs (CXCR4 and CXCR7) in	

RT rainbow trout *Oncorhynchus mykiss*.":  
RL J. Leukoc. Biol. 65:684-690(1999).  
DR EMBL, AJ003159; CAA05917.1; -.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PRO0237; GPCRHHODOPS.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KM Receptor.  
SQ SEQUENCE 368 AA; 41523 MW; BE2BE2D4C47E821A CRC64;  
  
Query Match 32.2%; Score 586.5; DB 13; Length 368;  
Best Local Similarity 37.3%; Pred. No. 2,66-45;  
Matches 120; Conservative 58; Mismatches 125; Indels 19; Gaps 4;  
  
QY 22 YDYSQY-----ELICKEDEREFARVFLPFLTIVFVIGLAGNSMVAIYAYK 70  
DB 17 YDYDSFTPTVGEDVDNFMCDKSAVRAFRQYDEPPLWMSYIILGGLNLTFTWVIYLFHR 76  
QY 71 KO-RKTDVYILNLAVADLLFLTPFPAANAAGWLTGKIMCKTSLATLNPFSGMQF 129  
DB 77 ORLKMTDIIYLLNLAVLFLGLTFLPAVANDQMSFGLCKVTSAFYKINFPSSML 136  
QY 130 IACISIDRYAVATKPSQSGVGK-----CWICFCVMAAILSLIPOLVFTYND--NA 182  
DB 137 LTGICVDVRYVIVQTMAQNSKQRLSCSKYVCACWLLAVLALPEMFPAVXELDQF 196  
QY 183 RCIPFPRYLGTSMKALLQMLEICIGFVFPFLMGVCYFTARTLMKPNIKISRLPYL 242  
DB 197 YCTWYVMSNONNRKRTIVLGHQICWGFCLPLVMVFCYAGIIRLLTKRSPQKKALAVI 256  
QY 243 LTVAVFLVLTQLPNIVYFCRAIDIIYSLLTSCMSKRMDAIQVTSIALFHSGLNPL 302  
DB 257 LVVAVAVFLSQLPNVSVLWMEATQANSTQDCAAKRFNVSVQVLSKLATYHACLNPFL 316  
QY 303 YVFMGASFKNYVMKAKYKYSW 324  
DB 317 YVFGVFRFRDILKLLRIYHCW 338  
  
RESULT 7  
Q9N0Z0  
ID Q9N0Z0 PRELIMINARY; PRT; 343 AA.  
AC Q9N0Z0;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
STRL33.  
OS *Cercocobus torquatus* atys (Red-crowned mangabey) (Sooty mangabey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutaria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Cercocobus.  
OX NCBI\_Taxid=9531;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20261727; Pubmed=10799581;  
RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,  
RA Kirchhoff F.;  
RT "Slain immunodeficiency virus utilizes human and sooty mangabey but  
not rhesus macaque STRL33 for efficient entry.";  
RL J. Virol. 74:5075-5082(2000).  
[2]  
RP SEQUENCE FROM N.A.  
RX Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,  
RA Kirchhoff F.;  
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF237559; AAF68392.1; -.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PRO0237; GPCRHHODOPS.  
DR PRINTS; PRO1568; LYMPHOTACTNR.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.

SEQUENCE 343 AA; 39589 MW; A75B7A0751C13455 CRC64;  
 Query Match 31.8%; Score 578; DB 6; Length 343;  
 Best Local Similarity 33.7%; Pred. No. 1.5e-44;  
 Matches 120; Conservative 73; Mismatches 131; Indels 32; Gaps 8;

10 DYYEENENMGATDYSGYELICIKEDVREFAKFLPVFLTIYFVIGLAGNSMVAIYAY 69  
 5 DHIEDDFNSFNDSSQOE-----HODELFQSKVFLPCMYLVFVCGVSGSLVVISIFY 60  
 70 KKORTKDYIILNLAVALDLLFTLPFAVANAAGVULGKINCKITSALTYTLNFSGMOF 129  
 61 HKQSLTDVFLVNLPLADLVFCTLPFWAYAGIHEWIFGQVMCKTLGVTYINFTSMI 120  
 130 LACISIDRYAVATKVP--QSGVGKPCW--IICFCVMAAILISTIPOLVYTV--NDNR 183  
 121 LTCITVDREFIVVATKAVNAQAARMTGWKVCILIMVLSLVSIPQIYGAVNFNDKLI 180  
 184 CIPFPRYLGTSKALIQMLEICIGFVFPFLMGVCYFITARLTMKMPNIKISRLPKVLL 243  
 181 C-----RYHDEISTVLAQTQMTGFLPLIMIVCYSAIKITLLHAGFGQKRSIKIIF 235  
 244 TVIVFIVTQLPYNIYVFCRAIDIIYSLITSCKNSKMDIAIOVTEISALFHSCLNPIY 303  
 236 LVMAVFLITQTPFNVLKIRSTHWEYAMTSFHYT-----IIVTEAIVLRAACLPVLY 289  
 304 VFMGASFKYVYMKAKKYG-----SWRRQROSVEEFPDSEPTSTFSI 350  
 290 AFVSLKRFKRWKLVKIDIGCLPIYGVSHQWSSEDSK--TFSASHNVETISMFL 343

## RESULT 8

09B016 PRELIMINARY; PRT; 351 AA.  
 AC 09B016;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Chemokine receptor CXCR6.  
 GN CXCR6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA MEDLINE=21177382; PubMed=11017100;  
 RA Matlobian M., David A., Engel S., Ryan J.E., Cyter J.G.;  
 RT "A transmembrane CXCR6 chemokine is a ligand for HIV-coreceptor Bnzo.";  
 RL Nat. Immunol. 1:298-304 (2000).  
 DR EMBL; AF301018; AAG34367.1; -.  
 DR MGD; MGI:1934582; Cxcr6.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 DR KMW Receptor.  
 SQ SEQUENCE 351 AA; 40468 MW; 565878837284C65A CRC64;

Query Match 31.1%; Score 566.5; DB 11; Length 351;  
 Best Local Similarity 35.4%; Pred. No. 1.7e-43;  
 Matches 127; Conservative 70; Mismatches 125; Indels 37; Gaps 10;

10 DYYEEN--ENMGTYDSQYELICIKEDV--EPAKFLPVFLTIYFVIGLAGNSMVAI 65  
 12 DGHYGDGFWLFPNDSNSQO-----ENKRFLEKFEVFLPCYIVLVFVFGGLGNSLVLI 64  
 66 YAYYKORTKDYIILNLAVALDLLFTLPFAVANAAGVULGKINCKITSALTYTLNFSV 125  
 65 YIFQKRLTIDVFLNPLADLVFCTLPFWAYAGIHEWIFGVWFKTLRGMTYINFTY 124

126 GMOFLACISIDRYAV--TVPSQSGVCKPCW--IICFCVMAAILISTIPOLVYTVND 180  
 125 SMLTLCITVDREFIVVATKAVNAQAARMTGWKVCILIMVLSLVSIPQIYGVNFNDKLI 183  
 181 NARCPFPRYLGTSKALIQMLEICIGFVFPFLMGVCYFITARLTMKMPNIKISRLPK 240  
 184 IDKLI---CQVHSEISTVLAQTQMTGFLPLIMIVCYSAIKITLLHAGFGQKRSIKI 240  
 241 VLLTVIVFIVTQLPYNIYVFCRAIDIIYSLITSCKNSKMDIAIOVTEISALFHSCLN 300  
 241 IIFLVAAVFLITQTPFNVLKIRSTHWEYAMTSFHYT-----IIVTEAIVLRAACLP 294  
 301 ILVFMGASFKYVYMKAKKYG-----SWRRQROSVEEFPDSEPTSTFSI 350  
 295 VLVAFVGLKFRKRWKLVKIDIGCLSHLGVSQWSSEDSK--TFSASHNVETISMFL 351

## RESULT 9

09BDS6 PRELIMINARY; PRT; 343 AA.  
 AC 09BDS6;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Orphan seven transmembrane receptor STRL3.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 NC NCB1\_TaxID=95411;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21134756; PubMed=11242524;  
 RA Made-Evans A.M., Russell J., Jenkins A., Javan C.;  
 RT "Cloning and sequencing of cynomolgus macaque ccr3, gp15, and strl33;  
 RT potential coreceptors for HIV type 1, HIV type 2, and STV."  
 RL AIDS Res. Hum. Retroviruses 17:371-375 (2001).  
 DR EMBL; AF291671; AAK25742.1; -.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE; PR01568; LYMPHOTACTIN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 DR KMW Receptor; Transmembrane.  
 SQ SEQUENCE 343 AA; 39472 MW; 0961328F948E7784 CRC64;

Query Match 31.1%; Score 566; DB 6; Length 343;  
 Best Local Similarity 33.1%; Pred. No. 1.8e-43;  
 Matches 118; Conservative 73; Mismatches 133; Indels 32; Gaps 8;

10 DYYEENENMGATDYSGYELICIKEDVREFAKFLPVFLTIYFVIGLAGNSMVAIYAY 69  
 5 DHIEDDFNSFNDSSQOE-----HODELFQSKVFLPCMYLVFVCGVSGSLVVISIFY 60  
 70 KKORTKDYIILNLAVALDLLFTLPFAVANAAGVULGKINCKITSALTYTLNFSGMOF 129  
 61 HKQSLTDVFLVNLPLADLVFCTLPFWAYAGIHEWIFGQVMCKTLGVTYINFTSMI 120  
 130 LACISIDRYAVATKVP--QSGVGKPCW--IICFCVMAAILISTIPOLVYTV--NDNR 183  
 121 LTCITVDREFIVVATKAVNAQAARMTGWKVCILIMVLSLVSIPQIYGAVNFNDKLI 180  
 184 CIPFPRYLGTSKALIQMLEICIGFVFPFLMGVCYFITARLTMKMPNIKISRLPKVLL 243  
 181 C-----GYHDEISTVLAQTQMTGFLPLIMIVCYSAIKITLLHAGFGQKRSIKIIF 235  
 244 TVIVFIVTQLPYNIYVFCRAIDIIYSLITSCKNSKMDIAIOVTEISALFHSCLNPIY 303  
 236 LVMAVFLITQTPFNVLKIRSTHWEYAMTSFHYT-----IIVTEAIVLRAACLPVLY 289  
 304 VFMGASFKYVYMKAKKYG-----SWRRQROSVEEFPDSEPTSTFSI 350

Db 290 AFVSLKFRKFWKLVKDIGCLPYLGVSHPWKSSEDNSK--TFSASHNVEATSMFOL 343

## RESULT 10

Q9ERH5 PRELIMINARY; PRT; 351 AA.  
 ID Q9ERH5  
 AC Q9ERH5  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Putative chemokine receptor.  
 GN CXCR6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=SPLEEN;  
 RA Sato H., Taniguchi M.;  
 RT "Molecular cloning of a putative chemokine receptor preferentially  
 expressed in mouse lymphocytes."  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF305709; AAC31284.1; -  
 DR MGD; MGI:1934582; Cxcr6.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PRINTS; PR01568; LYMPHOTACTNR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEPTOR\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 351 AA; 40511 MW; B00E3134D2B4D1ED CRC64;

Query Match 30.9%; Score 561.5; DB 11; Length 351;  
 Best Local Similarity 35.4%; Pred. No. 4.7e-43;  
 Matches 127; Conservative 69; Mismatches 126; Indels 37; Gaps 10;

QY 10 DYVVEEN--ENMGTYDYSQYELCIKEDVR--BFAKVFELVFLTVIVIGLAGNSMVVAI 65  
 Db 12 DGHESGFWLNNSSDSSQ-----ENKRFLEKVEFLFCVILVVFVFLGNSLVLI 64  
 QY 66 YAYYKQRTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVNLGKIMKITSALTYLNFVS 125  
 Db 65 YIFQKRLTLDVFLNPLADLVFVCTLPFWAYAGTYEWFVGVNCKTLRGMYTNMFYV 124  
 QY 126 GMDPLACISIDRYAV--TKVPSQGVGKPCW--ITFCVMAAILLSIPQIVFTVND 180  
 Db 125 SMLTLCITVDRLVAVQATKAFNRQAKWK--IMQVILCLIMVWSLVLSLPDIIGHVOD 183  
 QY 181 NARCIFFPRPLGTSMKALIQMLEICIGFVFPFLIMGVCFIARTLTKMPNKKISRPK 240  
 Db 184 IDKIL---COYHSEETWLVAVIOMTRGFPLPLTMILCTSGIILKILHARNQKHSLK 240  
 QY 241 VLVTVIVFIVTQLPYNIYVKRCRAIDIIYSLITSCNMSKEMDIAIQYTESIALFHSCLNP 300  
 Db 241 IIFLVAVFLLTQTPFLAMLIQSTSWETIIS-----FKYAIIVTEIAIAFRACLNP 294  
 QY 301 ILVYFGASFRNYVMKAYKYG-----SWRRQOSVEEPPFSEGTETSTFSI 350  
 Db 295 VLVAFVGLKFRKNVWKLMKIDIGCLSHLGVSOWKSEDSK--TCSASHNVEATSMFOL 351

## RESULT 11

Q9HCAS PRELIMINARY; PRT; 342 AA.  
 ID Q9HCAS  
 AC Q9HCAS  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Mutant G protein-coupled receptor STRL33.  
 GN STRL33.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97311099; PubMed=9166430;  
 RA Liao F., Alkhatib G., Peden K.W., Sharma G., Berger E.A., Farber J.M.;  
 RT "STRL33, A novel chemokine receptor-like protein, functions as a  
 fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-  
 1."  
 RL J. Exp. Med. 185:2015-2023 (1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA An P., Winkler C., O'Brien S.J.;  
 RT "The Influence of a STRL33 mutant on the course of HIV-1 infection."  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF029759; AAG21918.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PRINTS; PR01568; LYMPHOTACTNR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEPTOR\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 342 AA; 39279 MW; CE149633D01D20AA CRC64;

Query Match 30.8%; Score 560; DB 4; Length 342;  
 Best Local Similarity 33.1%; Pred. No. 6.3e-43;  
 Matches 117; Conservative 75; Mismatches 130; Indels 32; Gaps 8;

QY 12 YVEENMGTYDYSQYELCIKEDVR--BFAKVFELVFLTVIVIGLAGNSMVVAIYAYYK 71  
 Db 6 YHEDYGFSPDSSQGE-----HDFLQSKVFLPCMYLVVFCVGLVGSILVLSIFYHK 61  
 QY 72 QRTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVNLGKIMKITSALTYLNFVSQMDPLA 131  
 Db 62 LQSLIDVFLVNLPLADLVFVCTLPFWAYAGTYEWFVGVNCKTLRGMYTNMFYV 121  
 QY 132 CISIDRYAVVFKVPS--QSGVGKPCW--ITFCVMAAILLSIPQIVFTVND--NDNACI 185  
 Db 122 CITVDRLVAVQATKAFNRQAKWK--IMQVILCLIMVWSLVLSLPDIIGHVOD 180  
 QY 186 PIFPRYLGTSMKALIQMLEICIGFVFPFLIMGVCFIARTLTKMPNKKISRPK 245  
 Db 181 ---GYHBEAISTVVLAVQATKAFNRQAKWK--IMQVILCLIMVWSLVLSLPDIIGHVOD 236  
 QY 246 VLVTVIVTQLPYNIYVKRCRAIDIIYSLITSCNMSKEMDIAIQYTESIALFHSCLNP 305  
 Db 237 MAVFLLTQTPFLAMLIQSTSWETIIS-----IMVTEAIYVLRACLNPLVYAF 290  
 QY 306 MWASFRNYVMKAYKYG-----SWRRQOSVEEPPFSEGTETSTFSI 350  
 Db 291 VSLKFRKFWKLVKDIGCLPYLGVSHPWKSSEDNSK--TFSASHNVEATSMFOL 342

## RESULT 12

Q9TV16 PRELIMINARY; PRT; 342 AA.  
 ID Q9TV16  
 AC Q9TV16  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE G protein-coupled receptor STRL33.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=STRL33 (BONZO);  
 RA Brussels A., Pretet J.L., Girard M., Butor C.;  
 RT "Sequences and Predicted Structures of Chimpanzee STRL33 (Bonzo) and



RT 9P15 (BOB).";  
 RL AIDS Res. Hum. Retroviruses 15:0-0(1999).  
 DR EMBL; AF084229; AAD52041.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; LYMPHOTACTNR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 342 AA; 39273 MW; 5B58003797806B2A CRC64;  
 Query Match 30.7%; Score 559; DB 6; Length 342;  
 Best Local Similarity 33.1%; Pred. No. 7, 8e-43;  
 Matches 117; Conservative 74; Mismatches 131; Indels 32; Gaps 8;  
 QY 12 YEEENENGTVDYSQYELICIKEDVREFAKFLPVFLTIIVFVIGLAGNSMVAIYVKK 71  
 DB YHEDYGNFSNDSQEE---HDFLQFSKVFLECMYLVFVCGLVGNSIVLVISIFVHK 61  
 QY 72 QRTIDVYIINLAADLLFLTPFMAVNAHGVNGKIMCKITSLALTYLNFVSGQFLA 131  
 DB 62 LOSLIDVFLVNLPLADLVFCTLPFMAVYAGIHEWFGQVCKSLGITYINFTSMILIT 121  
 QY 132 CISIDRYVAATKPS--QSGVGRPCW--IICFCVMAAIIISIPOLVFYTV--NDNARCI 185  
 DB 122 CTVDRITVVKATKANKQAQKRTNGKVTSLIIVSLVSLPQIIYGVNPLDKLIC- 180  
 QY 186 PIFPRYLGTSMKALIQMLEICIGFVFPFLINGVCYFITARLTKMKNPKISRLPKVLLTV 245  
 DB 181 ---GYHDEAISTVLAQTQMTLGFPLPLTWICYSVILIKTLIAGFGQGRSIIKIIFLV 236  
 QY 246 VIVFIVQPLPNIVKFCRAIDITISLITSCMSKMDIAIQTESIALPHSCNPLIYVF 305  
 DB 237 MAVFLITQMPENMLKLRSTHWEYAMTISFHYT-----INVTIAIYLRACLPLVIAF 230  
 QY 306 MGAFKRYVMVAKKYG-----SWRQROSEVEFPDSEGPTEPTSTFSI 350  
 DB 291 VSLFRKRFKVLVDIGCLPLVIGVSHQKSEDSK--TFSASINVAATSMFOL 342  
 RESULT 13  
 Q9PUBO PRELIMINARY; PRT; 358 AA.  
 ID Q9PUBO  
 AC Q9PUBO  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE CXC chemokine receptor 4.  
 GN CXCR4.  
 OS Acipenser ruthenus (sterlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;  
 OC Acipenser.  
 NCBI\_TaxID=7906;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20368347; PubMed=10906389;  
 RA Alabjev B.Y., Najashin A.M., Mechetina L.V., Taranin A.V.;  
 RT "Cloning of a CXCR4 homolog in chondrosteian fish and characterization  
 of the CXCR4-specific structural features."  
 RL Dev. Comp. Immunol. 24:765-770(2000).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; AJ294948; CAB60252.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR01558; CHEMOKINER11.  
 DR PRINTS; PR00237; GPCRHOPOPSN.  
 DR PRINTS; PR01568; LYMPHOTACTNR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.

SQ SEQUENCE 358 AA; 40448 MW; 7B3B9B962453008 CRC64;  
 Query Match 29.9%; Score 544; DB 13; Length 358;  
 Best Local Similarity 35.5%; Pred. No. 1, 9e-41;  
 Matches 125; Conservative 64; Mismatches 145; Indels 18; Gaps 7;  
 QY 8 STDYEEEN-ENNGTYDYSQYELICIKEDVREFAKFLPVFLTIIVFVIGLAGNSMVAIY 66  
 DB 7 TVDFEENNTGSGSGDYSQYDEVCKRMINGDLRKIFLPTVYITIIIFWGIENGVLVITW 66  
 QY 67 AYKKQRTKTYIINLAADLLFLTPFMAVNAHGVNGKIMCKITSLALTYLNFVSG 126  
 DB 67 G-YQKTKMTDTRRLHLLIADLLEFVTLFPMAVDASSWYGGFLCKVNSIYVNLVSS 125  
 QY 127 MQLACISIDRYVAATKPSQSGVGRPC---WICFCVMAAIIISIPOLVFYTVNDN 181  
 DB 126 VILAFISFDRKLAIVARATNGH---KPRKLAEKIIVGVWLPATLILVPLVFAQVHDE 182  
 QY 182 A---RCIPFPRYLGTSMKALIQMLEICIGFVFPFLINGVCYFITARLTKM-MKNPKIS 237  
 DB 183 GTRMMCDRYVPSGSGNIMWTIFRFQHIFVGLVLPGLVITLCYCIITRLSGSKGLQRR 242  
 QY 238 PLKVLTVIVIVQPLPNIVKFCRAIDITISLITSCMSKMDIAIQTESIALPHSC 297  
 DB 243 ALKTTIILIAFLICWLPICAIIVDTIVLVNIQYNTLQHNETWTFVIBGLAIFHC 302  
 QY 298 LNPILYVFMGAFKRYVMVAKKYGSMRQROSEVEFPDSEGPTEPTSTFS 349  
 DB 303 LNSILYAFIVGFK---KSAKSALTIVNSRGSLSLKILSKNRGGISVSTSS 350  
 RESULT 14  
 Q91ZHA PRELIMINARY; PRT; 360 AA.  
 ID Q91ZHA  
 AC Q91ZHA  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE C-C chemokine receptor 4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LEW;  
 RA Garcia G.E., Chen S., Xia Y., Harrison J., Wilson C.B., Johnson R.J.,  
 RA Bacon K.B., Feng L.;  
 RT "Monoclonal cell-infiltrate inhibition by blocking macrophage-derived  
 RT chemokine results in attenuation of developing crescentic  
 RT glomerulonephritis."  
 RL Submitted (Oct-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF432872; AAL30398.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR01559; DUFFYANTIGEN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 360 AA; 41218 MW; 5095C6CD299E1F8B CRC64;  
 Query Match 29.4%; Score 534.5; DB 11; Length 360;  
 Best Local Similarity 34.7%; Pred. No. 1, 4e-40;  
 Matches 113; Conservative 67; Mismatches 127; Indels 19; Gaps 6;  
 QY 3 LEONSTDYEEENENGTVDYSQYELICIKEDVREFAKFLPVFLTIIVFVIGLAGNSW 62  
 DB 1 MNAETEVDITQDETEVNSYFDESLEPKPTKEGIRAFGEVFLPPLYSVLFGLGNSV 60  
 QY 63 VAIYAYKKQRTKTYIINLAADLLFLTPFMAVNAHGVNGKIMCKITSLALTYLN 122  
 DB 61 VVLPFKRLKSKNTDYLINLAISDLFLVLSLPMGVYAADQWVGIGLCKIISMWYLVG 120

QY 123 FVSGMQLACISIDRYAVTKV-----PSQGVGKPCWIIICFCVMAAILLSIPOLVF 175  
 DB 121 FVSGIFIMLSIDRYALVAVFSLRARTLTGVL-----ITSLSITSVAFAPALPGLF 175  
 QY 176 YTV--NNNARCIPFPRLYGTSMKALIQMLEI-CIGFVFPFLMGVCYFTARTLMKMP 231  
 DB 176 STCDTENHNYCKTOYS--VNSTKWKVSLSEINVLGIVPLGIMLFCYSMIITLTHCK 233  
 QY 232 NIKISRPKVLTVIVTQLPYNIKPCRAIDIIISLTSQNSKMDIAIQVETSI 291  
 DB 234 NEKKRAVRMFAVVVLGFWTPYNNVLFETL-VELSVLQDCTLERIDYALQATETL 292  
 QY 292 ALFHSCNPLIYVFMGASPKYVVKV 317  
 DB 293 AFHCCNPLIYVFLGKFRKYIAQL 318

RESULT 15  
 Q8VHP3 PRELIMINARY; PRT; 361 AA.  
 AC Q8VHP3;  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE CC-chemokine receptor 4.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
 NCBI\_TaxId=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Jopling L.A., Sabroe I., Andrew D.P., Mitchell T.J., Li Y.,  
 RA Hodge M.R., Williams T.J., Pease J.E.;  
 RT "The identification, characterization and distribution of guinea pig  
 RT CCR4 and epitope mapping of a blocking antibody."  
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF431971; AAL57488.1;  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 DR KMW Receptor.  
 SQ SEQUENCE 361 AA; 41064 MW; 9304897D4FDF6839 CRC64;

Query Match 29.1%; Score 529; DB 11; Length 361;  
 Best Local Similarity 36.0%; Pred. No. 4.4e-40;  
 Matches 118; Conservative 66; Mismatches 104; Indels 40; Gaps 10;

QY 9 TDYYEENENMGTYDYSQYELICIKEDVREFAKVFLPVFLTVFVIGLAGNSMVAIYAY 68  
 DB 17 SNYNYESSVGP-----CTKGTGKAFGELFLPPLVSLVFLFGLLNSVAVLVLFK 67  
 QY 69 YKKQRTKTYITLAVADLLFTLPMAVNAVHGVNLGKIMCKITSAIYTLNFSQMG 128  
 DB 68 YKRLRSMYDVLNLMAISDLFLVSLPFWGYAADQWVFGVCKMSIYLVGVSIGIF 127  
 QY 129 FLACISIDRYAVTV-----KVPSSQ-GVGGKPCWIIICFCVMAAILLSIPOLVF--YTV 178  
 DB 128 FIVLMSIDRYALVAVFSLRARTLTGVL-----ITSLSITSVAFAPALPGLFSTCYTE 182  
 QY 179 NDNARCIPFPRLYGTSMK-ALIQMLEI-CIGFVFPFLMGVCYFTARTLMKMPNIKIS 236  
 DB 183 RNHTSC---KRYNSANTWVKVLSLEINILGIVPLGIMLFCYSMIITLTHCKSKKN 239  
 QY 237 RPLKVLTVIVTQLPYNIKPCRAIDIIISLTSQNSKMDIAIQVETSI 291  
 DB 240 KAVKQIPAVVVLGFWTPYNNVLF-----LYTVLVELVLQDCELEKVIDPALQATETL 293  
 QY 292 ALFHSCNPLIYVFMGASPKYVVKV 319  
 DB 294 AFHCCNPLIYVFLGKFRKYIAQL 321

RESULT 16  
 Q9YGC3 PRELIMINARY; PRT; 358 AA.  
 AC Q9YGC3;  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Chemokine receptor 4.  
 GN CXCR4.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NCBI\_TaxId=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Moepfs B., Knoefle K., Brown M., Knoefel W., Gierschik P.;  
 RT "Expression of the CXCR chemokine receptor 4 during early Xenopus  
 RT laevis embryogenesis: a possible role of chemokine receptors as  
 RT regulators of development and differentiation."  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; Y17895; CAA76923.1; -  
 DR EMBL; Y17895; CAA76923.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHOPOPSN.  
 DR PRINTS; PR01568; LYMPHOTACNR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
 SQ SEQUENCE 358 AA; 40078 MW; 2E9E3448AE40ECB1 CRC64;

Query Match 28.6%; Score 520.5; DB 13; Length 358;  
 Best Local Similarity 35.9%; Pred. No. 2.6e-39;  
 Matches 108; Conservative 61; Mismatches 121; Indels 11; Gaps 6;

QY 19 NGTYDYSQYELICIKEDVREFAKVFLPVFLTVFVIGLAGNSMVAIYAYKKQRTKDV 78  
 DB 20 NSCGDFEDFIEPCFMEHNSDFNRIFLPITYSFIFLGIIGNLVAVVWGYYKKSRITMDK 79  
 QY 79 YILNLAVADLLFTLPMAVNAVHGVNLGKIMCKITSAIYTLNFSQMGQLACISIDRY 138  
 DB 80 YKRLHLSVADLFLVFLPMSVDAIIGWFKERLCAVHVIYTVNLYSVLILAFISLDY 139  
 QY 139 VAVTVPSQSGVGPCK--WIIICFCVMAAILLSIPOLVFYVND-NAR--CIPFPRLYGT 193  
 DB 140 LAIVAHNTSQSGRKMALADKVVYAGVWLPALLTVPDLVFAVSDENQGFCDRIYPIENR 199  
 QY 194 TSMKALIQMLEICIGFVFPFLMGVCYFTARTLMKMPNIKISRLKVLTVIVTQ 253  
 DB 200 EFWTGFRLHTTVGLIPGLIILICVVISKSHSGKHQRKALKTIVTILAFACW 259  
 QY 254 LPYNIKPCRAID--IISLIT-SQNSKMDIAIQVETSIALHSCNPLIYVFMGASF 310  
 DB 260 LPYVY--CLTDTTPEMLGLVKGDCIEMTUNLMAISTEALAFHCCNPLIYVFLGAKF 316  
 QY 311 K 311  
 DB 317 K 317

RESULT 17  
 Q9ULY8 PRELIMINARY; PRT; 355 AA.  
 AC Q9ULY8;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)





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QY 128 QFLACISIDRYAVATKVPSSQSGVCKPC--WICRCVMAAIIISIPQVYVY--NDNA 182
DB 120 LILAFISIDRLALVHATNSORPERKLAERKVVGVWIPALPLIPDFIPANVSEADDKY 179
QY 183 RCIPFIPRYVGTSMKALIQMLEICIGFVPELIMGVCFYFARTLKMMPNIKISRLPKVL 242
DB 180 ICDRFYFNDLWV--VVFQOHIMVGLILPGIVILSCYCIISLTKSHQKQKALKKT 236
QY 243 LTVVIVFIVTQLPYNIKFCRAIDIIYSLITSCNMSKRDIAIQVTSIALFHSCLNPIL 302
DB 237 VILLIAFACWLPYIIGISIDSFILIEIRQGEFENTVHKWISITETALAFHCCINPIL 296
QY 303 YVFMGASFK 311
DB 297 YAFIAGAKFK 305

RESULT 22
Q9MZNO PRELIMINARY; PRT; 347 AA.
AC Q9MZNO;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Chemokine receptor CXCR4 (Fragment).
GN CXCR4.
OS Alouatta seniculus (Howler monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Alouattinae;
OC Alouatta.
OX NCBI_TaxID=9503;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF172233; AAF89353.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR003006; IG_MEC.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1558; CHEMOKINER11.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PRINTS; PRO1568; LYMPHOTACTINR.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
KW NON_TER
FT
SQ SEQUENCE 347 AA; 39242 MW; 9F41BCDC75032E2B CRC64;

Query Match 27.7%; Score 503.5; DB 6; Length 347;
Best local Similarity 34.6%; Pred. No. 8.8e-38;
Matches 107; Conservative 58; Mismatches 133; Indels 11; Gaps 4;

```

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QY 243 LTVVIVFIVTQLPYNIKFCRAIDIIYSLITSCNMSKRDIAIQVTSIALFHSCLNPIL 302
DB 237 VILLIAFACWLPYIIGISIDSFILIEIRQGEFENTVHKWISITETALAFHCCINPIL 296
QY 303 YVFMGASFK 311
DB 297 YAFIAGAKFK 305

RESULT 23
Q9TV44 PRELIMINARY; PRT; 352 AA.
AC Q9TV44;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CC Chemokine receptor type 5.
GN CCR5.
OS Cercopithecus patas.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=27677;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9935215; PubMed=10408730;
RC STRAIN=04;
RX Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with SIV
RT carrier status in African nonhuman primates";
RL Aids Res. Hum. Retroviruses 15:931-939 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=04;
RA Muller-Trutwin M.C., Corbet S., Hansen J., Diop O.,
RA Georges-Courbot M.-C., Barre-Sinoussi F., Fomsgaard A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035220; AAD44013.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40747 MW; 3A56B90D3528D94C CRC64;

Query Match 27.7%; Score 503.5; DB 6; Length 352;
Best local Similarity 33.1%; Pred. No. 8.9e-38;
Matches 117; Conservative 67; Mismatches 124; Indels 45; Gaps 12;

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Db 296 IYAFVGEKFRVYLVFQKHTAKRCCKW-----CS1-----FQGAPEBASSVYT 340

## RESULT 24

Q9MZP1 PRELIMINARY; PRT; 347 AA.  
 ID Q9MZP1;  
 AC Q9MZP1;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Chemokine receptor CXCR4 (Fragment).  
 GN CXCR4.  
 OS Mandibullus leucophaeus (Drill) (Papio leucophaeus).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Mandibullus.  
 NCBI\_TaxID=9568;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;  
 RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in  
 RT Primates.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; AF172222; AAF89342.1; -;  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PRO1558; CHEMOKINER11.  
 DR PRINTS; PRO0237; GPCR\_RHODOPSN.  
 DR PRINTS; PRO1568; LYMPHOTACTNR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECPT\_P1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECPT\_P1\_2; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
 FT NON\_TER 1  
 SQ SEQUENCE 347 AA; 39273 MW; 0AE971AD1B565B4 CRC64;

Query Match 27.6%; Score 502.5; DB 6; Length 347;  
 Best Local Similarity 34.3%; Pred. No. 1.1e-37;

Matches 107; Conservative 60; Mismatches 128; Indels 17; Gaps 5;

QY 8 STDYVEENENNGTYDSQYELICIKEDVREPAKVPFLVFLTVFVIGLAGNSMVAIYA 67  
 Db 3 TSDNYTEE---MGSGDYDSIKEPCFRENAHFNRIFLPTIYSIIFLGIYNGGLVILWVG 59  
 QY 68 YKKORTKTDVYIINLAVADLLFTLPFAVNAVAVHGVGLGKIMCKITSAIYTLNFSQGM 127  
 Db 60 YOKLRSMTDKRYRLHLSVADLLFVITLPFAVNAVAVHGVGLGKIMCKITSAIYTLNFSQGM 119  
 QY 128 QPLACISIDRYAVAVTKVPSQGVGKPC---WICFCVMAAIIISIPOLVFTYV---N 179  
 Db 120 LILAFISIDRYALVAVHANSQ---KPKRLAEKVVYGVWIPALLITIPDIFPAVSSEAD 176  
 QY 180 DNARCIPIFRYIGTSKALIMLEICIGFVPEPLMGVCYFRTARTLMKMPNIXSRPL 239  
 Db 177 DRPICRFYNDLMV---VVFQFQHMVGLILPGIYILSCYIIISKLSKHQKRAKLT 233  
 QY 240 KVLITVIVFIVTQLPYNIYVFCRAIDIIYSLITSCMSKMDIAIQTVESIALFHSCLN 299  
 Db 234 KTVIIVLILAFACWLPYIIGISIDISFTLLETIRQGCFFENTVHKWISTEALAFHCCIN 293  
 QY 300 PILYVEMGASFK 311  
 Db 294 PILYAFGAKFK 305

## RESULT 25

Q9MZM9 PRELIMINARY; PRT; 347 AA.  
 ID Q9MZM9;  
 AC Q9MZM9;

DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Chemokine receptor CXCR4 (Fragment).  
 GN CXCR4.  
 OS Ateles paniscus (Black spider monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.  
 NCBI\_TaxID=9510;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;  
 RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in  
 RT Primates.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; AF172234; AAF89354.1; -;  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PRO1558; CHEMOKINER11.  
 DR PRINTS; PRO0237; GPCR\_RHODOPSN.  
 DR PRINTS; PRO1568; LYMPHOTACTNR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECPT\_P1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECPT\_P1\_2; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
 FT NON\_TER 1  
 SQ SEQUENCE 347 AA; 39317 MW; B84037A04490A1D1 CRC64;

Query Match 27.6%; Score 502.5; DB 6; Length 347;  
 Best Local Similarity 34.6%; Pred. No. 1.1e-37;

Matches 107; Conservative 58; Mismatches 133; Indels 11; Gaps 4;

QY 8 STDYVEENENNGTYDSQYELICIKEDVREPAKVPFLVFLTVFVIGLAGNSMVAIYA 67  
 Db 3 TSDNYTEE---MGSGDYDSIKEPCFRENAHFNRIFLPTIYSIIFLGIYNGGLVILWVG 59  
 QY 68 YKKORTKTDVYIINLAVADLLFTLPFAVNAVAVHGVGLGKIMCKITSAIYTLNFSQGM 127  
 Db 60 YOKLRSMTDKRYRLHLSVADLLFVITLPFAVNAVAVHGVGLGKIMCKITSAIYTLNFSQGM 119  
 QY 128 QPLACISIDRYAVAVTKVPSQGVGKPC---WICFCVMAAIIISIPOLVFTYV---DNA 182  
 Db 120 LILAFISIDRYALVAVHANSQ---KPKRLAEKVVYGVWIPALLITIPDIFPAVSSEADRY 179  
 QY 183 RCIPIFRYIGTSKALIMLEICIGFVPEPLMGVCYFRTARTLMKMPNIXSRPLKVL 242  
 Db 180 ICDFRYPDLMV---VVFQFQHMVGLILPGIYILSCYIIISKLSKHQKRAKLT 236  
 QY 243 LTVIVFIVTQLPYNIYVFCRAIDIIYSLITSCMSKMDIAIQTVESIALFHSCLN 302  
 Db 237 VILIVLILAFACWLPYIIGISIDISFTLLETIRQGCFFENTVHKWISTEALAFHCCIN 296  
 QY 303 YVFMGASFK 311  
 Db 297 YAFGAKFK 305

## RESULT 26

Q9MZM8 PRELIMINARY; PRT; 347 AA.  
 ID Q9MZM8;  
 AC Q9MZM8;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Chemokine receptor CXCR4 (Fragment).  
 GN CXCR4.  
 OS Callithrix jacchus (Common marmoset).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.  
 NCBI\_TaxID=9483;







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QY 128 QFLACISIDRYVAATKVPSSQGVGKPC--WICFCVMAAAILSLIPOLVFTYV--NDNA 182
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 LILAFISLSDRYLAIVATNSQGRPKLAELKVYVGVWIPALLTIPDFIFANVSEADRY 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 RCIPFIPRYLGTSMKALIQMLEICIGFVDFPLMGVCYFTARTLMKMPNIKISRLKVL 242
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 ICDRFYENDLWV---VVFQFOHIMVGLIPGIVILSCYCIISKLSHSGHQKRAKLT 236
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 243 LTVVIVFIVTOLPYNIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNPIL 302
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 VILIAFPACMLPYIIGISIDSFILLETIKQCGEFENTVHKMISTEALAFHCCCLNPIL 296
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 303 YVFMGASFK 311
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 YAFLGAKFK 305
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 31
Q9MZN2 PRELIMINARY; PRT; 347 AA.
AC Q9MZN2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Chemokine receptor CXCR4 (Fragment).
GN CXCR4.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT Primates.;
RT Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF172232; AAF89351.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PRO1558; CHEMOKINER11.
DR PRINTS: PRO0237; GPCRHHODOPSN.
DR PRINTS: PRO1568; LYMPHOTACTNR.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL2; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON TER
SQ SEQUENCE 347 AA; 39209 MW; D853326462E15B22 CRC64;

Query Match 27.5%; Score 500.5; DB 6; Length 347;
Best Local Similarity 34.6%; Pred. No. 1.6e-37;
Matches 107; Conservative 57; Mismatches 134; Indels 11; Gaps 4;

QY 8 STDYVEENENAGTYDYQYELICKEDEVREFAKVELVFLITVYVIGLAGNSMVAIYA 67
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 TSDNYTEE---MGSGDYDSIKEPCFREBNANFNKILEPTIYSILFTIGIVGGLVILWMG 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 68 YKKKORTKDVYIILNLAVALDLLFTLPFMAVNAVHGVNLGKIMCKITSAIYTLNPFVSGM 127
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 YKKKRSMTDKYRLHLSADLLFVITLFPMAVDANVWYFENFLCKAHVITYTNLVS 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 128 QFLACISIDRYVAATKVPSSQGVGKPC--WICFCVMAAAILSLIPOLVFTYV--NDNA 182
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 LILAFISLSDRYLAIVATNSQGRPKLAELKVYVGVWIPALLTIPDFIFANVSEADRY 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 RCIPFIPRYLGTSMKALIQMLEICIGFVDFPLMGVCYFTARTLMKMPNIKISRLKVL 242
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 ICDRFYENDLWV---VVFQFOHIMVGLIPGIVILSCYCIISKLSHSGHQKRAKLT 236
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 243 LTVVIVFIVTOLPYNIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNPIL 302
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 VILIAFPACMLPYIIGISIDSFILLETIKQCGEFENTVHKMISTEALAFHCCCLNPIL 296
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 303 YVFMGASFK 311
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 YAFLGAKFK 305
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 33
```

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Db 237 VILIAFPACMLPYIIGISIDSFILLETIKQCGEFENTVHKMISTEALAFHCCCLNPIL 296
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 303 YVFMGASFK 311
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 YAFLGAKFK 305
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 32
Q9MZN1 PRELIMINARY; PRT; 347 AA.
AC Q9MZN1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Chemokine receptor CXCR4 (Fragment).
GN CXCR4.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT Primates.;
RT Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF172232; AAF89352.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PRO1558; CHEMOKINER11.
DR PRINTS: PRO0237; GPCRHHODOPSN.
DR PRINTS: PRO1568; LYMPHOTACTNR.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL2; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON TER
SQ SEQUENCE 347 AA; 39209 MW; D853326462E15B22 CRC64;

Query Match 27.5%; Score 500.5; DB 6; Length 347;
Best Local Similarity 34.6%; Pred. No. 1.6e-37;
Matches 107; Conservative 57; Mismatches 134; Indels 11; Gaps 4;

QY 8 STDYVEENENAGTYDYQYELICKEDEVREFAKVELVFLITVYVIGLAGNSMVAIYA 67
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 TSDNYTEE---MGSGDYDSIKEPCFREBNANFNKILEPTIYSILFTIGIVGGLVILWMG 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 68 YKKKORTKDVYIILNLAVALDLLFTLPFMAVNAVHGVNLGKIMCKITSAIYTLNPFVSGM 127
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 YKKKRSMTDKYRLHLSADLLFVITLFPMAVDANVWYFENFLCKAHVITYTNLVS 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 128 QFLACISIDRYVAATKVPSSQGVGKPC--WICFCVMAAAILSLIPOLVFTYV--NDNA 182
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 LILAFISLSDRYLAIVATNSQGRPKLAELKVYVGVWIPALLTIPDFIFANVSEADRY 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 RCIPFIPRYLGTSMKALIQMLEICIGFVDFPLMGVCYFTARTLMKMPNIKISRLKVL 242
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 ICDRFYENDLWV---VVFQFOHIMVGLIPGIVILSCYCIISKLSHSGHQKRAKLT 236
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 243 LTVVIVFIVTOLPYNIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNPIL 302
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 VILIAFPACMLPYIIGISIDSFILLETIKQCGEFENTVHKMISTEALAFHCCCLNPIL 296
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 303 YVFMGASFK 311
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 YAFLGAKFK 305
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 33
```

Q9TS08 PRELIMINARY; PRT; 352 AA.  
 ID 09TS08  
 AC 09TS08  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE G-protein coupled receptor.  
 GN CXCR4.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Holtkamp N., Baier M., Werner A.;  
 RT "CXCR4 from African green monkey."  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL: AF019378; AAD01638.1;  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR003006; 1g\_MHC.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PRO0001; CHEMOKINER1.  
 DR PRINTS: PRO0237; GPCR\_RHODOPSIN.  
 DR PRINTS: PRO1568; LYMPHOTACTIN.  
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR\_F1\_1; 1.  
 DR PROSITE: PS00262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
 DR PROSITE: PS00290; 1g\_MHC; UNKNOWN\_1.  
 DR G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
 SK SEQUENCE 352 AA; 39624 MW; F240B86D6BC368F CRC64;

Query Match 27.5%; Score 500.5; DB 6; Length 352;  
 Best Local Similarity 34.3%; Pred. No. 1.7e-37;  
 Matches 107; Conservative 59; Mismatches 129; Indels 17; Gaps 5;

QY 8 STDYVEENEMNGYDYSQVELICIKEDVREFAKVPVFLTYFVIGLAGNSMVAIYA 67  
 DB 8 TSDVTEB---MGSQDYSIKEPCEBRENAHFNRIPLTYISIFLGIYONGVILVMG 64  
 QY 68 YKKKQRTKDYIINLAVADLLFLTPFMAVNAHGVGLGKINCKITSAIYTLNPFVSGM 127  
 DB 65 YOKLRSMWTKYRIHLVADLLFLTYLTPFMAVDAVAMWYFENFLCKAVHYITVNLVSSV 124  
 QY 128 QFLACISIDRVVAATKPSQSGVGKPC-----WICFCVMAAAILLSIPQVFTV---N 179  
 DB 125 LILAFISIDRLAIVAHATNSQ--KPRKLAEKVYVGVWIPALLTIPDIFASVSEAD 181  
 QY 180 DNACIPFFPYLGTSMKALIQMLEICIGFVFPFLMGVCYFIFARTLMKPNIKISRL 239  
 DB 182 DRYICDRYPNDLWV--VVFQGHIMVGLIPGIVILSCYCIISLKSQHGKQKAL 238  
 QY 240 KVLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCMSKRMIDIAIQVTSIALFHSCLN 299  
 DB 239 KTVYILIAFPACMLPYIGISIDSFILRIIKQCEFEFNTVHKWISITETALAFHCCLN 298  
 QY 300 PILVFMGASFK 311  
 DB 299 PILVAFGLAKFK 310

RESULT 34  
 Q9TUR8 PRELIMINARY; PRT; 339 AA.  
 ID 09TUR8  
 AC 09TUR8  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Cercopithecus aethiops vervet.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=100936;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
 RA Shidara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 RT species."  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF162020; AAD47775.1;  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PRO0237; GPCR\_RHODOPSIN.  
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR\_F1\_1; UNKNOWN\_1.  
 DR PROSITE: PS00262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
 DR PROSITE: PS00262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
 KW Receptor.  
 FT NON TER 1  
 FT NON TER 1  
 FT NON TER 1  
 SQ SEQUENCE 339 AA; 39143 MW; 67F8A4546C8E560 CRC64;

Query Match 27.5%; Score 499.5; DB 6; Length 339;  
 Best Local Similarity 33.5%; Pred. No. 2e-37;  
 Matches 117; Conservative 70; Mismatches 125; Indels 37; Gaps 11;

QY 21 TYDYSQY-ELICIKEDVREFAKVPVFLTYFVIGLAGNSMVAIYAYKKQRTKDYV 79  
 DB 2 TYDINYTSEPOCKINVAQIARLLPPLXSLVIFIGFQGNILVILINCRGLKSLMTDII 61  
 QY 80 IINLAVADLLFLTPFMAVNAHGVGLGKINCKITSAIYTLNPFVSGMQLACISIDRV 139  
 DB 62 LNLAIISDILFLTPFMAVNAHGVGLGKINCKITSAIYTLNPFVSGMQLACISIDRV 121  
 QY 140 AYTKV-----PSQSGVGKPCWIIICFCVMAAAILLSIPQVFTV-----YTNNDAR 183  
 DB 122 AIVHAVFAIKARTVTFGV---VTSVITVVAVAVASLPRIIFRSQREGIHYT----- 170  
 QY 184 CIPFPRYLGTSMAKALIQMLEICIGFVFPFLMGVCYFIFARTLMKPN-IKISRLPKV 241  
 DB 171 GSHHP-YQYQPFMKNFQTLKIVILGVLPLVMWICVSGILKTLTRNRNKKHRAVRL 229  
 QY 242 LITVIVFIVTQLPYNIYKFCRAIDIIYSLITSCMSKRMIDIAIQVTSIALFHSCLNPI 301  
 DB 230 IFTIMIVFPLFAPYNIIVILNTFQEFGL-NNCSSNRLDQAMQVETTLGTHCCINPI 288  
 QY 302 LVFMGASFKNYVMVAKKYSWRQR-QSVBEFPFDESGTEPTST 349  
 DB 289 IYAFVGEKFRNYLVFQKHIAKFKCCSI---FQGEABERASSVYT 333

RESULT 35  
 Q9TUR4 PRELIMINARY; PRT; 339 AA.  
 ID 09TUR4  
 AC 09TUR4  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Mandrillus sphinx (Mandrill) (Papio sphinx).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Mandrillus.  
 OX NCBI\_TaxID=9561;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
 RA Shidara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 RT species."  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF162032; AAD47787.1;  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm 1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECIP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECIP\_F1\_2; 1.  
 DR Receptor.  
 FT NON TER 1 1  
 FT NON TER 339 339  
 SO SEQUENCE 339 AA; 39135 MW; 518626A2DEF1BFBE CRC64;

Query Match 27.5%; Score 499.5; DB 6; Length 339;  
 Best Local Similarity 32.5%; Pred. No. 2e-37;  
 Matches 113; Conservative 71; Mismatches 129; Indels 35; Gaps 9;

QY 21 TYDYSQ-ELICTEDREFAKVFLPVFLTIYVIGLAGSMVAIYAYKQRTKDYV 79  
 DB 2 TYDDYTSSECKQINVKQIDARLLPPLVSLVIFGVGNILVLLINKRKLKSMTDIY 61  
 QY 80 ILNLAVADLLFLTPFMAVAVAGVIGKIMCKITSALYTLNFGSMOFLACISIDRYV 139  
 DB 62 LNLALISDLFLTLVPMVAHAAQWDFGNIMCOLTGLYFIFGSGIFPIILLITDRYL 121  
 QY 140 AVTKV-----PSQGVKPCWITCCVMAAILSLPOLV-----YTVNDMAR 183  
 DB 122 AIVAVAFALKARVTFGV-----VTSVITWVAVAFSLPGIIFRSQREGILHYT----- 170  
 QY 184 CIPFPRVIGSMKALIQMLEICIGFVVPFLMGVCYFIARTLMKPN-IKISRLKVL 242  
 DB 171 CSSHPFSQVQFWKQFTLKVLIGLVPLLMWICYSGILKTLIRCKRKHRAVRLI 230  
 QY 243 LTVIVIVITQLPYNIYVFCRAIDIIYSLTSCNMSKMDIAIQVTESIALFHSCLNPIL 302  
 DB 231 FTIMIVFLFMAPNIVILNTFOEPFGL-NCCSSNRLDQAMQVETLGMTHCINPII 289  
 QY 303 YVNGASPKYVAVKAYGSGWRQR-QSVHEFPDSEGPPEPSTIS 349  
 DB 290 YAFVGEKERNYLVFQKHAKRFCKCSCI---FQGEAPRASSVYT 333

RESULT 36  
 Q9MZ03 PRELIMINARY; PRT; 347 AA.  
 AC Q9MZ03;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Chemokine receptor CXCR4 (Fragment).  
 GN Pygathrix avunculus (Tonkin snub-nosed monkey).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Pygathrix.  
 OC NCBI\_TaxID=66062;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;  
 RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in  
 RT Primates"; JOL-1999) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; AF172210; AAF89330.1; -;  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PRO1558; CHEMOKINER11.  
 DR PRINTS; PRO0237; GPCRHHODPSN.  
 DR PRINTS; PRO1568; LYMPHOTACTNR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECIP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECIP\_F1\_2; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
 KW NON TER 1 1  
 FT SEQUENCE 347 AA; 39205 MW; E96B6136541515C CRC64;

Query Match 27.5%; Score 499.5; DB 6; Length 347;  
 Best Local Similarity 34.3%; Pred. No. 2e-37;  
 Matches 107; Conservative 59; Mismatches 129; Indels 17; Gaps 5;

QY 8 STDYVEENMGTYDSQVELICTEDREFAKVFLPVFLTIYVIGLAGSMVAIYA 67  
 DB 3 TSDNYTEE---MGSDGYDSIKEPCFRENHAFNRIPLTIYSILFTGLVGNGLVLMG 59  
 QY 68 YKKORTKTDYVILNLAVADLLFLTPFMAVAVAGVIGKIMCKITSALYTLNFGSM 127  
 DB 60 YKKRSMSTDKRRLSLVADLLFVTLTPFMAVDVANNPFGNPLCKAHVITVNLVSSV 119  
 QY 128 QFLACISIDRYAVAVTKVPSQGVKPC-----WIIICVMAAILSLPOLVFTV---N 179  
 DB 120 LILALISDRYALAHVAVNSQ---KPRKLAEKVYVGVWIPALLITPDEFIFASVSEAD 176  
 QY 180 DNARCIPIPRVIGSMKALIQMLEICIGFVVPFLMGVCYFIARTLMKPNIKISRL 239  
 DB 177 DRVYCDREFVNDLWV---VVFQFHIMVGLIPGIVLSICYIIISKLSHGKQKRAL 233  
 QY 240 KYLLTVIVIVITQLPYNIYVFCRAIDIIYSLTSCNMSKMDIAIQVTESIALFHSCLN 299  
 DB 234 KTVVILILAFKACWLPYITIGSIDSFILIELIKQCEFEYVHKMISTELAFHCCLN 293  
 QY 300 PILYVFMGASF 311  
 DB 294 PILYVFLGAKFK 305

RESULT 37  
 Q9MZ02 PRELIMINARY; PRT; 347 AA.  
 AC Q9MZ02;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Chemokine receptor CXCR4 (Fragment).  
 GN Rhinophelus roxellanae.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Pygathrix.  
 OC NCBI\_TaxID=101279;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;  
 RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in  
 RT Primates"; JOL-1999) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; AF172211; AAF89331.1; -;  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PRO1558; CHEMOKINER11.  
 DR PRINTS; PRO0237; GPCRHHODPSN.  
 DR PRINTS; PRO1568; LYMPHOTACTNR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECIP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECIP\_F1\_2; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
 KW NON TER 1 1  
 FT SEQUENCE 347 AA; 39205 MW; E96B6136541515C CRC64;

Query Match 27.5%; Score 499.5; DB 6; Length 347;  
 Best Local Similarity 34.3%; Pred. No. 2e-37;  
 Matches 107; Conservative 59; Mismatches 129; Indels 17; Gaps 5;

QY 8 STDYVEENMGTYDSQVELICTEDREFAKVFLPVFLTIYVIGLAGSMVAIYA 67  
 DB 3 TSDNYTEE---MGSDGYDSIKEPCFRENHAFNRIPLTIYSILFTGLVGNGLVLMG 59

QY 68 YKKKORTKTDVYIINLAVADLLFTLPFMAVNAVHGVNLCKIMCKITSAIYTLNFVSGM 127  
 DB 60 YKKLRSMTDKRYRLHLSDVADLLFTLPFMAVNAVHGVNLCKIMCKITSAIYTLNFVSGM 119  
 QY 128 QFLACISIDRYVAVTKVPSQSGVGKPC-----WICFCVMAAILISIPOLVFYTV--N 179  
 DB 120 LILAFISIDRYLAIVHATNSQ---KPRKLLAEKVYVGVWIPALLLTIPDFIFASVSEAD 176  
 QY 180 DNARCIPIFPRYLGTSMKALIQMLEICGFVVPFLMGVCYFIFARTLMKPNIKISRL 239  
 DB 177 DRYICDRFPNDLWV---VVFQPHIMVGLIPGIVILSCYIIISKLSHGQKQKAL 233  
 QY 240 KVLTVVIVFIVTOLPYNIIVKFCRAIDIIYSILTSCKNSKMDIAIOVTESIALFHSCLN 299  
 DB 234 KTVVILILAFACWLPYIIGISIDSFILIEIKQGCERFENVHMKISTITLALAFHCCLN 293  
 QY 300 PILYVFMGASF 311  
 DB 294 PILYAFLAGAKFK 305

## RESULT 38

Q9MZQ1 PRELIMINARY; PRT; 347 AA.  
 AC Q9MZQ1;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Chemokine receptor CXCR4 (Fragment).  
 GN CXCR4.  
 OS Pygathrix bieti (Black snub-nosed monkey) (Rhinothecus bieti).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Colobinae;  
 OC Pygathrix.  
 NC NCBI\_TaxID=61621;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;  
 RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in  
 RT Primates";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL: AF172212; AAF89332.1; -;  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR00306; IG\_MHC.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PRO1558; CHEMOKINER11.  
 DR PRINTS: PRO0237; GPCR\_RHODOPSN.  
 DR PRINTS: PRO1568; LYMPHOTACTNR.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECPT\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECPT\_F1\_2; 1.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
 DR KEGG: G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 347 AA; 39205 MW; E96B6136541515C CRC64;

Query Match 27.5%; Score 499.5; DB 6; Length 347;  
 Best Local Similarity 34.3%; Pred. No. 2e-37;  
 Matches 107; Conservative 59; Mismatches 129; Indels 17; Gaps 5;  
 QY 8 STDVYEEENNGTYDSQYELICIKEDVREFAVFLPVFLTIVFVIGLAGNSMVVAIYA 67  
 DB 3 TSDNVTTEE---MGSGDYDSIKPCFRENHAFNRIPLPTYSIIIFLIGVINGVLIVMG 59  
 QY 68 YKKKORTKTDVYIINLAVADLLFTLPFMAVNAVHGVNLCKIMCKITSAIYTLNFVSGM 127  
 DB 60 YKKLRSMTDKRYRLHLSDVADLLFTLPFMAVNAVHGVNLCKIMCKITSAIYTLNFVSGM 119  
 QY 128 QFLACISIDRYVAVTKVPSQSGVGKPC-----WICFCVMAAILISIPOLVFYTV--N 179  
 DB 120 LILAFISIDRYLAIVHATNSQ---KPRKLLAEKVYVGVWIPALLLTIPDFIFASVSEAD 176

QY 180 DNARCIPIFPRYLGTSMKALIQMLEICGFVVPFLMGVCYFIFARTLMKPNIKISRL 239  
 DB 177 DRYICDRFPNDLWV---VVFQPHIMVGLIPGIVILSCYIIISKLSHGQKQKAL 233  
 QY 240 KVLTVVIVFIVTOLPYNIIVKFCRAIDIIYSILTSCKNSKMDIAIOVTESIALFHSCLN 299  
 DB 234 KTVVILILAFACWLPYIIGISIDSFILIEIKQGCERFENVHMKISTITLALAFHCCLN 293  
 QY 300 PILYVFMGASF 311  
 DB 294 PILYAFLAGAKFK 305

## RESULT 39

Q9MZQ0 PRELIMINARY; PRT; 347 AA.  
 AC Q9MZQ0;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Chemokine receptor CXCR4 (Fragment).  
 GN CXCR4.  
 OS Pygathrix nemaeus (Dove langur).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Colobinae;  
 OC Pygathrix.  
 NC NCBI\_TaxID=54133;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;  
 RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in  
 RT Primates";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL: AF172213; AAF89333.1; -;  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR00306; IG\_MHC.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PRO1558; CHEMOKINER11.  
 DR PRINTS: PRO0237; GPCR\_RHODOPSN.  
 DR PRINTS: PRO1568; LYMPHOTACTNR.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECPT\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECPT\_F1\_2; 1.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
 DR KEGG: G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 347 AA; 39205 MW; E96B6136541515C CRC64;

Query Match 27.5%; Score 499.5; DB 6; Length 347;  
 Best Local Similarity 34.3%; Pred. No. 2e-37;  
 Matches 107; Conservative 59; Mismatches 129; Indels 17; Gaps 5;  
 QY 8 STDVYEEENNGTYDSQYELICIKEDVREFAVFLPVFLTIVFVIGLAGNSMVVAIYA 67  
 DB 3 TSDNVTTEE---MGSGDYDSIKPCFRENHAFNRIPLPTYSIIIFLIGVINGVLIVMG 59  
 QY 68 YKKKORTKTDVYIINLAVADLLFTLPFMAVNAVHGVNLCKIMCKITSAIYTLNFVSGM 127  
 DB 60 YKKLRSMTDKRYRLHLSDVADLLFTLPFMAVNAVHGVNLCKIMCKITSAIYTLNFVSGM 119  
 QY 128 QFLACISIDRYVAVTKVPSQSGVGKPC-----WICFCVMAAILISIPOLVFYTV--N 179  
 DB 120 LILAFISIDRYLAIVHATNSQ---KPRKLLAEKVYVGVWIPALLLTIPDFIFASVSEAD 176  
 QY 180 DNARCIPIFPRYLGTSMKALIQMLEICGFVVPFLMGVCYFIFARTLMKPNIKISRL 239  
 DB 177 DRYICDRFPNDLWV---VVFQPHIMVGLIPGIVILSCYIIISKLSHGQKQKAL 233  
 QY 240 KVLTVVIVFIVTOLPYNIIVKFCRAIDIIYSILTSCKNSKMDIAIOVTESIALFHSCLN 299  
 DB 234 KTVVILILAFACWLPYIIGISIDSFILIEIKQGCERFENVHMKISTITLALAFHCCLN 293

QY 300 PILYVFMGASFK 311  
Db 294 PILYAFLGAKFK 305

## RESULT 40

Q9MZP9 PRELIMINARY; PRT; 347 AA.  
AC Q9MZP9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)  
DE Chemokine receptor CXCR4 (Fragment).  
GN CXCR4.  
OS Nasalis larvatus (Proboscis monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
OC Nasalis.  
OX NCBI\_TaxID=43780;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;  
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in  
RT Primates."  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; AF172214; AAF89334.1; -;  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PRO1558; CHEMOKINER1.  
DR PRINTS; PRO0237; GPCR\_RHODOPSN.  
DR PRINTS; PRO1568; LYMPHOTACTIN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KM G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
FT NON\_TER  
SQ SEQUENCE 347 AA; 39205 MW; E96B6136541515C CRC64;

Query Match 27.5%; Score 499.5; DB 6; Length 347;  
Best Local Similarity 34.3%; Pred. No. 2e-37;  
Matches 107; Conservative 59; Mismatches 129; Indels 17; Gaps 5;

QY 8 STDYVEENENNGYDYVSOVELICIKEDVREFAKFLPFLTYFVIGLAGNSMVAIYA 67  
Db 3 TSDNYTEE--MGSQDYDSIKPCFRENAHFRIPLPIYSIFLTGIVGNGLVILVMG 59  
QY 68 YKKQRTKTDVYIINLVADLLFLTPFWANVAVHGVGLKIMCKITSAIYTLNLFVSGM 127  
Db 60 YQKLRSTDTKRLHLSTVADLLFVITLPPWADVAVANNYFQNFCLKAVHVIYTNLYSSV 119  
QY 128 QFLACISIDRYVAVYKVPSSQSGVKPC---WIICFVWMAAILLSIPQLVFTV---N 179  
Db 120 LILAFISIDRYLAIVHATNSQ--KPRKLAEKVVYGVWIPALLTIPDFIFASVSEAD 176  
QY 180 DNARCIPIFPFYLTGSMKALIQMLEICIGFVFPFLMGVCFTIARTLMKPNIKISRP 239  
Db 177 DRYICDRFPYNDLWV--VVFQHIWGLIPGIVILSCYCIISKLSHSGHQKRAL 233  
QY 240 KVLTVVVFVLTQLPYNIIVAFCAIDIIYSLTSCNMSKRMDAIOVTESIALFHSCLN 239  
Db 234 KTYVLLIAFPACWLPYITGISIDSFILITIKGCEFEFNTVHKWISITELAFHCCLN 293  
QY 300 PILYVFMGASFK 311  
Db 294 PILYAFLGAKFK 305

Search completed: March 17, 2003, 16:27:42  
Job time : 36 secs



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## OM protein - protein search, using sw model

Run on: March 17, 2003, 16:27:06 ; Search time 14 Seconds

(without alignments)  
1152.302 Million cell updates/sec

Title: US-09-721-495b-2

Perfect score: 1819  
Sequence: 1 MALFQNSQSDYYEENEMNG.....VEPPFDSGPTPTFTSI 350

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 135 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1819	100.0	350	10	US-09-796-338A-8
3	1814	99.7	349	10	US-09-765-994-4
4	761	41.8	175	9	US-09-989-442-108
5	761	41.8	175	9	US-09-852-865-91
6	761	41.8	175	10	US-09-764-853-584
7	637	35.0	357	9	US-09-966-755-2
8	637	35.0	357	10	US-09-903-377-2
9	637	35.0	357	10	US-09-952-385-2
10	637	35.0	357	12	US-10-000-759A-2
11	581	31.9	342	10	US-09-852-156-4
12	569	31.3	342	10	US-09-852-156-6
13	560	30.8	342	10	US-09-852-156-2
14	560	30.8	342	10	US-09-940-063-2
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16	537.5	29.5	360	9	US-09-764-413-20
17	537.5	29.5	360	10	US-09-837-446-2
18	537.5	29.5	360	10	US-09-796-744-17
19	532.5	29.3	360	10	US-09-938-719-10
20	532.5	29.3	360	10	US-09-939-226-10
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22	526.5	28.9	362	9	US-09-898-751A-4
23	525	28.9	362	10	US-09-931-381A-18
24	522.5	28.7	355	10	US-09-789-482-4
25	522.5	28.7	355	10	US-09-789-486-4
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97 365 20.1 364 10 US-10-218-574-11 Sequence 11, Appl  
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99 362 19.9 351 10 US-09-944-807-2 Sequence 2, Appl  
100 357 19.6 360 10 US-09-852-156-8 Sequence 8, Appl  
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102 343 18.9 302 9 US-10-024-494-10 Sequence 30, Appl  
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127 323 17.8 405 10 US-09-866-871-84 Sequence 84, Appl  
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## ALIGNMENTS

RESULT 1  
US-09-765-994-2  
; Sequence 2, Application US/09765994  
; Patent No. US20010016336A1  
; GENERAL INFORMATION:  
; APPLICANT: ELIIS, CATHERINE  
; TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR  
; FILE REFERENCE: GH-70225-C1  
; CURRENT APPLICATION NUMBER: US/09/765,994  
; CURRENT FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/055,895  
; PRIOR FILING DATE: 1997-08-15  
; PRIOR APPLICATION NUMBER: 08/962,922  
; PRIOR FILING DATE: 1997-10-27  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-765-994-2

Query Match 100.0%; Score 1819; DB 10; Length 350;  
Best Local Similarity 100.0%; Pred. No. 5,7e-153;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 2  
US-09-796-338a-8  
; Sequence 8, Application US/09796338A  
; Patent No. US20020061522A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR  
; FILE REFERENCE: 10448-020001  
; CURRENT APPLICATION NUMBER: US/09/796,338A  
; CURRENT FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/186,059  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-796-338a-8  
Query Match 100.0%; Score 1819; DB 10; Length 350;  
Best Local Similarity 100.0%; Pred. No. 5,7e-153;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 M A L E Q N O S T D Y Y E E N E N G T D Y S O Y E L I C K E V R E P A K F L P V L T I V F I G L A G N S 60  
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DB 181 N A R C I P I P R Y I G T S M K A L I O M L E I C I G F V V P F L M G V C Y F I T A T L M K M P I K S R P L K 240  
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DB 301 I L Y V F M G A S F K N Y V N K V A K K Y S W R R O R O S V E E P F D S E G P T E P T S P S I 350



Db 301 LLYVFMGASFKNYVMKAKKYGSMRQRQSVSEFPDSEPTSTFSGI 350

US-09-765-994-4  
Sequence 4, Application US/09765994  
Patent No. US20010016336A1

GENERAL INFORMATION:  
APPLICANT: ELI LILLY, CATHERINE

TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR  
FILE REFERENCE: GH-70225-C1

CURRENT APPLICATION NUMBER: US/09/765,994  
CURRENT FILING DATE: 2001-01-19

PRIOR APPLICATION NUMBER: 60/055,895  
PRIOR FILING DATE: 1997-08-15

PRIOR APPLICATION NUMBER: 08/962,922  
PRIOR FILING DATE: 1997-10-27

NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PASCSEQ for Windows Version 3.0

SEQ ID NO 4  
LENGTH: 349  
TYPE: PRT

ORGANISM: HOMO SAPIENS  
US-09-765-994-4

Query Match 99.7%; Score 1814; DB 10; Length 349;  
Best Local Similarity 100.0%; Pred. No. 1,6e-152;  
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ALEONOSTDYVEENENGTVDYSQVELICIKEDVREFAKVPVFLTVFVIGLAGNSM 60

QY 62 VVAIYAYKKKRTKTDVYLNLAVADLLFTLPFMAVNAVHGVGLKINCKITSAIYTL 121  
Db 61 VVAIYAYKKKRTKTDVYLNLAVADLLFTLPFMAVNAVHGVGLKINCKITSAIYTL 120

QY 122 NFVSGMQLACISIDRYAVATKVPDSQGVKPCWITICPCWMAAILISTQVLYFTYNDN 181  
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QY 182 ARCPPIPRVYGTSMKALIQMLEICIGVVPFLMGVCYFTARTLKKMPKIKSRPLKV 241  
Db 181 ARCPPIPRVYGTSMKALIQMLEICIGVVPFLMGVCYFTARTLKKMPKIKSRPLKV 240

QY 242 LLLTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNPI 301  
Db 241 LLLTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNPI 300

QY 302 LLYVFMGASFKNYVMKAKKYGSMRQRQSVSEFPDSEPTSTFSGI 350  
Db 301 LLYVFMGASFKNYVMKAKKYGSMRQRQSVSEFPDSEPTSTFSGI 349

RESULT 4  
US-09-969-442-108  
Sequence 108, Application US/09969442  
Publication No. US20030013649A1

GENERAL INFORMATION:  
APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: P4208

CURRENT APPLICATION NUMBER: US/09/969,442  
CURRENT FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31

PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/214,886  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 60/217,487

PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,758  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,963  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/217,496  
PRIOR FILING DATE: 2000-07-11  
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PRIOR FILING DATE: 2000-08-14  
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PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/225,757  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/226,868  
PRIOR FILING DATE: 2000-08-22  
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PRIOR APPLICATION NUMBER: 60/241,809  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/249,299  
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PRIOR APPLICATION NUMBER: 60/236,327  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/241,785  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/244,617  
PRIOR FILING DATE: 2000-11-01  
PRIOR APPLICATION NUMBER: 60/225,268  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,368  
PRIOR FILING DATE: 2000-09-29  
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PRIOR FILING DATE: 2000-12-08  
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PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,345  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,287  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,513  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/231,413  
PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/229,509  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/236,367  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/237,039  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,038  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/236,370  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/236,802  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,037  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,040  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/240,960  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/239,935  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/239,937  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/241,787  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,474  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/246,532  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/249,216  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,210  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/226,681  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,759  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/225,213  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/227,182  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,214  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/235,836  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/230,438  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/215,135  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 60/225,266  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/249,218  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,208  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,213  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,212  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,207  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,245  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,244  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,217  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,211  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,215  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,264  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,214

PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,297  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/232,400  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/231,242  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/232,081  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/232,080  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/231,414  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/231,244  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/233,064  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/233,063  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,397  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,399  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,401  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/241,808  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,826  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,786  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,221  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,475  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/231,243  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/233,065  
PRIOR FILING DATE: 2000-09-14

Query Match 41.8%; Score 761; DB 9; Length 175;  
Best Local Similarity 96.1%; Pred. No. 5.1e-60;  
Matches 148; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 197 KALIMLEICIGFVVPFLIMGVCYFRTMTMKQPNKISRLKVLTVVIVITOLPY 256  
DB 22 ESIDSMLEICIGFVVPFLIMGVCYFRTMTMKQPNKISRLKVLTVVIVITOLPY 81  
QY 257 NIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNPILVYFMGASFKNYMK 316  
DB 82 NIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNPILVYFMGASFKNYMK 141  
QY 317 VAKKYGWRORQSVVEFPFDEGTEPTSTFSI 350  
DB 142 VAKKYGWRORQSVVEFPFDEGTEPTSTFSI 175

RESULT 5  
US-10-073-865-91  
Sequence 91, Application US/10073865  
Publication No. US2003004904A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PYZ09C1  
CURRENT APPLICATION NUMBER: US/10/073,865  
PRIOR FILING DATE: 2002-02-14  
Prior Application removed - See file Wrapper or Palm  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 91  
LENGTH: 175  
TYPE: PRT

```

? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (16)
? OTHER_INFORMATION: Xaa equals any of the naturally occurring L-amino acids
? NAME/KEY: misc_feature
? LOCATION: (19)
? OTHER_INFORMATION: Xaa equals any of the naturally occurring L-amino acids
? OS-10-073-865-91

```

Query Match	41.8%;	Score 761;	DB 9;	Length 175;
Best Local Similarity	96.1%;	Pred. No. 5.1e-60;		
Matches 148;	Conservative 3;	Mismatches 3;	Indels 0;	Gaps 0

Qy	197	KALQMEICIGFVPEFLIMGCEFTARTLTKMPNIKISPLKVLTVVVFVLTOLPY	256
	...		
Db	22	ESIDSMETCIGFVPEFLIMGVCFHTERTLTKMPNIKISPLKVLTVVVFVLTOLPY	81
Qy	257	NIVFCRAIDIIYSILTSCKNSKAMDIAIQVTESIALFHSCLNEDILVYFGASPKYVMK	316
Db	82	NIVFCRAIDIIYSILTSCKNSKAMDIAIQVTESIALFHSCLNEDILVYFGASPKYVMK	141
Qy	317	VAKKIGSWRROROSVYEEFPDSEGETESTPESI	350
Db	142	VAKKIGSWRROROSVYEEFPDSEGETESTPESI	175

```

RESULT 6
US-09-764-853-584
: Sequence 584. Application US/09764853
: Patent No. US20020090672A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: P206
: CURRENT APPLICATION NUMBER: US/09/764,853
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 939
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 584
: LENGTH: 175
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (16)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (19)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: US-09-764-853-584

```

Query Match	41.8%;	Score 761;	DB 10;	Length 175;
Best Local Similarity	96.1%;	Pred. No. 5.1e-60;		
Matches 148;	Conservative 3;	Mismatches 3;	Indels 0;	Gaps 0;

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QY 197 KAL10MELCIGFVVPFLIMGVCYITFARLTKMKNISPLKVLTVVFLVTOJPY 250
:::
Db 22 ESIDMELCIGFVVPFLIMGVCYITFARLTKMKNISPLKVLTVVFLVTOJPY 81

QY 257 NIVKCRADIIYSLITSCNNSKRDIA1QVTESTALFHSCLNPILYFMGASEKNYMK 310
|||||
Db 82 NIVKCRADIIYSLITSCNNSKRDIA1QVTESTALFHSCLNPILYFMGASEKNYMK 140

QY 317 VAKKGTSMRROQSVEEFPDSEGTPEPTSTSI 350
|||||
Db 142 VAKKGTSMRROQSVEEFPDSEGTPEPTSTSI 175
```

RESULT 7  
US-09-966-755-2  
; Sequence 2, Application US/09966755

```

Publication No. US20030022238A1
GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: ANTI-GR-9-6 ANTIBODIES AND METHODS OF
IDENTIFYING AGENTS WHICH MODULATE GR-9-6 FUNCTION
FILE REFERENCE: LKS98-16
CURRENT APPLICATION NUMBER: US/09/966,755
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-09-966-755-2

```

Query Match	35.0%;	Score 637;	DB 9;	Length 357;
Best Local Similarity	36.5%;	Pred. No. 1e-48;		
Matches 119;	Conservative 74;	Mismatches 115;	Indels 18;	Gaps 4

[illegible]

```

1 RESULT 8
2
3 ; Sequence 2, Application US/09903377
4 ; Patent No. US20020116727A1
5 ;
6 ; GENERAL INFORMATION:
7 ;
8 ; APPLICANT: Allen, Keith D.
9 ;
10 ; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHEMOKINE
11 ; TITLE OF INVENTION: RECEPTOR 9A GENE DISRUPTIONS
12 ;
13 ; FILE REFERENCE: R-365
14 ;
15 ; CURRENT APPLICATION NUMBER: US/09/903,377
16 ;
17 ; CURRENT FILING DATE: 2001-07-10
18 ;
19 ; PRIOR APPLICATION NUMBER: US 60/217,255
20 ;
21 ; PRIOR FILING DATE: 2000-07-10
22 ;
23 ; PRIOR APPLICATION NUMBER: US 60/221,483
24 ;
25 ; PRIOR FILING DATE: 2000-07-27
26 ;
27 ; PRIOR APPLICATION NUMBER: US 60/262,113
28 ;
29 ; PRIOR FILING DATE: 2001-01-16
30 ;
31 ; NUMBER OF SEQ ID NOS: 4
32 ;
33 ; SOFTWARE: FastSeq for Windows Version 4.0
34 ;
35 ; SEQ ID NO 2
36 ;
37 ; LENGTH: 357
38 ;
39 ; TYPE: PRT
40 ;
41 ; ORGANISM: Artificial Sequence
42 ;
43 ; FEATURE:

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OTHER INFORMATION: Targeting vector  
US-09-903-377-2

Query Match	35.0%;	Score 637;	DB 10;	Length 3577
Best Local Similarity	36.5%;	Pred. No. 1e-48;		
Matches 119;	Conservative	74;	Mismatches 115;	Indels 1

Oy	10	DYVYE - NENNGTIDYSGYEILCI MEDYERAEKAEFLPEFLTIVIVIGIAGSMVAIYAY	68
Db	4	DYGSSTJSMEDYVNFNTDPYCEGNVNRQGRASHFLPEFLYLVYIVGALNSIYIIVYMY	63
Oy	69	YKQKQRTDVIYIINLAVADLLFLPLPWAVNAVHGVLGKIMCKITSALYTLNFWGMO	128
Db	64	CTRVYTMIDMFLMLAIADLLFLVTLPLWAIADQWQFOTFMCKVNSMKNFYCYVL	123
Oy	129	FLACISIDRYAVAVTEVPQSQGVKRCW-----IICFCVMAAILLSIPOLVFYTVN	179
Db	124	LIMCSVDRYIAIINQ-----AMRAHTWBEKRLYSXWYCFIWIWLAALCIPELYSQIK	178
Oy	180	DN---ARCIPIPRYLYGTSMKALIQMTEICGFVVPFLIMGVCFYTARTLMKMPNIIKIS	236
Db	179	EESGIAITCTWYYPDSERFKLSAVITLVKVIIGFELPFVMAACVYIIIIHTLIQKKSKH	238
Oy	237	RPLKLTIVYVIVFYIOTLOPVNIYKFCRAIDIIYSITSNNKSKMDIAIQVTSIALFHS	286
Db	239	KALKATITIVLVFVYSQPPNYCIIIVQIIDAVNMFISNCANSTMIIDICFOTQIARFHS	288
Oy	297	CLNPLIYFPMQASFKNVYMKAKKTYG	322
Db	299	CLNPLVLYFVEGERFRDLVKTILKING	324

RESULT 9  
US-09-952-385-2

Patent No. US20020119504A1  
GENERAL INFORMATION:  
APPLICANT: Andrew, David P.  
APPLICANT: Zabel, Brian A.  
APPLICANT: Ponath, Paul D.  
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF  
TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION  
FILE REFERENCE: LKS98-16  
CURRENT APPLICATION NUMBER: US/09/952,385  
CURRENT FILING DATE: 2001-09-13  
PRIOR APPLICATION NUMBER: 09/266,464  
PRIOR FILING DATE: 1999-03-11  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 357  
TYPE: PR1  
ORGANISM: Homo sapiens  
IS-09-952-385-2

Query Match 35.0%; Score 637; DB 10; Length 357;  
Best Local Similarity 36.5%; Pred. No. 1e-48;  
Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps

QY 10 DYYVEE-NENMGITDYSYELCTCKEDVREPAKFLFVPLFTIVPVIGLAGNSMVAIYAY 68  
DB 4 DYSESTISMDYVNFENTDPYCEKNRRQPSHFLLPPLIYLVFTVALDNSLITLITWY 63  
QY 69 YKKORTKTIVYILNI,AAVADLLLFLETFPVAVNAVHGVWLGRKIMCKITSAIYTLNPFVSGMO 128  
DB 64 CTRVKTITDMFLMLAIADLLFLTLTFPFAIADQMKPOTFMCKVYVNSKNNFYSCVL 123  
QY 129 FLACISIDRYAAVNRKVSQSGVGKPCW-----IICGVMAAATLLSIIPOLVFVTYN 179  
DB 124 LIMCISIDRYAIADQ-----AMRAHTREKRLYSKAVCFITWLAALCIPELISQIK 178  
QY 180 DN---ARCIFFPYLGTSMKALIOMLEICIGFVPLVINGVCYFIPTARTLMKKNPIKIS 236

[illegible]

```

RESULT 10
US-10-000-759A-2
Sequence 2, Application US/10000759A
Patent No. US20020141991A1
GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: ANTIGR-9-6 ANTIBODIES AND METHODS OF
TITLE OF INVENTION: IDENTIFYING MODULATORS OF GR-9-6 FUNCTION
FILE REFERENCE: 1855.1064-003
CURRENT APPLICATION NUMBER: US/10/000,759A
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US/09/522,752
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: US 09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 357
TYPE: PR1
ORGANISM: Homo sapiens
US-10-000-759A-2

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	Oneary Match	35.0%	Score 637;	DB 12;	Length 357;	
	Best Local Similarity	36.5%*	Pred. NO. 1e-48;			
	Matches 119;	Conservative	74;	Mismatches 115;	Indels 18;	Gaps 4;
Oy	10 DYYEE-NENGVYDVSQYEYLICIKEDREFEAKFELPVFLTFIVGILAGNSMVAIVAY	68				
Dd	4 DYSESTSSMEDVYANFNPTDFCEKANNRQASHFLPLWLVIFGALGNLSVLIVMY	63				
Oy	69 YKKORTKVYILNIAVADLLFLTPFWAVNAVHGVLCIMCKITSAIYTLNFVSGMO	128				
Dd	64 CTRVKMTDMFLNLAIADLFLVTLPFWAIAADQMKFOTMPCKKNVSNMYKNFFSCLV	123				
Oy	129 FLACISIDRYVAATVPQSGVGRCW-----IIICCVMAAILLSIPQLVRYTYN	179				
Dd	124 LINCISVDVRYIAAQ----AMRAHTMEKEKLISKVCNCFETIWLAALCIPBILYSQIK	178				
Oy	180 DN---ARCPPEPRYIGTSKALIQMLEICIGFVFPFLINGVCYFTIARTIMAPNIKIS	236				
Dd	179 EESGIALCTMYPSDEBKTKASAVLTIKVILGFLLPFWAACTYIIITHILOAKSSSG	238				
Oy	237 RPLKVLLETVVFIIVTOLPYNIIVKFCRAIDIYSILITSNMSSKMDIAIQVESIALFFS	296				
Dd	239 KALKVTIIVLFVFLSQPFNYCILQLQTIDAYAMFINSCAVSTINDICHOYTOTIAFFHS	298				
Oy	297 CLNPILIVFMGASFKNYVMKVAKKKG	322				
Dd	299 CLNPVLIVVFGRFRRDVKTLLKNG	324				

RESULT 11  
 US-09-852-156-4  
 ; Sequence 4, Application US/0985215  
 ; Patent No. US20020076694A1  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Iltman, Dan R.  
 ;  
 ; Deng, Hongkui  
 ; Umutaz, Derya

Ramani, Vineet N.K.  
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS  
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF  
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES  
THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

Floor  
STREET: 411 Hackensack Ave, Continental Plaza, 4th

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/852,156

FILING DATE: 09-May-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1049-1-009NCIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 342 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: African Green Monkey

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-852-156-4

Query Match 31.9%; Score 581; DB 10; Length 342;

Best Local Similarity 34.2%; Pred. No. 8,2e-44;

Matches 121; Conservative 71; Mismatches 130; Indels 32; Gaps 8;

QY 12 YEEENEMNGTYDYSQYELICIKEDVREPAKVPFLPFLTIVFVIGLAGNSMVAIYAYKK 71

DB 6 HYEDNGFNSFNDSSQEE---HODPLQFSKVFPCMYLVFVCGLVGNSLVVISIFYHK 61

QY 72 QRTKTDVITLNAVADLLLTLPFAVNAVHGWLGKIMCKITSALYTLNFSGMOFLA 131

DB 62 LQSLDVEFLVNLPLADLVFVCTLPFAVAGIHEMTFGQVMCKTLLGTYTLNFSYMSLILT 121

QY 132 CISIDRYAVATKVPB--QSGVGKPCW--IICFCVMAAILISIPOLVFTV--NDNARCI 185

DB 122 CITVDRFIVVAKATAYNOQAKMTGKVICLLIWIISLVSLPQIIYGNVFNLDKILC- 180

QY 186 PIPIRFLIGSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIKISRPKLVLTV 245

DB 181 ----GYHDEEISTVLAQMTLGFPLPLAMIVCYSVIKTLILHAGGFQKHSIKIIFLV 236

QY 246 VIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKRDIAIQVTESIALFHSCLNPLIYVF 305

DB 237 MAVFLITQTPFNVLKILRSTHWEYAMTSFHYT-----IIVTEAIAYLRACLNPLVLYAF 290

QY 306 MCASFKNYMKVAKKYG-----SWRQROSVSEPPFDSGPTPTSTFSI 350

DB 291 VSLTKRKPNKVLKVDIGCLPYLGSHQKSSSDNKK--TFSSHNHVEATSMFOL 342

RESULT 12

US-09-852-156-6  
Sequence 6, Application US/09852156  
Patent No. US2002007694A1  
GENERAL INFORMATION:

APPLICANT: Littman, Dan R.

Deng, Hongkui

Unutmaz, Derya

Ramani, Vineet N.K.

Floor

STREET: 411 Hackensack Ave, Continental Plaza, 4th

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/852,156

FILING DATE: 09-May-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1049-1-009NCIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 342 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: pigtailed macaque

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-852-156-6

Query Match 31.3%; Score 569; DB 10; Length 342;

Best Local Similarity 33.6%; Pred. No. 9,4e-43;

Matches 119; Conservative 72; Mismatches 131; Indels 32; Gaps 8;

QY 12 YEEENEMNGTYDYSQYELICIKEDVREPAKVPFLPFLTIVFVIGLAGNSMVAIYAYKK 71

DB 6 HYEDNGFNSFNDSSQEE---HODPLQFSKVFPCMYLVFVCGLVGNSLVVISIFYHK 61

QY 72 QRTKTDVITLNAVADLLLTLPFAVNAVHGWLGKIMCKITSALYTLNFSGMOFLA 131

DB 62 LQSLDVEFLVNLPLADLVFVCTLPFAVAGIHEMTFGQVMCKTLLGTYTLNFSYMSLILT 121

QY 132 CISIDRYAVATKVPB--QSGVGKPCW--IICFCVMAAILISIPOLVFTV--NDNARCI 185

DB 122 CITVDRFIVVAKATAYNOQAKMTGKVICLLIWIISLVSLPQIIYGNVFNLDKILC- 180

QY 186 PIPIRFLIGSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIKISRPKLVLTV 245

DB 181 ----GYHDEEISTVLAQMTLGFPLPLAMIVCYSVIKTLILHAGGFQKHSIKIIFLV 236

QY 246 VIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKRDIAIQVTESIALFHSCLNPLIYVF 305

DB 237 MAVFLITQTPFNVLKILRSTHWEYAMTSFHYT-----IIVTEAIAYLRACLNPLVLYAF 290

RESULT 12

Oy 306 MGASFKNVYKAKKYG-----SWRROQSVSEFPDSEPTSTFSI 350  
 Db 291 VSLKRNKFWKLVKDIGCLPYIGVSHQKSEBNSK--TFASHNVEATSNFOL 342

# RESULT 13 US-09-852-156-2

; Sequence 2, Application US/09852156  
 ; Patent No. US20020076694A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Littman, Dan R.  
 ; Inventor: Deng, Hongkui  
 ; Unutmaz, Derya  
 ; Ramani, Vineet N K.

TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS  
 ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF  
 IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES  
 THEREOF

NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.  
 STREET: 411 Hackensack Ave, Continental Plaza, 4th  
 Floor  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/852,156  
 FILING DATE: 09-May-2001  
 CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 1049-1-009NCIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 342 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHEICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-852-156-2

Query Match 30.8%; Score 560; DB 10; Length 342;  
 Best Local Similarity 33.1%; Pred. No. 5.9e-42;  
 Matches 117; Conservative 75; Mismatches 130; Indels 32; Gaps 8;

Oy 12 YEEENMGTYDYSQVELCIKEDVREPAKVFLLPVFLTVVIGLAGSNVVAIYAYKK 71  
 Db 6 YHEDYGFSSFNDSQOE---HQDFLOFSKYFLPCMYLVVFCGLVGNLSLVVISTYHK 61  
 Oy 72 QRTKTDVYILNLAVALDLFLFTLPFMAVNAVHGVLGKIMKITSALTYTLNFSGMQFLA 131  
 Db 62 LOSLTDVFLVNLPLADLVFVCTLPFMAVYAGIHEWVFGQWCKSLGITYINFTSMILT 121  
 Oy 132 CISIDRYAVATKVP--QSGVGKPCW--IICFCVMAAILISIPOLVFYV--NDNARCI 165  
 Db 122 CITVDRFIVVATKAVYNAQAKMTWKVTSLLIIVISLVSIPOLIIYGNVFNLDKILIC- 180

Oy 186 PIFPRYIGTSMKALIQMLEICIGFVVPFLINGVCYFITARLTKMKNIKISRLKLLTV 245  
 Db 181 ----GYHDAISIVLATQMTIGFLPLTLTVCSVILIKTLHAGGQKRSLSKIIFLV 236  
 Oy 246 VIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIAIQVTSIALPHSLNPILYV 305  
 Db 237 MAVFLLTQMPFNLKMFIRSTHWEYAMTSFHYT-----IMVTEIAIALRACLNPLVYAF 290

Oy 306 MGASFKNVYKAKKYG-----SWRROQSVSEFPDSEPTSTFSI 350  
 Db 291 VSLKRNKFWKLVKDIGCLPYIGVSHQKSEBNSK--TFASHNVEATSNFOL 342

# RESULT 14 US-09-940-063-2

; Sequence 2, Application US/09940063  
 ; Patent No. US2002090657A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Briskin, Michael J.  
 ; APPLICANT: Murphy, Kristine E.  
 ; APPLICANT: Wilbanks, Alyson M.

APPLICANT: Wu, Lijun  
 TITLE OF INVENTION: No. US2002090657A1e1 Antibodies and ligands for "Bonzo"

FILE REFERENCE: 1855.1070-000  
 CURRENT APPLICATION NUMBER: US/09/940,063  
 PRIOR FILING DATE: 2001-08-27  
 PRIOR APPLICATION NUMBER: 09/449,437

NUMBER OF SEQ ID NOS: 18  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 2

LENGTH: 342  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-940-063-2

Query Match 30.8%; Score 560; DB 10; Length 342;  
 Best Local Similarity 33.1%; Pred. No. 5.9e-42;  
 Matches 117; Conservative 75; Mismatches 130; Indels 32; Gaps 8;

Oy 12 YEEENMGTYDYSQVELCIKEDVREPAKVFLLPVFLTVVIGLAGSNVVAIYAYKK 71  
 Db 6 YHEDYGFSSFNDSQOE---HQDFLOFSKYFLPCMYLVVFCGLVGNLSLVVISTYHK 61  
 Oy 72 QRTKTDVYILNLAVALDLFLFTLPFMAVNAVHGVLGKIMKITSALTYTLNFSGMQFLA 131  
 Db 62 LOSLTDVFLVNLPLADLVFVCTLPFMAVYAGIHEWVFGQWCKSLGITYINFTSMILT 121  
 Oy 132 CISIDRYAVATKVP--QSGVGKPCW--IICFCVMAAILISIPOLVFYV--NDNARCI 185  
 Db 122 CITVDRFIVVATKAVYNAQAKMTWKVTSLLIIVISLVSIPOLIIYGNVFNLDKILIC- 180  
 Oy 186 PIFPRYIGTSMKALIQMLEICIGFVVPFLINGVCYFITARLTKMKNIKISRLKLLTV 245  
 Db 181 ----GYHDAISIVLATQMTIGFLPLTLTVCSVILIKTLHAGGQKRSLSKIIFLV 236  
 Oy 246 VIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIAIQVTSIALPHSLNPILYV 305  
 Db 237 MAVFLLTQMPFNLKMFIRSTHWEYAMTSFHYT-----IMVTEIAIALRACLNPLVYAF 290  
 Oy 306 MGASFKNVYKAKKYG-----SWRROQSVSEFPDSEPTSTFSI 350  
 Db 291 VSLKRNKFWKLVKDIGCLPYIGVSHQKSEBNSK--TFASHNVEATSNFOL 342

# RESULT 15 US-10-120-394-20

; Sequence 20, Application US/10120394  
 ; Patent No. US20020160015A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wells, Timothy N.C.  
 ; Power, Christine A.

```

TITLE OF INVENTION: CHEMOKINE RECEPTOR ABLE TO BIND TO MCP-1, MIP-1 ALPHA AND/OR RANTES AND ITS USES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 No. US20020160015alth Giebe Rd. 8th floor
City: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/120,394
FILING DATE: 12-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/614,256
FILING DATE: 12-JUL-2000
APPLICATION NUMBER: US 08/875,573
FILING DATE: 31-OCT-1997
APPLICATION NUMBER: PCT/GB96/00143
FILING DATE: 24-JAN-1996
APPLICATION NUMBER: GB 9501683.8
FILING DATE: 27-JAN-1995
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-120-394-20
Query Match 29.5%; Score 537.5; DB 9; Length 360;
Best Local Similarity 35.8%; Pred. No. 66-40;
Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps
QY 10 DYVYENENMGVYDYSQVELLICKEDVRFAVFLPVFLTIYFVIGLAGSNMVAIYAY 69
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 8 DTTDESISNYVLESIPKPKCTKEGKFGELFPLPYSLVFPVGLGNSVAVLVLFK 67
QY 70 KKQRTKTDVYIINLAVADLLFLTFPFMAVNAVHGVLAGKINCKITSAIYTLNFSGMQF 129
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 KRLRSMITDYYILNLAIISDLLFVSLPFWGYAADQVWFGIGLCKMISMYVLGVGYGIRF 127
QY 130 IACISIDRYVAATKV-----PSQSGVGKPCWITFCVWMAAILISIQLVF--YTN 179
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 128 VMLMSIDRYLAIYHVAVFSLRARTLTGV-----ITSLATWSVAVFASLPGLFSTCYTER 182
QY 180 DNARCIPIPRVLTGSMKALLIQLEI-CIGFVYVFLIMGVCPITARTMTMKPNKISRP 238
DB 183 NHFYCKTKRS--LNSTTWKVLSSLELNIIIGLVLPGLIMLFCYSMIRITLQHCNEKNKA 240
QY 233 LKVLTLTVIVFTVLTQLPYNIYVKFCRAIDITISLITSCNNSKRMIDIAIQTESIATLPHSCL 298
DB 241 VGMIRFVAVVLPFLGFWPPNIVLFLETL-VELBVLQDCTERYLDVAIQTETLTAFAVHCL 299
QY 299 NPILYVFMGASPKNYVMYKAK 319
DB 300 NPILYVFLGKFRKYLQLFK 320
RESULT 16
US-09-764-413-20
; Sequence 20, Application US/09764413
; Publication No. US20020187930A1
GENERAL INFORMATION:
APPLICANT: Wells, Timothy N.C.
Power, Christine A.

```

```

TITLE OF INVENTION: A CHEMOKINE RECEPTOR ABLE TO BIND TO MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 No. US20020187930Alth Glebe Rd. 8th floor
City: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,413
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/875,573
FILING DATE: <Unknown>
APPLICATION NUMBER: GB 9501683.8
FILING DATE: 27-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-172
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-764-413-20

Query Match 29.5%; Score 537.5; DB 9; Length 360;
Best Local Similarity 35.8%; Pred. No. 6e-40;
Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps 6.

QY 10 DYVHEENMGTYDSQVELLCIKEDVAPKAVLPVPLTIYFVGLGNSVVAIVAY 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 8 DTLDESISNYVYESIPKQCKEGIAFGELFLPILYSIVFVGLGNSVVAIVLEKY 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 KQORTKTVYILINLAVADLLLEFTLPFVAVAVAHGVLGKIMCKITSLTYLNFVSGMOF 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 KRLNSMTVYILINLAISDLVFLVSLPFPGYAAADQWVGLGCKKIMSWVLYLFGISGIRF 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 130 LACISIDRYVAATKY-----PSQSGVGKPCWIIICFCVMAAILLSIPQLVF---YTVN 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 128 VWLMSIDRYLAIVHAFVSLRARTLYGV-----ITSLATWSVAVFPASLPGFLSTCYTER 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 180 DNARCIPIFPRLTGLSGMALLQMLEI-CIGFVFPPLINGVCYCFIARTLMKPNKISRP 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 183 NHTYKTKYS-INSTWKVLSLEINILGVLPGLIMLFCYSMIRTLQCKNEKKAKA 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 239 LKVLTVVIVFIVTOLPNVIVFCALDIILYSLTSCNMSKMDIAIQVTESIALFHSCL 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 241 VAMTAVVVLFPGFPTPINIVIFLETL-VELEVLDQCFERIVLDVAIQATETLAFVHCL 299
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 299 NPIIVFMGASFKNYVMKAVK 319
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 300 NPIIVFMGASFKNYVMKAVK 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 17
US-09-837-446-2
; Sequence 2, Application US/09837446
; Patent No. US20020019341A1

```





TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. US20020106742A1e  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-938-719-10

Query Match 29.3%; Score 532.5; DB 10; Length 360;  
Best Local Similarity 35.8%; Pred. No. 1.7e-39;  
Matches 115; Conservative 62; Mismatches 125; Indels 19; Gaps 6;

QY 10 DYVEENEMNGTYDSQYELICIKEDVREPAKVFPLPVLTIVFVIGLAGNSMVAIYAY 69  
DB 8 DTTDESISVNYLYESIPKCTKEGKAFGEFLPLPLYSIVAEVFGILGNSVVLVLFKY 67  
QY 70 KQCKRTDVYILNLAADLLFTLPFMAVNAVHGVGKIMCKITSAIYTLNPFVGMQF 129  
DB 68 KRIRSMTDVYILNLAISDLFLVFSLPFGYAADQWVFGIGICMISMTYLVGFYSIGIF 127  
QY 130 IACISIDRYAVATKVPSSQ-----GVGKPCWIIICFVMAAAILSLIPOLVF---YTVN 179  
DB 128 VMIMSIDRYALIVHAVEXXXARTIYGV-----ITSLATWSVAVFPASLPGFIFSTCYTER 182  
QY 180 DNARCIPIPRYIGTSMKALIQMLEI-CIGFVVPFLMGVCYFTTARTLMKMPNIXSRP 238  
DB 183 NHTYCKTKYS--INSTWVKVLSLEINILGLVPLGIMLFCYSMTIRTLQHCNKKKNKA 240  
QY 239 LKVLITVIVVIFVLPQPNIVKFCRAIDIIYSLITSCNMSKRMDAIQVTSIALFHSCL 298  
DB 241 VKMIFAVVAVFLGFWTPPNIVFLFETL--VELEVIQDCTFERIDYALQATETLAFVHCL 299  
QY 299 NPILYVFMGASFKNYVMKVAK 319  
DB 300 NPILYVFLGKFKRYITIQLFK 320

RESULT 20  
US-09-939-226-10  
Sequence 10, Application US/09939226  
Patent No. US20020110805A1  
GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL

PARMENTIER, MARC

VASSART, GILBERT

LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/939,226

FILING DATE: 24-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626,939

FILING DATE: 2000-07-27

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: <Unknown>

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 360 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. US20020110805A1e  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-939-226-10

Query Match 29.3%; Score 532.5; DB 10; Length 360;  
Best Local Similarity 35.8%; Pred. No. 1.7e-39;  
Matches 115; Conservative 62; Mismatches 125; Indels 19; Gaps 6;

QY 10 DYVEENEMNGTYDSQYELICIKEDVREPAKVFPLPVLTIVFVIGLAGNSMVAIYAY 69  
DB 8 DTTDESISVNYLYESIPKCTKEGKAFGEFLPLPLYSIVAEVFGILGNSVVLVLFKY 67  
QY 70 KQCKRTDVYILNLAADLLFTLPFMAVNAVHGVGKIMCKITSAIYTLNPFVGMQF 129  
DB 68 KRIRSMTDVYILNLAISDLFLVFSLPFGYAADQWVFGIGICMISMTYLVGFYSIGIF 127  
QY 130 IACISIDRYAVATKVPSSQ-----GVGKPCWIIICFVMAAAILSLIPOLVF---YTVN 179  
DB 128 VMIMSIDRYALIVHAVEXXXARTIYGV-----ITSLATWSVAVFPASLPGFIFSTCYTER 182  
QY 180 DNARCIPIPRYIGTSMKALIQMLEI-CIGFVVPFLMGVCYFTTARTLMKMPNIXSRP 238  
DB 183 NHTYCKTKYS--INSTWVKVLSLEINILGLVPLGIMLFCYSMTIRTLQHCNKKKNKA 240  
QY 239 LKVLITVIVVIFVLPQPNIVKFCRAIDIIYSLITSCNMSKRMDAIQVTSIALFHSCL 298  
DB 241 VKMIFAVVAVFLGFWTPPNIVFLFETL--VELEVIQDCTFERIDYALQATETLAFVHCL 299  
QY 299 NPILYVFMGASFKNYVMKVAK 319  
DB 300 NPILYVFLGKFKRYITIQLFK 320

RESULT 21  
US-09-938-703-10  
Sequence 10, Application US/09938703  
Patent No. US20020110870A1  
GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL

PARMENTIER, MARC

VASSART, GILBERT

LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,703

FILING DATE: 24-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626,939

FILING DATE: 2000-07-27

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: <Unknown>

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

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SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20020110870A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-938-703-10

```

```

Query Match      29.3% Score 532.5; DB 10; Length 360;
Best Local Similarity 35.8%; Pred. No. 1.7e-39;
Matches 115; Conservative 62; Mismatches 125; Indels 19; Gaps 6;

```

```

QY 10 DYVEENENMGTYDYSQYELICIKEDVREFAKFLPVPLTIIVFVIGLAGNSMVAIYAY 69
DB 8 DTLTDESISNYVLYESI PKCTKEGIAFGLPLPLYSIVFVGLIGNSVAVLVLFKY 67
QY 70 KKQRTKDVYILNLAVALDLLFTLPFWAVNAHGVLGKIMCKITSLATLNFVSGMOF 129
DB 68 KRISMVDVYILNLAISDLTFVFSLPFWGYAADQWFGIGICIMISMYLVGVSIGIF 127
QY 130 LACTSIDRYVAVTKVPSQS-----GVGKPCWIIICFWMAAILLSIPOLVF---YTVN 179
DB 128 VMWSIDRYLAIVAHVEXXAKRTIIVG-----ITSLATMSVAVFAPIPGFIFSTCTER 182
QY 180 DNARCIPIFPYRLGTSMKALIQMLEI-CIGFVVPFLIMGVCFYFARTMKMPNIKISRP 238
DB 183 NHTYCKTKYS--LNSTWKVLSLEINILGLVILGIMLFCYSMIITLQCKKEKNKA 240
QY 239 LKVLTVIVIVITQLPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTESIALPFSCL 298
DB 241 VKMIFAVVVLFGFWTPYNIYVLFETL-VELEVIDQCTFFERYLDYALQVETTLAFVHCL 299
QY 299 NPILYVFMGASFKNYVMKVAR 319
DB 300 NPILYFLEKFRKIYIOLFK 320

```

## RESULT 22

```

US-09-898-751A-4
Sequence 4, Application US/09898751A
Patent No. US20020160024A1
GENERAL INFORMATION:
APPLICANT: Oldham, Elizabeth R.
APPLICANT: Soco, Hortensia
APPLICANT: Liu, Ying
APPLICANT: Hudak, Susan A.
APPLICANT: Homey, Bernhard
APPLICANT: Morales, Janine M.
APPLICANT: Kellerman, Strid-Almee
APPLICANT: McEvoy, Leslie M.
APPLICANT: Bowman, Edward P.
TITLE OF INVENTION: CHEMOKINE AND RECEPTOR USES; COMPOSITIONS; METHODS
FILE REFERENCE: DX0882X
CURRENT APPLICATION NUMBER: US/09/898, 751A
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: US09/471,549
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US60/136,570
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: US60/113,858
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 362
TYPE: PRT
ORGANISM: Mus musculus
US-09-898-751A-4

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Query Match      28.9% Score 526.5; DB 9; Length 362;
Best Local Similarity 34.5%; Pred. No. 5.6e-39;

```

```

Matches 121; Conservative 66; Mismatches 133; Indels 31; Gaps 7;

```

```

QY 22 YDYSQYEL-----ICIKEDVREFAKFLPVPLTIIVFVIGLAGNSMVAIY-AYYKKQRTK 75
DB 17 YDEBAVSVPPELICYKADVQAFSRAFPVSILWAVLGLAGNGLVATHTLAARTTRSP 76
QY 76 TDVYIILNLAVALDLLFTLPFWAVNAHGVLGKIMCKITSLATLNFVSGMOFLACISI 135
DB 77 TSVHLOALADLLATLTLTFPMAAGALQGMNIGSTTCRAIGLVSASHAGFLPLACISA 136
QY 136 DRVVAATK-VPSQSGVGR--CWIIICFWMAAILLSIPOLVF---TVNDNARCIPIFP 189
DB 137 DRVVAATKALPGQRPSPSRHLYSVFWMLATLALPALFSPDGRREGORRRLIFP 196
QY 190 RYLGTSMKALIQMLEI-CIGFVVPFLIMGVCFYFARTMKMPNIKISPLKVLTLVIV 249
DB 197 ESLTQTVKASAVAQVAVGFLPLGVMAACVALGRTLLAARGPERRBALRVVALVAVF 256
QY 250 IYTQLPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTESIALPFSCLNPLVYFMGAS 309
DB 257 VVIQLPYSIALLDITADLLAARERSCSSKRDLLALVTGGLTVRCSLNPLVLAFLGLR 316
QY 310 FKNYVMKVKAKYGSN-----RROQSVYEEFPDSEGTPEPTSFESI 350
DB 317 FRDRLRLQGGGCGCPKPNPGRGCRRLRLS-----SCSAFTETHSL 358

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## RESULT 23

```

US-09-931-381A-18
Sequence 18, Application US/09931381A
Patent No. US20020137107A1
GENERAL INFORMATION:
APPLICANT: Butcher, Eugene C.
APPLICANT: Kunkel, Eric J.
APPLICANT: Pan, Junliang
APPLICANT: Soler-Ferran, Dulce
TITLE OF INVENTION: Method for Identifying Agents which
TITLE OF INVENTION: Modulate Chemokine "WCC"-Induced Functions of CCR3 and/or
FILE REFERENCE: 1855.2010-003
CURRENT APPLICATION NUMBER: US/09/931,381A
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: U.S. 09/638,914
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 362
TYPE: PRT
ORGANISM: Homo sapiens
US-09-931-381A-18

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Query Match      28.9% Score 525; DB 10; Length 362;
Best Local Similarity 32.9%; Pred. No. 7.6e-39;
Matches 121; Conservative 67; Mismatches 152; Indels 28; Gaps 6;

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QY 1 MALEQNSTDYVEENMGTYDYSQYELICIKEDVREFAKFLPVPLTIIVFVIGLAGNS 60
DB 1 MGEATEQVSMGHSYGDDEDAASAPPELCYKADVQAFSRAFPQSVSLVTAALAGLAGNG 60
QY 61 MVAIY-AYYKKQRTKDVYIILNLAVALDLLFTLPFWAVNAHGVLGKIMCKITSLAY 119
DB 61 LVATHTLAARRAARSPTSHTLQTLADLLATLTFPMAAGALQGMNIGSATCRISGLY 120
QY 120 TINFVSGMOFLACISIDRVVAATKV-----PSSQSGVGRKWCWIIICFWMAAILLSIPOLVF 175
DB 121 SASFHAAGFLFLACISADRVVAATRALPAGRPSTPGR-AHLVSVVWLSSLALPALLF 179
QY 176 YTVND---NARCIPIFPYRLGTSMKALIQMLEI-CIGFVVPFLIMGVCFYFARTMKMPN 232
DB 180 SQDQREGGRRCRLIFPELITQTVKASAVAQVAVGFLPLGVMAACVALGRTLLAARG 239
QY 233 IKISRLKVLTLTVIVITQLPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTESIA 292

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```

Db 240 PERRARLVVAALVAALVVLQLPYSALLLDLADLLAARSRSCPASRKKXVALLVTSIGA 299
Qy 293 LPHSCNLPILYVFGASPKYVMKVAK-----KYSWROROSVEPFDSGPT 342
Db 300 LARGCLNPVLYAFILGRPRDLRLKLGSSPSGPPRRCCPRRPLS-----SCS 350
Qy 343 EPTSTFSI 350
Db 351 APTETHSL 358

```

```

RESULT 24
US-09-789-482-4
; Sequence 4, Application US/09789482
; Patent No. US20020054875A1
; GENERAL INFORMATION:
; APPLICANT: Koch, Alisa E.
; APPLICANT: Ruth, Jeffrey H.
; APPLICANT: Rottman, James B.
; TITLE OF INVENTION: Therapeutic Methods That Target
; FILE REFERENCE: 3238.1000-003
; CURRENT APPLICATION NUMBER: US/09/789,482
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 60/183,568
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-482-4

```

```

Query Match 28.7%; Score 522.5; DB 10; Length 355;
Best Local Similarity 36.4%; Pred. No. 1.2e-38;
Matches 112; Conservative 57; Mismatches 122; Indels 17; Gaps 5;

```

```

Qy 22 YDSQVELICKEVDREFAKVPFLPVFLIVFVIGLAGNSMVAIYAAYKKORTKTDVYL 81
Db 12 FEYDDLAECYIGDIVVGTIVLSIFSVIPAIGVGLVAVPLMTSKKPKSVTDIYLL 71
Qy 82 NLAVADLLFLPFWAVNAVHGWLGKIMCKITSALTYNFVSGMOFLACISIDRYAV 141
Db 72 NLALSDLLFVATLPFWTHYLNKGLHNAMCKFTTAPFFIGFSGIFPITVISIDRYLAI 131
Qy 142 TKVPS-----QSGVGKPCWIIICVWMAAILSLPOLVFTVNDNARCIPIPRYLGT 194
Db 132 VLAANSNNRTVQHG-----TISLGWMAAILVAAPQFMFTKOKEN-ECIGDYEVLOE 185
Qy 195 SMKLLIOWLEICIGFVPELIMGVCFITARTLMKMPKISRPLKVLTVIVFVTQL 254
Db 186 IWPVLRNVTNPLGLPLIMSYCFRIQTLFSCNKKHAKAKIKLLLVIVFPLFWT 245
Qy 255 PYNIVKFCRAIDIIYSLTSCMSKRMDAIOVTESIALFHSCLNPILYVFGASPKYV 314
Db 246 PYNWVIFLETIK-LYDFPSCDMRDLRLALSVETVAFSHCCNPLIYAFAGEKFRYL 304
Qy 315 MKVAKKYG 322
Db 305 YHL---YG 309

```

```

RESULT 25
US-09-789-486-4
; Sequence 4, Application US/09789486
; Patent No. US2002005456A1
; GENERAL INFORMATION:
; APPLICANT: Koch, Alisa E.
; TITLE OF INVENTION: Therapeutic Methods That Target
; FILE REFERENCE: 3238.1000-004

```

```

; CURRENT APPLICATION NUMBER: US/09/789,486
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 60/183,568
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-486-4

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```

Query Match 28.7%; Score 522.5; DB 10; Length 355;
Best Local Similarity 36.4%; Pred. No. 1.2e-38;
Matches 112; Conservative 57; Mismatches 122; Indels 17; Gaps 5;

```

```

Qy 22 YDSQVELICKEVDREFAKVPFLPVFLIVFVIGLAGNSMVAIYAAYKKORTKTDVYL 81
Db 12 FEYDDLAECYIGDIVVGTIVLSIFSVIPAIGVGLVAVPLMTSKKPKSVTDIYLL 71
Qy 82 NLAVADLLFLPFWAVNAVHGWLGKIMCKITSALTYNFVSGMOFLACISIDRYAV 141
Db 72 NLALSDLLFVATLPFWTHYLNKGLHNAMCKFTTAPFFIGFSGIFPITVISIDRYLAI 131
Qy 142 TKVPS-----QSGVGKPCWIIICVWMAAILSLPOLVFTVNDNARCIPIPRYLGT 194
Db 132 VLAANSNNRTVQHG-----TISLGWMAAILVAAPQFMFTKOKEN-ECIGDYEVLOE 185
Qy 195 SMKLLIOWLEICIGFVPELIMGVCFITARTLMKMPKISRPLKVLTVIVFVTQL 254
Db 186 IWPVLRNVTNPLGLPLIMSYCFRIQTLFSCNKKHAKAKIKLLLVIVFPLFWT 245
Qy 255 PYNIVKFCRAIDIIYSLTSCMSKRMDAIOVTESIALFHSCLNPILYVFGASPKYV 314
Db 246 PYNWVIFLETIK-LYDFPSCDMRDLRLALSVETVAFSHCCNPLIYAFAGEKFRYL 304
Qy 315 MKVAKKYG 322
Db 305 YHL---YG 309

```

```

RESULT 26
US-09-898-751A-2
; Sequence 2, Application US/09898751A
; Patent No. US2002016024A1
; GENERAL INFORMATION:
; APPLICANT: Oldham, Elizabeth R.
; APPLICANT: Soto, Hortensia
; APPLICANT: Liu, Ying
; APPLICANT: Hudak, Susan A.
; APPLICANT: Homey, Bernhard
; APPLICANT: Morales, Janine M.
; APPLICANT: Kellerman, Strid-Aimee
; APPLICANT: McEvoy, Leslie M.
; APPLICANT: Bowman, Edward P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: CHEMOKINE AND RECEPTOR USES; COMPOSITIONS; METHODS
; FILE REFERENCE: DX0882XK
; CURRENT APPLICATION NUMBER: US/09/898,751A
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: US09/471,549
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US60/136,570
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: US60/113,858
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent version 3.1
; SEQ ID NO 2
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-751A-2

```

Query Match	28.5%	Score 518.5	DB 9	Length 362
Best Local Similarity	33.6%	Pred. No. 2,9e-38		
Matches 123	Conservative 66	Mismatches 146	Indels 31	Gaps

QY	3	LEONOSTDYVEENENNGTYDVSQVELICIKEDVREFAKVPFLVLTIVFVIGLANSKV	62
DB	6	LEQVSGHSGSGBEED---AYSAPPELPETLCYKADVCQAFRPOPSVSLTAAAGLNGNGIV	62
QY	63	VAYI-AVYKKORKTKDVTYLTNLAVADLLCLFTLPFAVAVAHVGMVGIKMCITSALYLT	121
DB	63	LATHLAAAPPAASPPSSAHLQLALADLLALTLTFPAAGAGQMSIGSCTCTTISGLYSA	122
QY	122	NFVSGMQFLACISIDRYVAVTKV---PSQSGVKXCWIIICFCVMAAILTISIPLVFT	177
DB	123	SPHAGFLFIACISADRYVAIARLPAQPRPPTFGR-AHIVSYIVMLSLLLALPALLFQ	181
QY	178	VND---NACPIPIFRYLTGSMKALIQMLEICGFVPEPLMGVCYFTARTLTMKPNIK	234
DB	182	DQOREGQRCLIPFEGELQTVKGASAVAOVALGFLPLGVNVAACVALLGRITLARGPE	241
QY	235	ISRPFLVLTIVVIFVLTOLPYNIIVKFCRAIDIIYSLITSCNMKSKMDIAIOVTESIALF	294
DB	242	RRRALRVVAALVAAPFVLDLPYSIALMLDPTADLLARENSCPASRKYDAVLLVTSGLALA	301
QY	295	HSCLPILIVFMGASHKXNYMKVAK-----KYSGWRORQSVVEEFPDSEGPTEP	344
DB	302	RCGLNPVLVAFLGRQDLRRLLRGGSSPQGPORCGCPRRBRLS-----SCSAP	352
QY	345	TSTST 350	
DB	353	TETHSL 358	

```

RESULT 27
US-09-931-381A-20
; Sequence 20, Application US/09931381A
; Patent No. US20020137107A1
; GENERAL INFORMATION:
; APPLICANT: Butcher, Eugene C.
; APPLICANT: Kunkel, Eric J.
; APPLICANT: Pan, Junliang
; APPLICANT: Soler-Ferran, Dulce
; TITLE OF INVENTION: Method for Identifying Agents which
; TITLE OF INVENTION: Modulate Chemokine "MCC"-Induced Functions of CCR3 and/or
; FILE REFERENCE: 1855.2010-003
; CURRENT APPLICATION NUMBER: US/09/931,381A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: U.S. 09/638,914
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-931-381A-20

Query Match      28.3%; Score 515.5; DB 10; Length 361;
Best Local Similarity 33.1%; Pred. No. 5.2e-38;
Matches 122; Conservative 67; Mismatches 149; Indels 31; Gaps 8;

Oy      1 M A L E O N O S T D Y Y E N E M N G T Y D V S Q Y E L I C I K E D V R E F A K F L P V F L T I F V I G I A G N S      60
Db      1 M G T A T E V S M G H I S G P E D A I S A E P L P E I C Y A D V Q A S R A F O S V S I T Y A A L G I A G N G      60
Oy      61 M V A I Y - A Y Y K Q K T D V Y I L N L A V A D I L L F T L P F W A V N A V H G V L G K I M C K I T S A L Y      119
Db      61 I V L A T H L A R R A A R S P T S A H L Q L A L A D I L L A T L T P F A A A G A L Q G M S I G S A T C R T I S G L Y      120
Oy      120 T L N F S G M Q E L A C T I S I R Y A V N K V - - - - P S O G V G K P C M I I C F C W M A A I L S I P Q L V F      175
Db      120 T L N F S G M Q E L A C T I S I R Y A V N K V - - - - P S O G V G K P C M I I C F C W M A A I L S I P Q L V F      175

```

```

Db 121 SASFHAGFLFIACISABRYVAIAARALPAGGRPSIPGR -ALHVSIVLWLSLILALPALLF 179
Qy 176 YTVND--NARCIIIPRRLYGLTSMKALIOMLTEICIGRVFVFLMGVCYFIARTAL -MKMP 231
Db 180 SQDGOREGQRRCRLIFPEGLTQYIVKGASAAVOALGFALPLGVMVACYALGLGRTLLARGP 239
Qy 232 NIKISRPKLVLAVVIVFIVTOLPYNIIVKFCRAIDIIYSLITSCKMSKMDIAIOVTESI 291
Db 240 ERR--RAIRVVALLVAFAFVILQLEPYSLALLLDPADLLAERSCPSKRDVALVLTSGL 297
Qy 292 ALFHSCINPLIIVYMGASFKNYVMKVAK-----KYGSMRRQROSVIEEPFDSGCP 341
Db 298 ALARCGINPLVLYAFILGIRFODLIRLLRGSCSPGPOPRGRCRRRLTS-----SC 348
Qy 342 TEPTSTESI 350
Db 349 SAPTEIHSGL 357

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```

1      RESULT 28
2      US-09-104-063-4
3      Sequence 4, Application US/09104063
4      Patent No. US20020168356A1
5      GENERAL INFORMATION:
6      APPLICANT: Lee, James
7      APPLICANT: Wood, William I.
8      TITLE OF INVENTION: PFA4 Receptors
9      NUMBER OF SEQUENCES: 6
10     CORRESPONDENCE ADDRESS:
11     ADDRESSEE: Genentech, Inc.
12     STREET: 1 DNA Way
13     CITY: South San Francisco
14     STATE: California
15     COUNTRY: USA
16     ZIP: 94080
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
19     COMPUTER: IBM PC compatible
20     OPERATING SYSTEM: PC-DOS/MS-DOS
21     SOFTWARE: WinPatIn (Genentech)
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/09/104,063
24     FILING DATE: 24-June-1998
25     CLASSIFICATION:
26     PRIOR APPLICATION DATA:
27     APPLICATION NUMBER: 08/701265
28     FILING DATE: 22-AUG-1996
29     PRIOR APPLICATION DATA:
30     APPLICATION NUMBER: 08/664228
31     FILING DATE: 06-JUN-1996
32     PRIOR APPLICATION DATA:
33     APPLICATION NUMBER: 08/076093
34     FILING DATE: 11-JUN-1993
35     PRIOR APPLICATION DATA:
36     APPLICATION NUMBER: 07/810782
37     FILING DATE: 19-DEC-1991
38     ATTORNEY/AGENT INFORMATION:
39     NAME: Love, Richard B.
40     REGISTRATION NUMBER: 34,659
41     REFERENCE/DOCKET NUMBER: P0706P2C2
42     TELECOMMUNICATION INFORMATION:
43     TELEPHONE: 415/225-5530
44     TELEFAX: 415/952-9881
45     TELEX: 910/371-7168
46     INFORMATION FOR SEQ ID NO: 4:
47     SEQUENCE CHARACTERISTICS:
48     LENGTH: 352 amino acids
49     TYPE: Amino Acid
50     TOPOLOGY: Linear
51     US-09-104-063-4
52
53     Query Match      27.5%;   Score 500.5;   DB 9;   Length 352
54     Best Local Similarity 34.6%;   Pred. No. 1,1e-36;

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; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-37

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Query Match	27.4%;	Score 498.5;	DB 9;	Length 352;
Best Local Similarity	34.6%;	Pred. No. 1.6e-36;		
Matches 107;	Conservative 56;	Mismatches 135;	Indels 11;	Gaps 4.

[illegible]

```

RESULT 32
US-09-870-759-144
; Sequence 144, Application US/09870759
; Patent No. US2002017551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 144
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-870-759-144

```

Query Match	27.4%;	Score 498.5;	DB 9;	Length 352;
Best Local Similarity	34.6%;	Pred. No. 1.6e-36;		
Matches 107;	Conservative 56;	Mismatches 135;	Indels 11;	Gaps 4;

[illegible][illegible]

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1      RESULT 33
2      US-09-938-719-7
3      ; Sequence 7, Application US/09938719
4      ; Patent No. US20020106742A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: SAMSON, MICHEL
7      ; PARMENTIER, MARC
8      ; VASSART, GILBERT
9      ; LIBERT, FREDERICK
10     ; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
11     ; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
12     ;
13     ; NUMBER OF SEQUENCES: 17
14     ; CORRESPONDENCE ADDRESSES:
15     ; ADDRESSEE: Knobbe, Martens, Olson & Bear
16     ; STREET: 620 Newport Center Drive 16th Floor
17     ; CITY: Newport Beach
18     ; STATE: CA
19     ; COUNTRY: U.S.A.
20     ; ZIP: 92660
21     ;
22     ; COMPUTER READABLE FORM:
23     ; MEDIUM TYPE: Floppy disk
24     ; COMPUTER: IBM PC compatible
25     ; OPERATING SYSTEM: PC-DOS/MS-DOS
26     ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
27     ;
28     ; CURRENT APPLICATION DATA:
29     ; APPLICATION NUMBER: US/09/938,719
30     ; FILING DATE: 24-Aug-2001
31     ; CLASSIFICATION: <Unknown>
32     ;
33     ; PRIORITY INFORMATION:
34     ; APPLICATION NUMBER: 09/626,939
35     ; FILING DATE: 27-JULY-2000
36     ; ATTORNEY/AGENT INFORMATION:
37     ; NAME: Altman, Daniel E
38     ; REGISTRATION NUMBER: 34,115
39     ; REFERENCE/DOCKET NUMBER: <Unknown>
40     ;
41     ; INFORMATION FOR SEQ ID NO: 7:
42     ;
43     ; SEQUENCE CHARACTERISTICS:
44     ;
45     ; LENGTH: 360 amino acids
46     ; TYPE: amino acid
47     ; STRANDEDNESS: single
48     ; TOPOLOGY: linear
49     ;
50     ; MOLECULE TYPE: NO. US20020106742A1
51     ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
52     ;
53     ; US-09-938-719-7

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Query Match	27.3%;	Score 497;	DB 10;	Length 360;
Best Local Similarity	33.5%;	Pred. No. 2.2e-36;		
Matches 107;	Conservative 63;	Mismatches 121;	Indels 28;	Gaps 8

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QY 17 ENMGTVDSQYELLICIEDDAEFNAKVPFLPVLTIVIGLAGNSWVAHVAYYKKQRKT 76
DQ 19 EVTFEPDY-DYAGPCHKDVAQICAOQLLPBLSYALVIFGPVGNMVLVILINCKKELCLT 77
QY 77 DVTIINLAVADILLFLLPFLPKAVAVNAVHGWVLGKIMKINSALVTLNPFVSGMQLACISID 136
DQ 78 DVLINLAISDLLFTITFLPLMAHSAANEWEFGNAKMLFTGLYHGFYGGGJFFIILLTID 137
QY 137 RYAAVTKV-----PESGSGVKRCWCILCCVMAAILISIPQLVFYVNNAR---CIP 186
DQ 138 RYAAIVHAVALKARTVTFGV-----VTSVITLVAVAFSAVGIIIFTRCKQEDSVYVCGP 192
QY 187 IPR---YIGTSMKLLIOMLEICIGFVVPPLINGVCYFIFTARTLMKMN-IKISRPLKVL 244

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[illegible]

Db	193	YEPGMMNFHTIMINI-----LGLVLPFLIMVICYSGILKTLIRCRNEKGRHRAVRVI	245
Qy	243	LTVIVIVFVTLQPNIVYFCGALIDIIYSLITSCNMSKMDIAIQVTESTIALFHSLNPLT	302
Db	246	FTIMIVYFLFWTPFNIVILLNTFOEFPEGL-SNCESTSQLDQAIQVETLGMTHCINPLII	304
Qy	303	YVFMGASFKNVYMKVAKKY	321
Db	305	YAFVGEKFRRTISVFFRKH	323
RESULT 35			
		US-09-938-703-7	
		; Sequence 7, Application US/09938703	
		; Patent No. US20020110870A1	
		GENERAL INFORMATION:	
		APPLICANT: SAMSON, MICHEL	
		PARMENTIER, MARC	
		VASSART, GILBERT	
		LIBERT, FREDERICK	
		TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR	
		AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR	
		NUMBER OF SEQUENCES: 17	
		CORRESPONDENCE ADDRESS:	
		ADDRESSEE: Knobbe, Martens, Olson & Bear	
		STREET: 620 Newport Center Drive	
		16th Floor	
		CITY: Newport Beach	
		STATE: CA	
		COUNTRY: U.S.A.	
		ZIP: 92660	
		COMPUTER READABLE FORM:	
		MEDIUM TYPE: Floppy disk	
		COMPUTER: IBM PC compatible	
		OPERATING SYSTEM: PC-DOS/MS-DOS	
		SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)	
		CURRENT APPLICATION DATA:	
		APPLICATION NUMBER: US/09/938,703	
		FILING DATE: 24-Aug-2001	
		CLASSIFICATION: <unknown>	
		PRIOR APPLICATION DATA:	
		APPLICATION NUMBER: 09/626,939	
		FILING DATE: 2000-07-27	
		ATTORNEY/AGENT INFORMATION:	
		NAME: Altman, Daniel E	
		REGISTRATION NUMBER: 34,115	
		REFERENCE/DOCKET NUMBER: <unknown>	
		INFORMATION FOR SEQ ID NO: 7:	
		SEQUENCE CHARACTERISTICS:	
		LENGTH: 360 amino acids	
		TYPE: amino acid	
		STRANDEDNESS: single	
		TOPOLOGY: linear	
		MOLECULE TYPE: No. US20020110870A1e	
		SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
		US-09-938-703-7	
Qy	17	EMNGTYDSQVELICIKDDVREFAVPLIPVLITIVFVGLAGNSWVAIYAYKKQRTKT	76
Db	19	EYTFPFDY-DYGAPCHKDKVQIGAQILLPPLYSLVIFGFVGNMLVALLINCKKLCIT	77
Qy	77	DYIINLNVADLLLETPFMAVNVAVHGMVLGKINCKITLSALYTLNPFVSGMQLACISID	136
Db	78	DIYILNLISDLITITITPLMAHSANEMVGNMCKLFTGTYHIGYGFIFILLITID	137
Qy	137	RYVAATKV-----PSQSGVGKPCWIIICFVMAAILISIPQLVFTYVNDNAR--CIP	186
Db	138	RYLAIVHVAVFALKARTVTFGV-----VTSVITLVAVFASVPGIIFTRCQEKEDSVYVCGP	192

QY 187 IFPR---YLGTSMKALIQMLEICIGFVVPFLIMGVCYFTIARTLMKMN-IKISRLPLKVL 242  
 Db 193 YFPRGNNHFTIMRNI-----LGLVPLILIMVICYSGILKTLRLCRNEKRRRAVRVI 245  
 QY 243 LTVIVIVITQLPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNPIIL 302  
 Db 246 FTIMIVYFLFWTPYNIIVILLNTFOEFGL-SNCESTSQLDQATVETLGTWTHCCINPII 304  
 QY 303 YVFMGASFKNYVMKAKKY 321  
 Db 305 YAFVGEKFRRIYSVFPK 323

RESULT 36  
 US-09-104-792-3  
 ; Sequence 3, Application US/09104792  
 ; Patent No. US20020019026A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soppet, Daniel R.  
 ; APPLICANT: Yi, Li  
 ; APPLICANT: Ruben, Steven M.  
 ; APPLICANT: Rosen, Craig A.  
 ; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
 ; ADDRESS: STUART & OLSTEIN  
 ; STREET: 6 Becker Farm Road  
 ; CITY: Roseland  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 07068

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/104,792  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/461,244  
 ; FILING DATE: 05-JUN-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ferraro, Gregory D.  
 ; REGISTRATION NUMBER: 36,134  
 ; REFERENCE/DOCKET NUMBER: 325800-445  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 201-994-1744  
 ; TELEFAX: 201-994-1700  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 347 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-104-792-3

Query Match 27.0%; Score 492; DB 10; Length 347;  
 Best Local Similarity 33.5%; Pred. No. 5.9e-36;  
 Matches 107; Conservative 62; Mismatches 122; Indels 28; Gaps 8;

QY 17 EMNGTYDSQYELICIKEDVREFAKVLPFLITIVFVIGLAGNSNVAIYAYKKQRTKT 76  
 Db 6 EVTTFFDY-DYGAPCHKEDVQIGQLPPLYSIVFIFGVGNMLVLLILNCKKTKCLT 64  
 QY 77 DVIILNLAVADLLFLTPFPAVNAVHGVLGKIMCKITSAIYTLNPFVSGNQFLACISID 136  
 Db 65 DIYILNLAISDLLFLITPLMAHSANENWFGNMCCKFTGLYHIGYFGGIFFIILLTID 124  
 QY 137 RYVAVTKV-----PSQGVGKPCMIICFVMAAILLSIPOLVFTYVNDNAR---CIP 186

Db 125 RYLAIVHAVALKARTVTFGV-----VTSVITWLVAVASVPGIITFTCQKEDSVYVCGP 179  
 QY 187 IFPR---YLGTSMKALIQMLEICIGFVVPFLIMGVCYFTIARTLMKMN-IKISRLPLKVL 242  
 Db 180 YFPRGNNHFTIMRNI-----LGLVPLILIMVICYSGILKTLRLCRNEKRRRAVRVI 232  
 QY 243 LTVIVIVITQLPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNPIIL 302  
 Db 233 FTIMIVYFLFWTPYNIIVILLNTFOEFGL-SNCESTSQLDQATVETLGTWTHCCINPII 291  
 QY 303 YVFMGASFKNYVMKAKKY 321  
 Db 292 YAFVGEKFRRIYSVFPK 310

RESULT 37  
 US-09-131-827A-2  
 ; Sequence 2, Application US/09131827A  
 ; Patent No. US20020038469A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dean, Michael  
 ; APPLICANT: O'Brien, Stephen J.  
 ; APPLICANT: Smith, Michael  
 ; APPLICANT: Carrington, Mary  
 ; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A  
 ; FILE REFERENCE: 14014.0333  
 ; CURRENT APPLICATION NUMBER: US/09/131,827A  
 ; CURRENT FILING DATE: 1998-08-10  
 ; PRIOR APPLICATION NUMBER: 60/055,659  
 ; PRIOR FILING DATE: 1997-08-14  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 360  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-131-827A-2

Query Match 27.0%; Score 492; DB 10; Length 360;  
 Best Local Similarity 33.5%; Pred. No. 6.2e-36;  
 Matches 107; Conservative 62; Mismatches 122; Indels 28; Gaps 8;  
 QY 17 EMNGTYDSQYELICIKEDVREFAKVLPFLITIVFVIGLAGNSNVAIYAYKKQRTKT 76  
 Db 19 EVTTFFDY-DYGAPCHKEDVQIGQLPPLYSIVFIFGVGNMLVLLILNCKKTKCLT 77  
 QY 77 DVIILNLAVADLLFLTPFPAVNAVHGVLGKIMCKITSAIYTLNPFVSGNQFLACISID 136  
 Db 78 DIYILNLAISDLLFLITPLMAHSANENWFGNMCCKFTGLYHIGYFGGIFFIILLTID 137  
 QY 137 RYVAVTKV-----PSQGVGKPCMIICFVMAAILLSIPOLVFTYVNDNAR---CIP 186  
 Db 138 RYLAIVHAVALKARTVTFGV-----VTSVITWLVAVASVPGIITFTCQKEDSVYVCGP 192  
 QY 187 IFPR---YLGTSMKALIQMLEICIGFVVPFLIMGVCYFTIARTLMKMN-IKISRLPLKVL 242  
 Db 193 YFPRGNNHFTIMRNI-----LGLVPLILIMVICYSGILKTLRLCRNEKRRRAVRVI 245  
 QY 243 LTVIVIVITQLPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNPIIL 302  
 Db 246 FTIMIVYFLFWTPYNIIVILLNTFOEFGL-SNCESTSQLDQATVETLGTWTHCCINPII 304  
 QY 303 YVFMGASFKNYVMKAKKY 321  
 Db 305 YAFVGEKFRRIYSVFPK 323

RESULT 38  
 US-10-106-623-20  
 ; Sequence 20, Application US/10106623  
 ; Patent No. US20020150888A1



GENERAL INFORMATION:  
APPLICANT: Gray, Patrick W.  
Schweickart, Vicky L.  
Report: Carol J.  
TITLE OF INVENTION: Chemokine Receptor Materials and Methods  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
City: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/106,623  
FILING DATE: 26-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/771,276  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: No. US20020150888Aland, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/33670  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-0448  
TELEFAX: 312-474-6300  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
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Query Match 27.0%; Score 491.5; DB 12; Length 352;  
Best Local Similarity 32.2%; Pred. No. 6.6e-36;  
Matches 112; Conservative 70; Mismatches 131; Indels 35; Gaps 9;  
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QY 243 LTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCKMSKMDIAIQVTSIALFHSCLNPL 302  
Db 238 FTIMIVFELMAPNIVILNTPQEFGL-NKCSSNRLLQAMQVTEITLGMTHCCINPII 296  
QY 303 YVFMGASFKNYVMKAKKYSWRQR-OSVEEPPDSGTEPTSTPS 349  
Db 297 YAFVGEKFRNYLVFQKHIAKRFCKCSI-----FOQAEPRASVYT 340  
RESULT 39  
US-09-131-827A-20  
Sequence 20, Application US/09131827A

Patent No. US20020038469A1  
GENERAL INFORMATION:  
APPLICANT: Dean, Michael  
APPLICANT: O'Brien, Stephen J.  
APPLICANT: Smith, Michael  
APPLICANT: Carrington, Mary  
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A  
FILE REFERENCE: 14014.0333  
CURRENT APPLICATION NUMBER: US/09/131,827A  
CURRENT FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/055,659  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 360  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-131-827A-20  
Query Match 27.0%; Score 491; DB 10; Length 360;  
Best Local Similarity 33.2%; Pred. No. 7.5e-36;  
Matches 106; Conservative 63; Mismatches 122; Indels 28; Gaps 8;  
Db 17 ENNGTYDSQYELICIKEDVREFAKFLPVFLTIVFVIGLANSWVAIYAYKKQRTKT 76  
Db 19 EYTFEPDY-DYGAPCHKRDVKQIGAQLPPLYSIVFIFGVGNMLVILLINCKRLKCLT 77  
QY 77 DYIILNLAVADLLFLPFAVAVAVHGVNLGKIMCKITSLALYTLNFGSQOFLACISID 136  
Db 78 DYIILNLALISDLFLITPLMAHSAANSEWFGNAACKLFTGLYHGYGGIIFILLITD 137  
QY 137 RYVAVTKV-----PSQSGVKPCWIIICFCVMAAILISIPOLVFYVNDNAR---CIP 186  
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QY 187 IPRP---YLGTSMKALLQMLEICIGFVVPFLMGVCYFTRARTLMKMN-IKISRLPLXL 242  
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QY 243 LTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCKMSKMDIAIQVTSIALFHSCLNPL 302  
Db 246 FTIMIVFELMAPNIVILNTPQEFGL-SNCESTSQLDQATVTEITLGMTHCCINPII 304  
QY 303 YVFMGASFKNYVMKAKKYS 321  
Db 305 YAFVGEKFRNYLVFQKHIAKRFCKKH 323  
RESULT 40  
US-09-104-063-2  
Sequence 2, Application US/09104063  
Patent No. US20020168356A1  
GENERAL INFORMATION:  
APPLICANT: Lee, James  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: PFA4 Receptors  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
City: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/104,063



GenCore version 5.1.4 p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2003, 09:03:30 ; Search time 3812 Seconds

(without alignments)  
8756.799 Million cell updates/sec

Title: US-09-721-495B-1

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Sequence: 1 atgcttgcgaacagacacca.....ctcgaataaaaaaaam 1147

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 135 summaries

Database :

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1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_ses:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_ses:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pln:\*  
35: em\_hcg\_rod:\*  
36: em\_hcg\_man:\*  
37: em\_hcg\_vit:\*  
38: em\_sy:\*  
39: em\_hcgo\_hum:\*  
40: em\_hcgo\_mus:\*  
41: em\_hcgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1146.6	100.0	1147	6 AX113671	AX113671 Sequence
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4	1133.6	98.8	1839	6 AX244231	AX244231 Sequence
5	1133.6	98.8	1925	6 AX244232	AX244232 Sequence
6	1133.6	98.8	1925	6 AF193507	AF193507 Homo sapi
7	1133.6	98.8	2407	6 E30057	E30057 G protein c
8	1133.6	98.8	162029	9 AC020632	AC020632 Homo sapi
9	1132	98.7	1915	9 AF110640	AF110640 Homo sapi
10	1130.6	98.6	2156	6 E30058	E30058 G protein c
11	1124	98.0	1637	6 AX041923	AX041923 Sequence
12	1124	98.0	170546	2 AC074296	AC074296 Homo sapi
13	1124	98.0	178159	9 HSJ509119	HSJ509119 Human DNA
14	1113	97.0	1113	6 AX239641	AX239641 Sequence
15	1113	97.0	1113	6 AF233281	AF233281 Homo sapi
16	1090.6	95.1	1150	6 AX244230	AX244230 Sequence
17	1053	91.8	1053	6 AX239643	AX239643 Sequence
18	1053	91.8	1053	6 AX244219	AX244219 Sequence
19	939.2	81.9	1388	6 AX244225	S63848 G-protein c
20	886	77.2	2059	6 AX244221	AX244221 Sequence
21	831	72.4	797	6 AX244223	AX244223 Sequence
22	797	68.3	1138	10 AF306532	AF306532 Mus muscu
23	783.2	68.3	2351	10 AY072796	AY072796 Mus muscu
24	783.2	68.3	2351	10 AY072938	AY072938 Mus muscu
25	783.2	68.3	2351	10 AY072938	AY072938 Mus muscu
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27	597.6	52.1	604	6 AX244224	AX244224 Sequence
28	481	41.9	481	6 AX244222	AX244222 Sequence
29	470.4	41.0	161539	2 AC111816	AC111816 Rattus no
30	447.4	39.0	665	10 AF090348	AF090348 Rattus no
31	348.6	30.4	374	6 AX244228	AX244228 Sequence
32	347	30.3	347	6 AX113681	AX113681 Sequence
33	180.6	15.7	162393	2 AC111746	AC111746 Rattus no
34	180.2	15.7	1631	10 AF121670	AF121670 Rattus no
35	174.8	15.2	155206	2 AC125884	AC125884 Rattus no
36	169.2	14.8	1302	10 AB009369	AB009369 Mus muscu
37	169.2	14.8	1674	10 MSN22714	MSN22714 Mus muscu
38	166.2	14.5	1500	9 HSDNBLR2	X84702 H.sapiens B
39	166.2	14.5	1900	6 AR107241	AR107241 Sequence
40	166.2	14.5	1900	6 AR194341	AR194341 Sequence
41	166.2	14.5	2058	6 AR107232	AR107232 Sequence
42	166.2	14.5	2058	6 AR194332	AR194332 Sequence
43	166.2	14.5	2139	6 HUMERI1CDN	LJ1581 Human G pro
44	166.2	14.5	2160	6 AR107239	AR107239 Sequence
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49	164.8	14.4	1186	9 HSA132337	AJ132337 Homo sapi
50	164.8	14.4	2462	9 AF145440	AF145440 Homo sapi
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52	164.8	14.4	2577	6 AX454125	AX454125 Sequence
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55	164.8	14.4	209772	9 AC099782	AC099782 Homo sapi
56	164.6	14.4	2072	6 AX299842	AX299842 Sequence
57	164.6	14.4	2072	10 MUSEBI1CDN	LJ1580 Mus musculu
58	164.6	14.4	2085	6 AR107278	AR107278 Sequence
59	164.6	14.4	2085	6 AR194378	AR194378 Sequence
60	164.6	14.4	106991	2 AC016960	AC016960 Homo sapi
61	164.6	14.4	117612	10 AL591366	AL591366 Mouse DNA
62	164.6	14.4	179693	2 AL691511	AL691511 Mus muscu
63	161.6	13.9	2154	6 AX280857	AX280857 Sequence
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66	159.8	13.9	2154	9	HUMGPCRA	L08176 Human Epste
67	158.2	13.8	1325	5	AF294794	AF294794 Gallus ga
68	155.2	13.5	1004	9	AF178082	AF178082 Cercopit
69	155.2	13.5	1068	9	AB015943	AB015943 Chloroce
70	153.6	13.4	1044	9	AF172221	AF172221 Mandrillu
71	153.6	13.4	1059	6	AX256185	AX256185 Sequence
72	153.6	13.4	1059	6	AX482330	AX482330 Sequence
73	153.6	13.4	1059	6	AF025375	AF025375 Homo sapi
74	153.6	13.4	1225	9	HUMNVRCA	HUMNVRCA
75	153.6	13.4	1317	6	AR107259	AR107259 Sequence
76	153.6	13.4	1317	6	AR194359	AR194359 Sequence
77	153.6	13.4	1582	6	AX481810	AX481810 Sequence
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79	153.6	13.4	1645	9	HSNPYRLA	HSNPYRLA
80	153.6	13.4	1664	6	E37853	E37853 Anti-HIV ag
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83	153.6	13.4	1670	6	AX409496	AX409496 Sequence
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85	153.6	13.4	1679	6	AX287116	AX287116 Sequence
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87	153.6	13.4	1737	6	AR015970	AR015970 Sequence
88	153.6	13.4	1737	6	AR060748	AR060748 Sequence
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90	153.6	13.4	1737	6	AR103430	AR103430 Sequence
91	153.6	13.4	1737	6	I13753	I13753 Sequence 4
92	153.6	13.4	1737	6	I24455	I24455 Sequence 3
93	153.6	13.4	1944	6	E33806	E33806 Human splic
94	153.6	13.4	1950	9	AF147204	AF147204 Homo sapi
95	153.6	13.4	3733	9	HSCXCR4	Y14739 Homo sapien
96	153.6	13.4	5161	9	AF005058	AF005058 Homo sapi
97	153.6	13.4	8747	9	AF0052572	AF0052572 Homo sapi
98	153.6	13.4	8747	9	HSAA224869	AJ224869 Homo sapi
99	153.6	13.4	172281	9	AC068492	AC068492 Homo sapi
100	152.2	13.3	2751	6	AR107244	AR107244 Sequence
101	152.2	13.3	2751	6	AR194344	AR194344 Sequence
102	152	13.3	1044	9	AF172222	AF172222 Mandrillu
103	152	13.3	1044	9	AF172232	AF172232 Gorilla g
104	152	13.3	1087	9	PTU89798	U89798 Pan troglod
105	152	13.3	1102	9	AF348491	AF348491 Homo sapi
106	151.8	13.2	131989	2	AC107545	AC107545 Rattus no
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109	150.4	13.1	1044	9	AF172210	AF172210 Pygathrix
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111	150.4	13.1	1044	9	AF172212	AF172212 Pygathrix
112	150.4	13.1	1044	9	AF172216	AF172216 Presbytis
113	150.4	13.1	1044	9	AF172218	AF172218 Presbytis
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127	148.8	13.0	1044	9	AF172230	AF172230 Hylobates
128	148.8	13.0	1044	9	AF172231	AF172231 Pongo pyg
129	148.8	13.0	1087	9	AF001928	AF001928 Macaca mu
130	148.6	13.0	1608	4	MM013336	MM013336
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133	147.2	12.8	1059	9	MM073740	MM073740 Macaca mula
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## ALIGNMENTS

RESULT 1	AX113671	1147 bp	DNA	linear	PAT 01-MAY-2001
LOCUS	AX113671				
DEFINITION	Sequence 1 from Patent WO0127146.				
ACCESSION	AX113671				
VERSION	AX113671.1	GI:13939848			
KEYWORDS					
SOURCE					
ORGANISM	human.				
REFERENCE	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 1147)				
REFERENCE	Goelling, J., Dairaghi, D.J., Hanley, M., Miao, Z., Talbot, D. and				
REFERENCE	Schall, T.J.				
REFERENCE	Chemokine receptor				
REFERENCE	Patent: WO 0127146-A 1 19-APR-2001;				
REFERENCE	Chemocentryx, Inc. (US)				
TITLE	Chemokine receptor				
JOURNAL	Chemocentryx, Inc. (US)				
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	VWMAALILSIPLQVFTVNDNFARCIPLFPRYLSKMAIOMEICIGFVPLINGV				
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ORIGIN					
Query Match	100.0%; Score 1146.6; DB 6; Length 1147;				
Best Local Similarity	100.0%; Pred. No. 3.2e-278;				
Matches 1147; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
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QY	361 CTAAACTTTGCTCTGGAATGAGCTTCTGCTTGATCAGATAGATATGTGCGCA 420				
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QY	421 GTAACTAAGTCCCAACCAATCAAGAGTGGGAAACCAATGCTGATCATCTGTTCTGT 480				
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QY 1141 AAAAAAM 1147
DB 1141 AAAAAAM 1147

RESULT 2
AX203742 1147 bp DNA linear PART 30-AUG-2001
LOCUS Sequence 1 from Patent WO0146698.
DEFINITION AX203742
ACCESSION AX203742
VERSION AX203742.1 GI:15393190
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1147)
AUTHORS Schall, T.J., Talbot, D., Miao, Z., and Wei, Z.
TITLE Tetrahedral ligands and methods of use
JOURNAL Patent: WO 0146698-A 1 28-JUN-2001;
Chemocentrix, Inc. (US)
FEATURES
source location/Qualifiers
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/note="unnamed protein product"
CDS

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BASE COUNT 344 a 244 c 222 g 336 t 1 others
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Query Match 100.0%; Score 1146.6; DB 6; Length 1147;
Best Local Similarity 100.0%; Pred. No. 3.2e-278;
Matches 1147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 LOCUS AX113673  
 DEFINITION Sequence 3 from Patent WO0127146.  
 ACCESSION AX113673  
 VERSION AX113673.1 GI:13939850  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 1147)  
 TITLE Gosling, J., Dairaghi, D.J., Hanley, M., Miao, Z., Talbot, D. and  
 Schall, T.J.  
 JOURNAL Chemokine receptor  
 Patent: WO 0127146-A 3 19-APR-2001;  
 Chemocentrix, Inc. (US)

FEATURES  
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 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /note="chemokine receptor (variant)"

BASE COUNT 342 a 244 c 225 g 335 t 1 others  
 ORIGIN

Query Match 98.8%; Score 113.8; DB 6; Length 1147;  
 Best Local Similarity 99.3%; Pred. No. 5.3e-275;  
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 LOCUS AX244231  
 DEFINITION Sequence 13 from Patent WO0166598.  
 ACCESSION AX244231  
 VERSION AX244231.1 GI:15859282  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1839)  
 AUTHORS Gray, P.W., Schweickart, V.L., Epp, A., Raport, C.J., Chantry, D. and Steiner, B.  
 TITLE Chemoattractant receptor characterization and cell selection materials and methods and chemokine receptor ccr1l materials and methods  
 JOURNAL Patent: WO 0166598-A 13 13-SEP-2001;  
 ICOS CORPORATION (US)  
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 BASE COUNT 594 a 355 c 353 g 537 t  
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 Query Match 98.8%; Score 1133.6; DB 6; Length 1839;  
 Best Local Similarity 99.6%; Pred. No. 5.9e-275;  
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 DEFINITION AX244232  
 ACCESSION AX244232  
 VERSION AX244232.1 GI:15859283  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1925)  
 AUTHORS Gray, P.W., Schweickart, V.L., Epp, A., Raport, C.J., Chantry, D. and Steiner, B.  
 TITLE Chemoattractant receptor characterization and cell selection materials and methods and chemokine receptor ccr1l materials and methods  
 JOURNAL Patent: WO 0166598-A 14 13-SEP-2001;  
 ICOS CORPORATION (US)  
 FEATURES Location/Qualifiers  
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 BASE COUNT 623 a 368 c 363 g 571 t  
 ORIGIN

Query Match 98.8%; Score 1133.6; DB 6; Length 1925;  
 Best Local Similarity 99.6%; Pred. No. 5.9e-275;  
 Matches 1136; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGCTTTGGAACAGAACAGTCAAGATTATTTATGAGAAATGAATGATGGC 60  
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RESULT 7  
 E30057 2407 bp DNA linear PAT 18-JUN-2001  
 LOCUS E30057 G protein conjugate receptor HPIA041.  
 DEFINITION E30057  
 ACCESSION E30057.1 GI:13025590  
 VERSION UP 199056377-A/1.  
 KEYWORDS  
 SOURCE unidentified.  
 ORGANISM  
 unclassified.  
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 G protein conjugate receptor HPIA041  
 Patent: JP 199056377-A 1 02-MAR-1999;  
 JOURNAL SMITHKLINE BEECHAM CORP  
 COMMENT  
 OS Unidentified  
 PN JP 199056377-A/1  
 PD 02-MAR-1999  
 PF 24-FEB-1998 JP 1998041506  
 PR 27-OCT-1997 US 08/962922,15-AUG-1997 US 60/055895 PI  
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 PC C12N15/09, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00,  
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 PC A61K39/395,  
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 CC Topology: Linear;  
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 AC020632.16 GI:17223153

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 1 (bases 1 to 162029)

## REFERENCE

AUTHORS  
 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,  
 Alston, J., Bimaga, K., Blankenburg, K., Bonin, D., Bouck, J.,  
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 Coyle, M.D., Dachorne, S.R., David, R., Davila, M.L., Davis, C.,  
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## TITLE

Williamson, A., Wlezyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y.,  
 Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstein, G. and  
 Gibbs, R.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 162029)  
 Worley, K.C.  
 Direct Submission  
 Submitted (07-JAN-2000) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 162029)  
 Worley, K.C.  
 Direct Submission  
 Submitted (01-DEC-2001) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 4 (bases 1 to 162029)  
 Worley, K.C.  
 Direct Submission  
 Submitted (05-DEC-2001) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
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 Worley, K.C.  
 Direct Submission  
 Submitted (31-JAN-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Dec 1, 2001 this sequence version replaced gi:17155009.  
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email  
 gc-help@bcm.tmc.edu

## REFERENCE

AUTHORS  
 TITLE  
 JOURNAL

## REFERENCE

AUTHORS  
 TITLE  
 JOURNAL

## REFERENCE

AUTHORS  
 TITLE  
 JOURNAL

## COMMENT

CLONE LENGTH: This sequence does not necessarily represent the  
 entire insert of this clone. Overlapping regions of clones are only  
 sequenced and submitted once, so the sequence for the remainder of  
 the insert may be found in the record for the adjacent clones.  
 Overlapping clones are noted at the beginning and end of the  
 Features listing.

## ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches  
 of a local database that includes entries from dbSTS, GDB, and  
 local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,  
 unpublised.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST  
 (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the  
 EST and cDNA sequences. Genes demonstrate at least two exons  
 flanked by consensus splice sites that maintained sequence  
 continuity across the splice junctions. Sequences that are not  
 identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum  
 standard of double strand coverage with a minimum of 2 clones and 2  
 reads with no ambiguities or 2 chemistries with a minimum of 2  
 clones and 3 reads with no ambiguities. If the sequence quality for  
 a region does not meet this standard, it will be indicated in the  
 annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality  
 standards - estimated error rate less than 1 per 10,000 bases.  
 Reports of lowest quality individual bases and measures of base  
 quality are listed below. Description of the metrics can be found  
 at URL: <http://gc.bcm.tmc.edu:8086/quality.info/genbank.annotation.html>.

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VERSION	E30058.1 GI:13025591			
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ORGANISM	unidentified.			
REFERENCE	1 (bases 1 to 2156)			
AUTHORS	Catharine, E. B.			
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Qy	604	ATGCTAAGATCTGATTTGATTTGTATGATACCTCTTATATATATGGGGGTGTCTACTTT						663
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VERSION	AX041923.1	GI:11340688						
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AUTHORS	1 (bases 1 to 1637)							
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JOURNAL	G-protein coupled receptor and method of using same							
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BASE COUNT      523 a      320 c      338 g      456 t
ORIGIN

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Query Match      98.0%; Score 1124; DB 6; Length 1637;
Best Local Similarity 99.1%; Pred. No. 1.6e-272;
Matches 1130; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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DB 228 ACTATGACTACAGTCAATATGAACTGATCTGATCAAGAGATGTCAGAGATTGCA 287
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DB 1068 ATCTTTATGTTTATTAAGGAGCATCTTTCAAAAATGATGTAAGAAAGTGGCAAGAA 1127
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LOCUS Homo sapiens chromosome 6 clone RP11-721P14, WORKING DRAFT
DEFINITION AC074296
AC074296
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KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE 1 (bases 1 to 170546)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 170546)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

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COMMENT On Aug 11, 2000 this sequence version replaced gi:9558680.

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0721P14
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 165208 bases at least Q40
Consensus quality: 166747 bases at least Q30
Consensus quality: 167535 bases at least Q20
Insert size: 16946; sum-of-contigs
Quality coverage: 5.93 in Q20 bases; agarose-fp
Quality coverage: 5.43 in Q20 bases; sum-of-contigs

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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**AUTHORS** Smith, M.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (02-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
 requests: clonerequests@sanger.ac.uk  
 On Feb 5, 2001 this sequence version replaced gi:12580848.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
 This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unseq' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; SW; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information can be found at http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Ch6  
 R3-509119 is from the library RPCI-3 constructed by the group of Pletzer de Jong. For further details see http://www.chori.org/bacpac/home.htm  
**VECTOR:** pCYPAC2  
 This sequence is the entire insert of clone RPI-509119.

**FEATURES**  
 Location/Qualifiers

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**Query Match** 98.0%; Score 1124; DB 9; Length 178159;  
**Best Local Similarity** 99.1%; Pred. No. 1.3e-272;  
**Matches 1130; Conservative** 0; Mismatches 10; Indels 0; Gaps 0;

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 VERSION AX239641.1 GI:15797314  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1113)  
 REFERENCE Glucksmann, M.A., Galvin, K.M. and Silos-Santiago, I.  
 1983, 52881, 2398, 45449, 50289, and 52872, G protein-coupled receptors and uses therefor  
 Patent: WO 0164882-A 7 07-SEP-2001;  
 Millennium Pharmaceuticals, Inc. (US)  
 JOURNAL Location/Qualifiers  
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CYETARTLMKMPNIKISRPILKVLTVIVFIVTOLPYNIVFCAIDIIIVSLITSCN
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BASE COUNT      325 a      239 c      220 g      329 t
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Query Match      97.0%; Score 1113; DB 6; Length 1113;
Best Local Similarity 100.0%; Pred. No. 9.4e-270;
Matches 1113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION   AF233281
ACCESSION    AF233281
VERSION      AF233281.1 GI:7274391
KEYWORDS     Homo sapiens.
SOURCE       Homo sapiens.
ORGANISM     Homo sapiens.
REFERENCE    1 (bases 1 to 1113)
AUTHORS      Gosling,J., Dairaghi,D.J., Wang,Y., Hanley,M., Talbot,D., Miao,Z.
              and Schall,T.J.
TITLE        Cutting edge: identification of a novel chemokine receptor that
              binds dendritic cell- and T cell-active chemokines including ELC,
              SLC, and TECK
              J. Immunol. 164 (6), 2851-2856 (2000)
JOURNAL      J. Immunol. 164 (6), 2851-2856 (2000)
MEDLINE      20171478
PUBMED       10706668
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AUTHORS      Schall,T.J.
TITLE        Direct Submision
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BASE COUNT   325 a      239 c      220 g      329 t
ORIGIN
Query Match   97.0%; Score 1113; DB 9; Length 1113;

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Best Local Similarity 100.0%; Pred. No. 9,4e-270;  
Matches 1113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 16  
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DEFINITION Sequence 12 from Patent WO016598.  
ACCESSION AX244230  
VERSION AX244230.1 GI:15859281  
KEYWORDS  
SOURCE  
human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1150)  
Gray, P.W., Schweickart, V.L., Epp, A., Raport, C.J., Chantry, D. and

Steiner, B.  
TITLE Chemosttractant receptor characterization and cell selection  
materials and methods and chemokine receptor ccr1l materials and  
methods  
Patent: WO 016598-A 12 13-SEP-2001;  
JOURNAL ICOS CORPORATION (US)

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LOCATION/Qualifiers  
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BASE COUNT 335 a 246 c 232 g 337 t  
ORIGIN

Query Match 95.1%; Score 1090.6; DB 6; Length 1150;  
Best Local Similarity 99.6%; Pred. No. 4.1e-264;  
Matches 1093; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 61 ATGTGAGAAATTTGCAAAAGTTTCTCTGATTTCTTCAATATGTTTGTCTATTG 163
QY 164 GACTTGACGGAATTTCCATGATGATGATGATGATGATGATGATGATGATG 223
Db 121 GACTTGACGGAATTTCCATGATGATGATGATGATGATGATGATGATGATG 223
QY 224 AAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 283
Db 181 AAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 283
QY 284 CTTTGTGGGCTGTTATGACAGTTTCAAGTGGGTTTATGAGGAAATATGTCAGAA 343
Db 241 CTTTGTGGGCTGTTATGACAGTTTCAAGTGGGTTTATGAGGAAATATGTCAGAA 343
QY 344 CTTTGTGGGCTGTTATGACAGTTTCAAGTGGGTTTATGAGGAAATATGTCAGAA 403
Db 301 CTTTGTGGGCTGTTATGACAGTTTCAAGTGGGTTTATGAGGAAATATGTCAGAA 403
QY 404 TAGACAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 463
Db 361 TAGACAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 463
QY 464 GGATCATCTGTTTCTGTTGATGATGATGATGATGATGATGATGATGATGATG 523
Db 421 GGATCATCTGTTTCTGTTGATGATGATGATGATGATGATGATGATGATGATG 523
QY 524 TTTTATAGTAATGACAAATGATGATGATGATGATGATGATGATGATGATGATG 583
Db 481 TTTTATAGTAATGACAAATGATGATGATGATGATGATGATGATGATGATGATG 583

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QY 584 CAATGAAGCATGATTCAATGCTAGAGATCTGATGGATTTTGTAGTACCTTTCTTA 643  
DB 541 CAATGAAGCATGATTCAATGCTAGAGATCTGATGGATTTTGTAGTACCTTTCTTA 600  
QY 644 TTATGGGGGTGTGCTACTTATTCACAGCAAGACACTCATGAGATGCCAAACATTAAAA 703  
DB 601 TTATGGGGGTGTGCTACTTATTCACAGCAAGACACTCATGAGATGCCAAACATTAAAA 660  
QY 704 TATCTGACCCCTTAAAAAGTTCTGTCTCAAGTCTTATAGTTTTCATTTCACCTCACTGC 763  
DB 661 TATCTGACCCCTTAAAAAGTTCTGTCTCAAGTCTTATAGTTTTCATTTCACCTCACTGC 720  
QY 764 CTATATACATTTGTCAGATGTCGCGAGCCATGACATCATCTACTCCCTGATCAGCAGCT 823  
DB 721 CTATATACATTTGTCAGATGTCGCGAGCCATGACATCATCTACTCCCTGATCAGCAGCT 780  
QY 824 GCAACATGACCAACGCGATGAGCATGCGCATCCAGTTCACAGAAAGCATGCACTCTTTC 883  
DB 781 GCAACATGACCAACGCGATGAGCATGCGCATCCAGTTCACAGAAAGCATGCACTCTTTC 840  
QY 884 ACAGCTGCTCCAAACCCCAATCTCTTATATGTTTATGAGAGATCTTCAAAATAGGTTA 943  
DB 841 ACAGCTGCTCCAAACCCCAATCTCTTATATGTTTATGAGAGATCTTCAAAATAGGTTA 900  
QY 944 TGAAGTGGCCAAAGATATGAGTCTGAGAGAGACAGACAAAGTGTGAGAGTTTC 1003  
DB 901 TGAAGTGGCCAAAGATATGAGTCTGAGAGAGACAGACAAAGTGTGAGAGTTTC 960  
QY 1004 CTTTGTGATTCGAGGGTCTTACAGAGCCAAACAGTACTTTTAAAGTTAAAGTAAACT 1063  
DB 961 CTTTGTGATTCGAGGGTCTTACAGAGCCAAACAGTACTTTTAAAGTTAAAGTAAACT 1020  
QY 1064 GCTCTGCTCTTGTCTTGTGATTCATATGATGATGATGATGATGATGATGATGATGATG 1123  
DB 1021 GCTCTGCTCTTGTCTTGTGATTCATATGATGATGATGATGATGATGATGATGATGATG 1080  
QY 1124 TTATTTGAAAAAATAA 1140  
DB 1081 TTATTTGAAAAAATAA 1097

RESULT 17  
AX239643 1053 bp DNA linear PAT 26-SEP-2001  
LOCUS AX239643  
DEFINITION Sequence 9 from Patent WO0164882.  
ACCESSION AX239643  
VERSION AX239643.1 GI:15797316  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS  
Glucksmann, M.A., Galvin, K.M. and Silos-Santiago, I.  
1983, 52881, 2398, 45449, 50289, and 52872, G protein-coupled  
receptors and uses therefor  
Patent: WO 0164882-A 9 07-SEP-2001;  
JOURNAL  
Millennium Pharmaceuticals, Inc. (US)  
FEATURES  
source  
1. 1053  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 308 a 226 c 210 g 309 t  
ORIGIN

Query Match 91.8%; Score 1053; DB 6; Length 1053;  
Best Local Similarity 100.0%; Pred. No. 1.2e-254;  
Matches 1053; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTTTGGAACAGAACAGTCAACAGATTATTTATGAGAAATGAAATGATGCG 60  
DB 1 ATGGCTTTGGAACAGAACAGTCAACAGATTATTTATGAGAAATGAAATGATGCG 60

QY 61 ACTATAGCTACAGTCAATATGAACTGATCTGTATCAAGAAGATGTCAGAAATTTGCA 120  
DB 61 ACTATAGCTACAGTCAATATGAACTGATCTGTATCAAGAAGATGTCAGAAATTTGCA 120  
QY 121 AAAGTTTCCCTCTGATTTTCCCAATAGTTTTCGATATGAGTGGCAATTC 180  
DB 121 AAAGTTTCCCTCTGATTTTCCCAATAGTTTTCGATATGAGTGGCAATTC 180  
QY 181 ATGGTAGGGAATTTATGCTTATTAAGAAAGAAAGAAAGAAAGAAAGATGTATATC 240  
DB 181 ATGGTAGGGAATTTATGCTTATTAAGAAAGAAAGAAAGAAAGAAAGATGTATATC 240  
QY 241 CTGAATTTGGCTGTAGAGATTTACTCTTATTTACTCTGCTTTTGGGCTGTTAT 300  
DB 241 CTGAATTTGGCTGTAGAGATTTACTCTTATTTACTCTGCTTTTGGGCTGTTAT 300  
QY 301 GCAATTTATGGGTGGGTTTATGGGAAAAATATGCAAAATTAATCTGAGCTTTATACA 360  
DB 301 GCAATTTATGGGTGGGTTTATGGGAAAAATATGCAAAATTAATCTGAGCTTTATACA 360  
QY 361 CTAACTTTGTCTCTGAGATGAGTTTCTGCTTGTATCAGCATGACAGATATGTGCA 420  
DB 361 CTAACTTTGTCTCTGAGATGAGTTTCTGCTTGTATCAGCATGACAGATATGTGCA 420  
QY 421 GTAATTAAGTCCCAAGCAATCAGAGTGGGAAAAACATGCTGATCATCTGTTCTGT 480  
DB 421 GTAATTAAGTCCCAAGCAATCAGAGTGGGAAAAACATGCTGATCATCTGTTCTGT 480  
QY 481 GTCTGATGAGTGGGATGCTGTCGAGATACCCGAGCTGGTTTATATAGTAAATGAC 540  
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QY 541 AATGCTAGGTGATTCCTCAATTTTCCCGCTACCTAGAACATCAATGAAGATTTGTT 600  
DB 541 AATGCTAGGTGATTCCTCAATTTTCCCGCTACCTAGAACATCAATGAAGATTTGTT 600  
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DB 601 CAATGCTAGATCTGATGATTTGATGATGATGATGATGATGATGATGATGATGATG 660  
QY 661 TTATTCAGAGCAAGGACATCATGAGATGCAAGATGCAAAATTAATATCTGACCCCTAAA 720  
DB 661 TTATTCAGAGCAAGGACATCATGAGATGCAAGATGCAAAATTAATATCTGACCCCTAAA 720  
QY 721 GTTCTGCTCAGAGTGTATATGATTTTCACTGATCACTGCTTATTAATGATGATGATG 780  
DB 721 GTTCTGCTCAGAGTGTATATGATTTTCACTGATCACTGCTTATTAATGATGATGATG 780  
QY 781 TTCTGCGGAGCCATGACATCATCTTACTCCCTGATCAGCAGCTGCAAGCAAGCAAGC 840  
DB 781 TTCTGCGGAGCCATGACATCATCTTACTCCCTGATCAGCAGCTGCAAGCAAGCAAGC 840  
QY 841 ATGGAATGCGCATCCCAATGACAGAAAGCATGCACTTTTCAAGCTGCTCAACCCA 900  
DB 841 ATGGAATGCGCATCCCAATGACAGAAAGCATGCACTTTTCAAGCTGCTCAACCCA 900  
QY 901 ATCTTTATGTTTATATGAGGACATCTTCAAAAATCTACGTTATGAAAGTGGCCAAAGAA 960  
DB 901 ATCTTTATGTTTATATGAGGACATCTTCAAAAATCTACGTTATGAAAGTGGCCAAAGAA 960  
QY 961 TATGGTCTCTGAGAGAGAGAGACAAAGTGTGAGAGAGTTTCTTTGATCTGAGGCT 1020  
DB 961 TATGGTCTCTGAGAGAGAGAGACAAAGTGTGAGAGAGTTTCTTTGATCTGAGGCT 1020  
QY 1021 CCTACAGAGCAACAGTACTTTTATGATTTAA 1053  
DB 1021 CCTACAGAGCAACAGTACTTTTATGATTTAA 1053

RESULT 18  
AX244219 1053 bp DNA linear PAT 28-SEP-2001  
LOCUS AX244219  
DEFINITION Sequence 1 from Patent WO0166598.



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Db 61 GGGCTGAGAGATTACTCTCTTATCTACCTGCGCTTTTGGGCTGTTAAAGCACTTCA 120
Qy 309 TGGGTGGGTTTGGGAAAATATATGCAAAAATTAATCTCAGCTTTTACACCTAACTT 368
Db 121 TGGGTGGGTTTGGGAAAATATATGCAAAAATTAATCTCAGCTTTTACACCTAACTT 180
Qy 369 TGTCTCGAATGAGATTCTGGCTTGTATCAGCATAGACATATGTGGAGTAATACTAA 428
Db 181 TGTCTCGAATGAGATTCTGGCTTGTATCAGCATAGACATATGTGGAGTAATACTAA 240
Qy 429 AGTCCCAAGCAATCAGAGATGGGAAAACCATGCTGATCATCTGTTCTGTCTGAT 488
Db 241 TGTCCCAAGCAATCAGAGATGGGAAAACCATGCTGATCATCTGTTCTGTCTGAT 300
Qy 489 GGTGCTGATCTTGTCTGAGCATACCCGAGCTGTTTATTAAGCTAAATAGCAATGCTAG 548
Db 301 GGTGCTGATCTTGTCTGAGCATACCCGAGCTGTTTATTAAGCTAAATAGCAATGCTAG 360
Qy 549 GTGATCTCCATTTTCCCGCTACCTAGGAAATCATGTAAGCAATGTAATGCT 608
Db 361 GTGATCTCCATTTTCCCGCTACCTAGGAAATCATGTAAGCAATGTAATGCT 420
Qy 609 AGAGATCTGATTTGATTTGATGACCTTTCTTATTAAGGGGCTGTCTACTTATCAC 668
Db 421 AGAGATCTGATTTGATTTGATGACCTTTCTTATTAAGGGGCTGTCTACTTATCAC 480
Qy 669 AGCAGAGACACTCTAGAAATGCGCAAACTTAAATATCTCGACCCCTAAAGTCTGCT 728
Db 481 GGCAGAGACACTCTAGAAATGCGCAAACTTAAATATCTCGACCCCTAAAGTCTGCT 540
Qy 729 CACAGTGTATAGTTTCTTATGTCATCTCACTGCTTATTAATGTCAGATTTGCTGCG 788
Db 541 CACAGTGTATAGTTTCTTATGTCATCTCACTGCTTATTAATGTCAGATTTGCTGCG 600
Qy 789 AGCCATGACATCATCTACTGCTGATCAGCTGACATGACATAGCAAAAGCATGACAT 848
Db 601 AGCCATGACATCATCTACTGCTGATCAGCTGACATGACATAGCAAAAGCATGACAT 660
Qy 849 CGCATCTCAAGTACAGAAAGCATGCGATCTTCAAGCTGCTCAAGCCATCTCTTAA 908
Db 661 CGCATCTCAAGTACAGAAAGCATGCGATCTTCAAGCTGCTCAAGCCATCTCTTAA 720
Qy 909 TGTTTTATGGAGCATCTTCAAAAATCTAGTTATGAAGTGGCCAAAGAAATATGGGCT 968
Db 721 TGTTTTATGGAGCATCTTCAAAAATCTAGTTATGAAGTGGCCAAAGAAATATGGGCT 780
Qy 969 CTGAGAGAAGCAGAGCAAAAGTGTGAGAGATTCTTTGATTTCTGAGGGCTTACAG 1028
Db 781 CTGAGAGAAGCAGAGCAAAAGTGTGAGAGATTCTTTGATTTCTGAGGGCTTACAG 840
Qy 1029 GCCAACCAGTACTTTTGAATTAAGTAAACTGCTGCTGCTTTTGGCTTGGATCATTA 1088
Db 841 GCCAACCAGTACTTTTGAATTAAGTAAACTGCTGCTGCTTTTGGCTTGGATCATTA 900
Qy 1089 TGAATGATGCTTCCCTCAATTAATAACTGATTAATCTGAAACTCAA 1140
Db 901 TGAATGATGCTTCCCTCAATTAATAACTGATTAATCTGAAACTCAA 952

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## RESULT 20

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LOCUS      S63848          2059 bp      mRNA      linear      MM 14-SEP-1993
DEFINITION G-protein coupled receptor type B (clone PPR1) [cattle, tongue,
            taste papillae, mRNA, 2059 nt].
ACCESSION  S63848
VERSION    S63848.1 GI:399710
KEYWORDS
SOURCE     Bos taurus tongue taste papillae.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.

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REFERENCE 1 (bases 1 to 2059)  
 AUTHORS Matsunaka, I., Mori, T., Aoki, U., Sato, T. and Kurihara, K.  
 TITLE Identification of novel members of G-protein coupled receptor  
 superfamily expressed in bovine taste tissue  
 JOURNAL Biochem. Biophys. Res. Commun. 194 (1), 504-511 (1993)  
 MEDLINE 93326166  
 PUBMED 8392843  
 REMARK GenBank staff at the National Library of Medicine created this  
 entry [NCBI gisbseq 135532] from the original journal article.  
 This sequence comes from Fig. 2.  
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 source  
 1..2059  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 1..2059  
 /gene="G-protein coupled receptor type B, GCR type B"  
 481..1533  
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 /note="This sequence comes from Fig. 2; GCR type B"  
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 HWVWLGIKIMCKVTSALYTVNFAVSGMOFLACISDRVAWVAIKADSGVSKPVNICFC  
 VVVAAILLSIPDLVFTVNHKRCVPIFPHLCTSKMAASIQILEIGFIPLIMAV  
 CYFTAKTLIKMFKISQPLKYLFTVIVFIETOLPYNIVKFCOAILDIISLITDCD  
 MSKMDVAIOTIESIALFHSCLNPLVLYVFMGTSFKYIMKVAKYSWRQRQNVBEI  
 PFESEDDTPEPTSTPST"

BASE COUNT 720 a 366 c 345 g 628 t  
 ORIGIN

Query Match 77.2%; Score 886; DB 4; Length 2059;  
 Best Local Similarity 87.4%; Pred. No. 1,5e-212;  
 Matches 970; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

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Qy 1 ATGGCTTTGGAACAGAACACAGTCAACAGATTATTTATGAGAAAATGAATGATGCC 60
Db 481 ATGGCTTTGGAATACACACAGTCAACAGATTATTTATGAGAAAATGAATGATGAC 540
Qy 61 ACTTATGACTACAGTCATATGAACTGATCTGTATCAAGAAGATGTCAGAAATTTGCA 120
Db 541 ACTCATGACTATGACATATGAAGTGTATTAAGAGAGGTAGAAAATTTGCA 600
Qy 121 AAAGTTTCCCTCCGTATTCCTCAATAGTTTTCGTCATTGAGCTTGCAGGCAATTC 180
Db 601 AAAGTTTCCCTCACTGCTCTTTCACATAGCTTTCATCATTTGACGGAATTC 660
Qy 181 ATGATAGTGGCAATTATGCTTATTAAGAAAGCAGAACCAAAACAGATGTATCATC 240
Db 661 ACTGATAGTGGCAATTATGCTTATTAAGAAAGCAGAACCAAAACAGATGTATCATC 720
Qy 241 CTGAATTTGGCTGTAGAGATTTACTCCTTCTATCACTGCTGCTTTTGGGCTGTTAT 300
Db 721 TTGAATTTGGCAGTGGCGAATTTATCTTCTATTCACCTTTGCGAGGTATAT 780
Qy 301 GCAGTTCAATGGGTGGGTTTGAAGAAATTAATGCAAAATTAATCACTTCAAGCTTGTACA 360
Db 781 GCAGTTCAATGGGTGGGTTTGAAGAAATTAATGCAAAATTAATCACTTGTGTACACA 840
Qy 361 CTAACTTTGCTCTGGAATGCAAGTTTGGCTGTATCAGCATAGACATATGTGGCA 420
Db 841 GTCAATTTTGTGTCTGGAATGCAAGTTTGGCTGTATCAGCATAGACATATGTGGCA 900
Qy 421 GTAACTTAAAGTCCCAAGTCAGAGTGGGAAAACCATGCTGGATCATCTGTTCTGTC 480
Db 901 GTAACTTAAAGTCCCAAGTCAGAGTGGGAAAACCATGCTGGATCATCTGTTCTGTC 960
Qy 481 GTCTGGAATGGCTGCATCTTGTGAGCATATCCCGAGCTGTTTATTAAGTAATGAC 540
Db 961 GTCTGGAATGGCTGCATCTTGTGAGCATATCCCGAGCTGTTTATTAAGTAATCAT 1020

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Db 1381 GTCCTAATGTTTTCATGAGAACCTCTTTAAATACTACATGATGAAAGTTGCCAAGAAA 1440  
Qy 961 TATGGGTCTCGGAGAGACAGACAAAGTGGAGAGATTCCTTTGATTCGAGGGT 1020  
Db 1441 TAGGGATCCCGAGAGAAACAAAGATGGAGAGATTCCTTTGATTCGAGGGT 1500  
Qy 1021 CTTACAGAGCCCAACGATCTTTTACATTTAAAGTAAAGTGTCTGCTTTGGCTTG 1080  
Db 1501 GCTACAGAGCCCAACGATCTTTTACATTTAAAGTAAAGTGTCTGCTTTGGCTTG 1560  
Qy 1081 GATACATATGATGATGCTTTCCCTCAAA 1110  
Db 1561 AATACACATGATGATGCTTTCCCTCAAA 1590

RESULT 22  
AX244223 831 bp DNA linear PAT 28-SEP-2001  
LOCUS Sequence 5 from Patent WO016598.  
DEFINITION AX244223  
ACCESSION AX244223  
VERSION AX244223.1 GI:15859274  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 831)  
AUTHORS Gray, P.W., Schweickart, V.L., Epp, A., Raport, C.J., Chantry, D. and  
Steiner, B.  
Chemottractant receptor characterization and cell selection  
materials and methods and chemokine receptor ccr1l materials and  
methods

JOURNAL Patient: WO 016598-A 5 13-SEP-2001;  
ICOS CORPORATION (US)  
FEATURES  
source Location/Qualifiers  
1..831  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 229 a 189 c 168 g 245 t  
ORIGIN

Query Match 72.4%; Score 831; DB 6; Length 831;  
Best Local Similarity 100.0%; Pred. No. 1.1e-198;  
Matches 831; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 CTGAATTTGGCTGAGAGATTTACTCTCTTCTATTCATCTGCTTTGGCTGTAAT 300  
Db 1 CTGAATTTGGCTGAGAGATTTACTCTCTTCTATTCATCTGCTTTGGCTGTAAT 60

Qy 301 GCAGTTACGAGGAGGTTTGGAGAAATATGCAAAATTAATCTTACGCTTGTACACA 360  
Db 61 GCAGTTACGAGGAGGTTTGGAGAAATATGCAAAATTAATCTTACGCTTGTACACA 120

Qy 361 CTTAACTTTGCTCTGAAATGCAATTTCTGGCTTGTATCAGATAGACAGATATGTGGCA 420  
Db 121 CTTAACTTTGCTCTGAAATGCAATTTCTGGCTTGTATCAGATAGACAGATATGTGGCA 180

Qy 421 GTAACCTAAAGTCCCAAGCATTCAGAGTGGAGAAACCAAGCTGGATCTGTTCTGT 480  
Db 181 GTAACCTAAAGTCCCAAGCATTCAGAGTGGAGAAACCAAGCTGGATCTGTTCTGT 240

Qy 481 GTCAGATGAGCTGCAATCTTCTGAGCATACCCAGCTGTTTATACAGTAAATGAC 540  
Db 241 GTCAGATGAGCTGCAATCTTCTGAGCATACCCAGCTGTTTATACAGTAAATGAC 300

Qy 541 AATGCTAGAGTCAATTCCTATTTCCCGCTACTAGGAATCAATGAAGCAATTAAT 600  
Db 301 AATGCTAGAGTCAATTCCTATTTCCCGCTACTAGGAATCAATGAAGCAATTAAT 360

Qy 601 CAAAGCTAGAGTCAATTCCTATTTGATGACCTTTCTATATAGAGGAGTGTGCTAC 660  
Db 361 CAAAGCTAGAGTCAATTCCTATTTGATGACCTTTCTATATAGAGGAGTGTGCTAC 420

Qy 661 TTTATCAAGCAAGAGACATCTGAGAAATGCCAAACATTAATAATATCGACCCCTAAA 720  
Db 421 TTTATCAAGCAAGAGACATCTGAGAAATGCCAAACATTAATAATATCGACCCCTAAA 480

Qy 721 GTCTGCTCAGAGCTGTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATG 780  
Db 481 GTCTGCTCAGAGCTGTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATG 540

Qy 781 TTTCGCGAGGCAATGACATCTACTCTCTGATGACCAAGCTGCAACATGAGCAAGCC 840  
Db 541 TTTCGCGAGGCAATGACATCTACTCTCTGATGACCAAGCTGCAACATGAGCAAGCC 600

Qy 841 ATGACATGCGCATTCAGATGACAGAAAGCATGCGCATCTTTTCAAGCTGCAAGCC 900  
Db 601 ATGACATGCGCATTCAGATGACAGAAAGCATGCGCATCTTTTCAAGCTGCAAGCC 660

Qy 901 ATCCCTTAATGTTTATGAGGAGCATCTTTCAAAACTACGTTATGAAAGTGGCCAGAAA 960  
Db 661 ATCCCTTAATGTTTATGAGGAGCATCTTTCAAAACTACGTTATGAAAGTGGCCAGAAA 720

Qy 961 TATGGGTCTCGGAGAGAGACAGAGCAAAAGTGTGAGAGAGTTCTTTTATGTTGAGGGT 1020  
Db 721 TATGGGTCTCGGAGAGAGACAGAGCAAAAGTGTGAGAGAGTTCTTTTATGTTGAGGGT 780

Qy 1021 CTTACAGAGCCCAACGATCTTTTACATTTAAAGTAAAGTGTCTGCTGCC 1071  
Db 781 CTTACAGAGCCCAACGATCTTTTACATTTAAAGTAAAGTGTCTGCTGCC 831

RESULT 23  
AX244229 797 bp DNA linear PAT 28-SEP-2001  
LOCUS Sequence 11 from Patent WO016598.  
DEFINITION AX244229  
ACCESSION AX244229  
VERSION AX244229.1 GI:15859280  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 797)  
AUTHORS Gray, P.W., Schweickart, V.L., Epp, A., Raport, C.J., Chantry, D. and  
Steiner, B.  
Chemottractant receptor characterization and cell selection  
materials and methods and chemokine receptor ccr1l materials and  
methods

JOURNAL Patient: WO 016598-A 11 13-SEP-2001;  
ICOS CORPORATION (US)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 230 a 168 c 155 g 244 t  
ORIGIN

Query Match 69.5%; Score 797; DB 6; Length 797;  
Best Local Similarity 100.0%; Pred. No. 4.7e-190;  
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GAACCACTGACAGATTTATTTATGAGAAATGAATGAATGACCTTATGATGACAG 74  
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Qy 75 TCAATATGACATGATCTGATCAAGAGATGTCAGAGATTTGCAAAAGTTTCTCTCC 134  
Db 61 TCAATATGACATGATCTGATCAAGAGATGTCAGAGATTTGCAAAAGTTTCTCTCC 120

Qy 135 TGTATTTCTCAAAATGTTTGTGATGATGATGATGATGATGATGATGATGATGATG 194  
Db 121 TGTATTTCTCAAAATGTTTGTGATGATGATGATGATGATGATGATGATGATGATG 180

Qy 195 TTATGCTTATCAAGAAACAGAAACCAAAACAGATGATGATGATGATGATGATGATG 254



Db 181 TTATGCTTATTAACAAGAAACAGAACCAAAACAGATGTATCTGATTTGCTGT 240  
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 Db 241 AGCAGATTACTCCCTTATCTACCTGCTCTTTTGGCTGTATGCAATGCTATGCTG 300  
 QY 315 GGTTTTAAAGAAAATATGTCAGAAATATCTTACCTGTATGACACATTAACCTTTGCTC 374  
 Db 301 GGTTTTAAAGAAAATATGTCAGAAATATCTTACCTGTATGACACATTAACCTTTGCTC 360  
 QY 375 TGGATGCACTTTCTGCTTTATACAGATGACAGATATGTCGAGTAATGCTATGCTC 434  
 Db 361 TGGATGCACTTTCTGCTTTATACAGATGACAGATATGTCGAGTAATGCTATGCTC 420  
 QY 435 CAGCAATCAGAGTGGGAAAACCATGCTGATCATCTGTTCTGTCTGTAGATGCTG 494  
 Db 421 CAGCAATCAGAGTGGGAAAACCATGCTGATCATCTGTTCTGTCTGTAGATGCTG 480  
 QY 495 CATCTTCTGAGCATACCCAGCTGTTTATTAACAGTAATGACAAATGCTAGTGCAT 554  
 Db 481 CATCTTCTGAGCATACCCAGCTGTTTATTAACAGTAATGACAAATGCTAGTGCAT 540  
 QY 555 TCCCATTTTCCCGCTTACCTAGGAACATCAATGAAGCAATGATTTCAATGCTAGAT 614  
 Db 541 TCCCATTTTCCCGCTTACCTAGGAACATCAATGAAGCAATGATTTCAATGCTAGAT 600  
 QY 615 CTGATTTGATTTGATGACCTTTCTTATTAAGGGGGTGGCTACTTTATCAACAGAG 674  
 Db 601 CTGATTTGATTTGATGACCTTTCTTATTAAGGGGGTGGCTACTTTATCAACAGAG 660  
 QY 675 GACATCTGAGAAATGCAAAACATTAATAATATCTGACCCCTTAAAGTTGCTGACAGT 734  
 Db 661 GACATCTGAGAAATGCAAAACATTAATAATATCTGACCCCTTAAAGTTGCTGACAGT 720  
 QY 735 CGTTATGTTTCTATCTGCTCACTGCTTATTAATGATTTCAAGTTCTGCGGACCAT 794  
 Db 721 CGTTATGTTTCTATCTGCTCACTGCTTATTAATGATTTCAAGTTCTGCGGACCAT 780  
 QY 795 AGACATCATCTACTCC 811  
 Db 781 AGACATCATCTACTCC 797

RESULT 24  
 AF306532 1138 bp mRNA linear ROD 29-JUL-2001  
 LOCUS AF306532  
 DEFINITION Mus musculus chemokine receptor CCR11 mRNA, complete cds.  
 ACCESSION AF306532 GI:15028429  
 VERSION AF306532.1  
 KEYWORDS  
 SOURCE Mus musculus.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE  
 AUTHORS Dorf, M.E., Berman, M.A., Tanabe, S., Heesen, M., and Luo, Y.  
 TITLE Astrocytes express functional chemokine receptors  
 JOURNAL J. Neuroimmunol. 111 (1-2), 109-121 (2000)  
 MEDLINE 20519697  
 PUBMED 11063828  
 REFERENCE  
 AUTHORS Luo, Y., Berman, M.A., Fischer, F.R., Adromson-Jeeman, S.R.,  
 Kuziel, W.A., Gerard, C., and Dorf, M.E.  
 TITLE RANTES and eotaxin stimulate chemotaxis, chemokine/cytokine  
 synthesis, and receptor modulation in murine astrocytes  
 JOURNAL Unpublished  
 AUTHORS Berman, M.A., Dorf, M.E. and Rosenbaum, D.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-SEP-2000) Pathology, Harvard Medical School, 200  
 Longwood Ave., Boston, MA 02115, USA  
 FEATURES  
 source location/Qualifiers  
 1..1138

CDs  
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 CYASTARALIKMPIKSRPLRVILAVVPIYVITOLPYNVKCOAIDATYLITSD  
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BASE COUNT 278 a 295 c 269 g 295 t 1 others  
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Query Match 68.3%; Score 783.2; DB 10; Length 1138;  
 Best Local Similarity 83.3%; Pred. No. 1.3e-186;  
 Matches 890; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 1 ATGGCTTTGAAACAGAACAGTCAACAGATTAATATGAGAAATGAATGATGCG 60  
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 Db 110 ACTCAGACTACAGCAGTACGAAATGATCTGCAATAAAGAGATCAGGAGTTTGC 169  
 QY 121 AAAGTTTCCCTCCGTAATTCCTCAAAATAGTTTGCATGTAAGTTCGAGCAATTC 180  
 Db 170 AAAGTTTCCCTCCGTAATTCCTCAAAATAGTTTGCATGTAAGTTCGAGCAATTC 229  
 QY 181 ATGTAGTGGCAATTAATGCTTATTAACAAGAAACAAACAGATGATGATGATC 240  
 Db 230 GTAGTGTGGGATTTACGCTTATTAACAAGAAACAAACAGATGATGATGATC 289  
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 Db 290 CTGAATTTGGCTGATGAGATTTACTCTCTTATTAATCACTGCTCTTTTGGGCTGTTAAT 349  
 QY 301 GAGTTTATGGGATGAGTTTATGAGAAATATGAGAAATATCAAGCTTGTATGACA 360  
 Db 350 GAGTTTATGGGATGAGTTTATGAGAAATATGAGAAATATCAAGCTTGTATGACA 409  
 QY 361 CTAAATTTTGTCTCTGGAATGACATTTCTGCTTGTATGACATGACATGATGATGCA 420  
 Db 410 GTAAATTTTGTCTCTGGAATGACATTTCTGCTTGTATGACATGACATGATGATGCA 469  
 QY 421 GTAAATTTTGTCTCTGGAATGACATTTCTGCTTGTATGACATGACATGATGATGCA 480  
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Db	770	GTTCGCTCGGGGAGTGTGGTTTCAATTGCAACCAAGTGGCCCTAAACGTTGTTAAG	829
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Db	830	TTTCGCCAAGCCATAGATGATCATCTACTGATGATCACCAAGCTGCATATGACMAAAGC	889
Qy	841	ATGGAATCGGCATTCAGATGACAGAAAGACATCGCACTCTTTTCACAGCTGGCTCAACCCA	900
Db	890	ATGGAATGTCGCATTCAGATGACAGAGAGCATCGCGCTCTTCCACAGCTGGCTCAACCCC	949
Qy	901	ATCCTTATATGTTTTATGGAGGATCTTTCAAAACTACGTTATGAAAGTGGCCAGAAGAA	960
Db	950	ATCCGTATATGCTTCATGAGGAGCTCTTCAAAACTATATCATGAAAGTGGCCAGAAGAA	1009
Qy	961	TATGGGTCTGTGAGAGACAGAGACMAAAGTGTGAGAGATTCTTTTGATTCTGAGGCT	1020
Db	1010	TATGGATCTGTGAGAGACAGAGACAGAAACGTGAGAAAGATTCCTTTTGATTCTGAGGCT	1069
Qy	1021	CCTAAGAGCCAAACAGTACTTTTATGCAATTTAAAGATAAAGTAACTGGCTC	1068
Db	1070	CCTAAGAGCCAAACAGTCTTTTATCAATTTAAATATATAAAGTGGCTC	1117

RESULT	25		
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LOCUS	Ay072796	2351 bp	mRNA linear ROD 01-Apr-2002
DEFINITION	Mus musculus chemokine receptor	CXCR mRNA, complete cds.	
ACCESSION	Ay072796		
VERSION	Ay072796.1	GI:19879567	
KEYWORDS			
SOURCE	Mus musculus.		

ORGANISM: *Mus musculus*; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 2351)

REFERENCE: Thomson, J.R. and Nibbs, R.J. Characterization of mouse CCX CKR, a receptor for the

AUTHORS: Thomson, J.R. and Nibbs, R.J.

TITLE: Characterization of mouse CCX CKR, a receptor for the

**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 2351)  
**AUTHORS** Townson, J.R. and Nibbs, R.J.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (10-JAN-2002) CRC Beatson Laboratories, The Beatson  
Institute for Cancer Research, Garscube Estate, Switchback Road,  
Beairsteden, Glasgow, Scotland G61 1BD, UK

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Query Match	68.3%;	Score 783.2;	DB 10;	Length 2351;
Best Local Similarity	83.3%;	Pred. No. 1.2e-186;		
Matches 890;	Conservative 0;	Mismatches 178;	Indels 0;	Gaps 0

Oy	1	ATGCGTTTGGAAACGAACCACTGCACAAGATTATATTATGAGAAAAATGAATGATGGC	60
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Oy	61	ACTTATGACTACAGTCATATGAACTGATCTGTATCAAAGAAGTGTCAGAAATTGCCA	120
Db	812	ACTCACGACTACAGCCAGTAAGAGTAGATCTGCATATAAAGAAGAGTGACGCAGTTCCGA	871
Oy	121	AAAGTTTTCTTCCTCTGTATTCCTGCACAAATAGTTTTGCTCATTTGGACCTTGAGGGCAATGCC	180
Db	872	AAAGCTTCCTCCGCTCCGCTCTTTCACAGTGGCTTTGTACCTGGGCTGCGAGGGAACTCC	931
Oy	181	ATGGTAGTGGCAATTATAGCTTATGACCTATTAACAAGAACAGAAACCAAAAACAGATGTGTATC	240
Db	932	GTAATGTGGGCAATTACGCCCTATTAACAAGAAGAGAGACCAAGACCGATGTGTATC	991
Oy	241	CTGAATTTGGCTGTAGACAGATTACTCCTTCTATTCACTCTGGCTTTTGGGCTGTAT	300
Db	992	CTGAACCTGGCTGTAGACAGACTGTGTACTTCTGATCAAGCTGCCCTTTCTGGCAGTTTAT	1051
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Db	1052	GGAGTTCACGGATGATTTCTAGGCAAAATGATGTGCAAAGTACCTCAGCCCTGTACACG	1111
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Db	1232	GTCGTGATGGCCGCATCTTGTCTGAGCATACCCAGCTGTTTTTTATACAGTAAATGAC	1291
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Db	1712	TATGATATCTCGAAGAAAGACAGACAAAGTGTGAGAAATTCCTTTGATTTGTAGGGT	1771
Oy	1021	CTACAGAGCAACAGTACTTTTACATTTAAAGTAAACCTGCTCT	1068
Db	1772	CTACAGAGCAACAGTCTTTTACATTTAAATATTAACCTGCTCT	1819

RESULT 26  
AY072938 2392 bp mRNA linear, ROD 01-APR-2002  
LOCUS Mus musculus chemokine receptor CXCR mRNA, complete cds,  
DEFINITION alternatively spliced.  
ACCESSION AY072938  
VERSION AY072938.1 GI:19879586  
KEYWORDS  
SOURCE Mus musculus.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 2392)  
Townson, J.R. and Nibbs, R.J.  
Characterization of mouse CXCR, a receptor for the  
lymphocyte-attracting chemokines TECK (CCL25), SLC (CCL21) and  
MIP-3beta (CCL19): comparison to human CXCR  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2392)  
Townson, J.R. and Nibbs, R.J.  
Direct Submission  
Submitted (11-JAN-2002) CRC Beatson Laboratories, The Beatson  
Institute for Cancer Research, Gartcube Estate, Switchback Road,  
Beairston, Glasgow, Scotland G61 1BD, UK  
LOCATION/Qualifiers  
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Query Match 68.3%; Score 783.2; DB 10; Length 2392;  
Best Local Similarity 83.3%; Pred. No. 1.2e-186;  
Matches 890; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

Qy 301 GCAGTTCATGGGTGGTTTAAAGGAAATTAATGTCACAAATTAACCTGACCTGTGACACA 360  
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Qy 361 CTAAATCTGTGTCTGGAATGACATTTCTGGCTGTATACACATAGACATATATGTGCA 420  
Db 1153 GTAAACTTGTCTCGGGATGACATCTCTGGCTGTATACACATATGACATATATGTGCA 1212  
Qy 421 GTAACTAAAGTCCCGACCAATCAGAGATGGGAAACCAATGATGATCTGTCTGT 480  
Db 1213 ATTAACCAAGCCCCACGCAATCAGAGAGCGGAGACCTCTGTGATCATCTGTCTGT 1272  
Qy 481 GTCTGATGCTGCTCCATCTTCTGAGATACCCAGCTGTTTTTATACAGTAATGAC 540  
Db 1273 GTGTGATGACCGGCATCTTCTGAGATACCCAGCTGTTTTTATACAGTAATGAC 1332  
Qy 541 AATGCTAGATGATTCCTATTTCCCGCTACCTAGGAACATCAATGAAGCATTTGATT 600  
Db 1333 AATGCTAGATGATTCCTATTTCCCGCTACCTAGGAACATCTGGAAGCATTCATT 1392  
Qy 601 CAATGCTAGATGATTCCTATTTCCCGCTACCTAGGAACATCAATGAAGCATTTGATT 660  
Db 1393 CAGATGCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1452  
Qy 661 TTTATCAGACAGACACATCATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
Db 1453 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1512  
Qy 721 GTTCTGCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
Db 1513 GTTCTGCTGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1572  
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Db 1573 TTCTGCCAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1632  
Qy 841 ATGACATGCGCATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
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RESULT 27  
AX244227 604 bp DNA linear PAT 28-SEP-2001  
LOCUS AX244227  
DEFINITION Sequence 9 from Patent WO016598.  
ACCESSION AX244227  
VERSION AX244227.1 GI:15859278  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 604)  
Gray, P.W., Schweickart, V.L., Bpp, A., Raport, C.J., Chantry, D. and  
Steiner, B.  
Chemottractant receptor characterization and cell selection  
materials and methods and chemokine receptor ccr1 materials and  
TITILE  
JOURNAL Patent: WO 016598-A 9 13-SEP-2001;  
ICOS CORPORATION (US)  
FEATURES  
Location/Qualifiers





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 \* 62094 64233: contig of 2140 bp in length  
 \* 64234 64333: gap of unknown length  
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 \* 67137 68815: contig of 1679 bp in length  
 \* 68816 68915: gap of unknown length  
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 \* 72006 72105: gap of unknown length  
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 \* 74395 75652: contig of 1258 bp in length  
 \* 75653 75752: gap of unknown length  
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 \* 78892 78991: gap of unknown length  
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 \* 81020 81119: gap of unknown length  
 \* 81120 83805: contig of 2686 bp in length  
 \* 83806 83905: gap of unknown length  
 \* 83906 86227: contig of 2322 bp in length  
 \* 86228 86327: gap of unknown length  
 \* 86328 88307: contig of 1980 bp in length  
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## RESULT 30

AF090348

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

BASE COUNT

ORIGIN

142 a 183 c 163 g 177 t  
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 ACCESSION AX244228  
 VERSION AX244228.1 GI:15859279  
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REFERENCE 1 (bases 1 to 374)  
 Gray, P.W., Schweickart, V.L., Bpp, A., Raport, C.J., Chantry, D. and  
 Steiner, B.  
 Chemotactant receptor characterization and cell selection  
 materials and methods and chemokine receptor ccr1 materials and  
 methods Patent: WO 0166598-A 10 13-SEP-2001;  
 JOURNAL ICOS CORPORATION (US)  
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BASE COUNT 111 a 92 c 72 g 99 t  
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Query Match 30.4%; Score 348.6; DB 6; Length 374;  
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 Matches 351; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 786 CCGAGCCATAGACATCATCTACTCCCTGATCAACAGCTGCAACATGAGCAAGCATGGA 845  
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 QY 846 CATCGGCATCAAGTACAGAAAGCATGCGACTCTTTTACAGAGTGGCTTCAACCCATCT 905  
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 QY 906 TTATGTTTTATGGAGCATCTTTCAAAACTAGTTAAGAAAGTGGCAAGAAATATGG 965

DB 121 TTATGTTTTATGGAGCATCTTTCAAAACTAGTTAAGAAAGTGGCAAGAAATATGG 180  
 QY 966 GTCTGAGAGAGACAGAGCAAAAGTGTGAGAGTTCCTTTGATTCAGAGGCTTAC 1025  
 DB 181 GTCTGAGAGAGACAGAGCAAAAGTGTGAGAGTTCCTTTGATTCAGAGGCTTAC 240  
 QY 1026 AGAGCCAAACAGTACTTTTAAAGTTAAAGTTAAAGTCTCTGCTTTTGGATAC 1085  
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 QY 1086 ATATGAATGATGCTTTCCCTCAATTAATACATGCTTTTCTGAAAAAATAA 1140  
 DB 301 ATATGAATGATGCTTTCCCTCAATTAATACATGCTTTTCTGAAAAAATAA 355

RESULT 32  
 LOCUS AX113681 347 bp DNA linear PAT 01-MAY-2001  
 DEFINITION Sequence 11 from Patent WO0127146.  
 ACCESSION AX113681  
 VERSION AX113681.1 GI:13939854  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 347)  
 Gosling, J., Dalraghi, D.J., Hanley, M., Miao, Z., Talbot, D. and  
 Schall, T.J.  
 Chemokine receptor  
 Patent: WO 0127146-A 11 19-APR-2001;  
 JOURNAL Chemocentriyx, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..347  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /note="selected portion of SEQ ID NO:1"

BASE COUNT 109 a 60 c 70 g 108 t  
 ORIGIN

Query Match 30.3%; Score 347; DB 6; Length 347;  
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 Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTTTGGAACAGAACAGTCAACAGATTATTTATGAGAAATGAAATGAGC 60  
 DB 1 ATGGCTTTGGAACAGAACAGTCAACAGATTATTTATGAGAAATGAAATGAGC 60  
 QY 61 ACTATGACTACAGTCAATATGAACTGATCTGTATCAAGAAAGATGTGAGAAATTGCA 120  
 DB 61 ACTATGACTACAGTCAATATGAACTGATCTGTATCAAGAAAGATGTGAGAAATTGCA 120  
 QY 121 AAAGTTTCCCTGCTGATTCCTCAAGATAGTTTGTGCTAGTGGCACTGAGCAATTGC 180  
 DB 121 AAAGTTTCCCTGCTGATTCCTCAAGATAGTTTGTGCTAGTGGCACTGAGCAATTGC 180  
 QY 181 ATGTAGTGGCAATTTATGCTATTACAGAGAACAGAGAACCAAAACAGATGTGATATC 240  
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 QY 241 CTGAATTTGGCTGTAGAGATTTACTCTCTTATTTCACTGCTGCTTTTGGGCTGTTAT 300  
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 DB 301 GCAAGTTCATGGGTGGTTTATGAGGAAATTAATGCAAAATTAATCTTC 347

RESULT 33  
 LOCUS AC111746/c 162393 bp DNA linear HTG 13-JUL-2002  
 DEFINITION Rattus norvegicus clone CH230-15011, \*\*\* SEQUENCING IN PROGRESS

\*\*\*, 72 unordered pieces.

ACCESSION AC11746  
VERSION AC11746.2 GI:21736893  
KEYWORDS HTG; HTGS\_Phrase1.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus

REFERENCE  
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

1 (bases 1 to 162393)  
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,  
Alshrocks, S.L., Amaral, H.C., Are, J.R., Ayale, M., Banks, T.,  
Barbieri, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,  
Bouck, J., Bowie, S., Briviera, M., Brown, E., Brown, M., Bryant, N.P.,  
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,  
Carion, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,  
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,  
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,  
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,  
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,  
Doutwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,  
Earmhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,  
Fallis, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,  
Gabriel, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,  
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,  
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,  
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,  
Homs, F., Howard, S., Huber, U., Hulik, S., Hume, J., Jackson, L.E.,  
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,  
Karlssoon, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,  
Kratovich, J., Kureishi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,  
Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Loussegod, H.,  
Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,  
Maneshwar, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,  
Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M.,  
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,  
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,  
Nguyen, N., Nickerson, E., Nwokwenkwo, S., Oguh, M., Okunnu, G.,  
Ogunyeye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,  
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,  
Rivers, M., Rojals, A., Rojudoan, I., Rolle, M., Ruiz, S., Saverly, G.,  
Scherer, S., Scott, G., Shen, H., Shooshbari, N., Sisson, I.,  
Sodergren, E., Sonakke, T., Sparks, A., Stanley, H., Stone, H.,  
Stutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,  
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, R., Thomas, S.,  
Uman, K., Vasquez, L., Vera, V., Villalob, D., Vinson, R., Wang, Q.,  
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,  
Williams, G., Williamson, A., Wleczek, R., Woden, S., Worley, K.,  
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,  
Weinstock, G. and Gibbs, R.

TITLE  
JOURNAL

Unpublished  
2 (bases 1 to 162393)

REFERENCE  
AUTHORS

Worley, K.C.

## JOURNAL

Submitted (19-FEB-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

REFERENCE  
AUTHORS

Worley, K.C.

## JOURNAL

Submitted (13-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

## COMMENT

On Jul 12, 2002 this sequence version replaced gi:18701588.

Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
Center project name: GOAP  
Center clone name: CH230-15011

## Summary Statistics

Sequencing vector: plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 96609 bases at least Q40  
Consensus quality: 101360 bases at least Q30  
Consensus quality: 105362 bases at least Q20

NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

NOTE: This is a 'working draft' sequence. It currently  
consists of 72 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.

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2428	2527: gap of unknown length
2528	3635: contig of 1108 bp in length
3636	3735: gap of unknown length
3736	4821: contig of 1086 bp in length
4822	4921: gap of unknown length
4922	6640: contig of 1719 bp in length
6641	6740: gap of unknown length
6741	8216: contig of 1476 bp in length
8217	8316: gap of unknown length
8317	9346: contig of 1030 bp in length
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9447	10691: contig of 1245 bp in length
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11952	13509: contig of 1558 bp in length
13510	13609: gap of unknown length
13610	14869: contig of 1260 bp in length
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16376	17440: contig of 1065 bp in length
17441	17540: gap of unknown length
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20162	21232: contig of 1071 bp in length
21233	21332: gap of unknown length
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22379	22478: gap of unknown length
22479	23629: contig of 1151 bp in length
23630	23729: gap of unknown length
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24994	25093: gap of unknown length
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26449	26748: gap of unknown length
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31549	31648: gap of unknown length
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32916	33015: gap of unknown length
33016	34132: contig of 1117 bp in length
34133	34232: gap of unknown length
34233	35376: contig of 1144 bp in length
35377	35476: gap of unknown length
35477	36835: contig of 1359 bp in length
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36936	38119: contig of 1184 bp in length



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*      40049      40148: gap of unknown length
*      40149      41648: contig of 1500 bp in length
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*      45398      46533: contig of 1136 bp in length
*      46534      46633: gap of unknown length
*      46634      48451: contig of 1818 bp in length
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*      52067      52166: gap of unknown length
*      52167      53724: contig of 1558 bp in length
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*      53825      55350: contig of 1526 bp in length
*      55351      55450: gap of unknown length
*      55451      57835: contig of 2385 bp in length
*      57836      57935: gap of unknown length
*      57936      59470: contig of 1535 bp in length
*      59471      59570: gap of unknown length
*      59571      61049: contig of 1479 bp in length
*      61050      62619: contig of 1470 bp in length
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*      65226      66427: contig of 1202 bp in length
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*      71417      71516: gap of unknown length
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Query Match      15.7%; Score 180.6; DB 2; Length 162393;
Best Local Similarity 51.3%; Pred. No. 8.2e-35;
Matches 482; Conservative 0; Mismatches 439; Indels 18; Gaps 2;

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Qy 414 TGT-----GGCAGTAACATAAGTCCCGACCAATCAGAGTGGGAAAAACATG 461
Db 121245 TGTGGCAATCCGCGAGCGGTGTACGCCACCGGACCGCGCGCTTCATCATAG 121186
Qy 462 CTGATCATCTGTCTTGTGTGTGTGATGCGTCGCAATCTTGTGAGCATCCCACTGCT 521
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RESULT 34
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DEFINITION AF121670
VERSION AF121670.1 GI:7688548
KEYWORDS Rattus norvegicus.
SOURCE Rattus norvegicus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1631)
AUTHORS Gonzalez,A.M., Delgado,M.D., Iachowicz,J.E. and Sibley,D.R.
TITLE Cloning of AMG1, a new putative G-protein coupled receptor with
homology to the chemokine receptor superfamily
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1631)
AUTHORS Gonzalez,A.M., Delgado,M.D., Iachowicz,J.E. and Sibley,D.R.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-1999) Pharmacol. and Physiol., School of Med.
Univ. of Cantabria, Cardenal Herrera Oria, Santander, Cantabria
39011, Spain

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FEATURES

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ORIGIN

Query Match 15.7%; Score 180.2; DB 10; Length 1631;  
Best Local Similarity 51.5%; Pred. No. 1,2e-34;  
Matches 478; Conservative 0; Mismatches 433; Indels 18; Gaps 2;

67 GACTACAGTCAATATGAATGATCTGATCAAGAAAGTGTGAGAAATTTGCAAAAGTT 126  
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307 TTCTCCCTGATATCCACAAATAGTTTGTGATGACCTGAGCAATTCATGATGTA 366  
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667 ATAGCATCTGACCTTGGCTTTTCTCTCTATCCCTGAGCTGCTTACAGCGGCTC 726  
535 AATGCAATGTAGGTGATGCTCCATTTTCCCGCTCTCTGAGCAATCATGAAAGCA 594

Db 727 CAGAGAACAGCGCGGAGACACGTGAGATGCTCCCTGCTAGTCCCAAGTGAAGCC 786

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Db 787 TTGATGCCATCCAGAGTGGCCAGATGTTGTTGTTTACGCTTATAGCTGGATG 846

Qy 649 GGGGTGTGCTACTTTATCAGACAGACACTCATGAAGATGCCAAATTTAAATATCT 708

Db 847 AGTTCTGTACTACCTGTTATCATCCGACCTGCTCCAGCGGAAACCTTGAGCGGAAC 906

Qy 709 CGACCCCTAAAGTTGCTGCTCAGAGTGGTAAAGTTTCAATGCTACTCACTGCTTAT 768

Db 907 AAGGCATCAAGTGTATCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 966

Qy 769 AACATTGCAAGTTCTGCGGACCATAGACATCATCTTCCCTGATACAGCTGCAAC 828

Db 967 AATGGGTGTGTCTGCGCCACACCGTGGCCAAATTTCAACATCAACATPAGAGCTGGAC 1026

Qy 829 ATGACAAAGCATGACATGCTGCTCATCCAGTTCACAGAAAGATCGCATCTTCAAGC 888

Db 1027 AGCAGCAAGCATCAATGCTGCTGATGACCTGACATCAACAGCTGCTGCTGCTGCTG 1086

Qy 889 TGCCCAACCCCATCTTATGTTTATGAGACATCTTCAAAACTAGCTATGAAA 948

Db 1087 TGTGTCAACCTTCTTGTATGCTTCTATGCGGCTGCAAGTTCCGACGACCTCTTCAAG 1146

Qy 949 GTGGCAGAAATATGAGTCTGAGAG 977

Db 1147 CTCTTCAAGACTTGGGCTGCTGACGAG 1175

RESULT 35

AC125884

LOCUS

DEFINITION Rattus norvegicus clone CH230-260K22, \*\*\* SEQUENCING IN PROGRESS

AC125884

VERSION 1

KEYWORDS HTG, HTGS, PHASE1.

SOURCE Rattus norvegicus.

ORGANISM Rattus norvegicus

REFERENCE

AUTHORS

1 (bases 1 to 155206)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alpbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayala,M., Banks,T., Barbara,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Bunay,C., Burch,P., Butkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,D., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunatane,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,D., Hernandez,O., Hodgson,A., Hognes,M., Hollway,C., Hollins,B., Homai,F., Howard,S., Huber,J., Hulik,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvan,J., Kovar,C., Kratoch,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichsteig,O., Lieu,C., Liu,J., Liu,W., Louised,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Martinez,E., Maheshwari,M., Mapua,P., Martin,R., Marindale,A., Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Medora,M., Mei,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,A., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,B., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogul,M., Okunolu,G., Rattus.

Otáguye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,  
 Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y.,  
 Rivas, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G.,  
 Scherer, S., Scott, G., Shen, H., Shooshari, N., Sisson, I.,  
 Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,  
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,  
 Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,  
 Umanan, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, C.,  
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,  
 Williams, G., Williamson, A., Wleczky, R., Wooden, S., Worley, K.,  
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,  
 Weinstock, G., and Gibbs, R.  
 Direct Submission  
 2 (bases 1 to 155206)  
 Unpublished  
 Worley, K.C.  
 Direct Submission  
 Submitted (02-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 155206)  
 Worley, K.C.  
 Direct Submission  
 Submitted (23-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
 ----- Project Information  
 Center project name: GMSU  
 Center clone name: CH230-260K22  
 ----- Summary Statistics  
 Sequencing vector: Plasmid  
 Chemistry: Dye-terminator Big Dye: 100% of reads  
 Assembly program: Phrap; Version 0.990329  
 Consensus quality: 121477 bases at least Q40  
 Consensus quality: 126231 bases at least Q30  
 Consensus quality: 129386 bases at least Q20  
 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 47 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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2359	3692: contig of 1334 bp in length	20446	20545: gap of unknown length
3693	3792: gap of unknown length	20546	22581: contig of 2036 bp in length
3793	5454: contig of 1662 bp in length	22582	22681: gap of unknown length
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Best Local Similarity 53.1%; Pred. No. 2.4e-33; Indels 30; Gaps 4;

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AB009369

LOCUS

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 REFERENCE 1 (bases 1 to 1674)  
 Zaballos A.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-DEC-1997) Zaballos A., Immunologia y Oncologia, Centro Nacional de Biotecnologia, Universidad Autonoma de Madrid, Campus de Cantoblanco, 28049-Madrid, SPAIN  
 REFERENCE 2 (bases 1 to 1674)  
 Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F., Albar J.P., Ardayin C. and Marquez G.  
 TITLE Molecular cloning, functional characterization and mRNA expression analysis of the murine chemokine receptor CCR6 and its specific ligand MIP-3alpha  
 JOURNAL FEBS Lett. 440 (1-2), 188-194 (1998)  
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 PUBMED 9862452  
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REFERENCE 1 (bases 1 to 1500)  
 Burgeblat, R., Kempkes, B., Steube, K. and Lipp, M.  
 Expression of the chemokine receptor BLR2/EB1 is specifically  
 transactivated by Epstein-Barr virus nuclear antigen 2  
 JOURNAL Biochem. Biophys. Res. Commun. 215 (2), 737-743 (1995)  
 MEDLINE 96011839  
 PUBMED 7488016  
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 Lipp, M.  
 Direct Submission  
 TITLE Submitted (10-FEB-1995) M. Lipp, Max-Debrueck-Centrum fuer  
 JOURNAL Mol.Medizin, Robert-Rössle-Strasse 10, 13122 Berlin-Buch, FRG  
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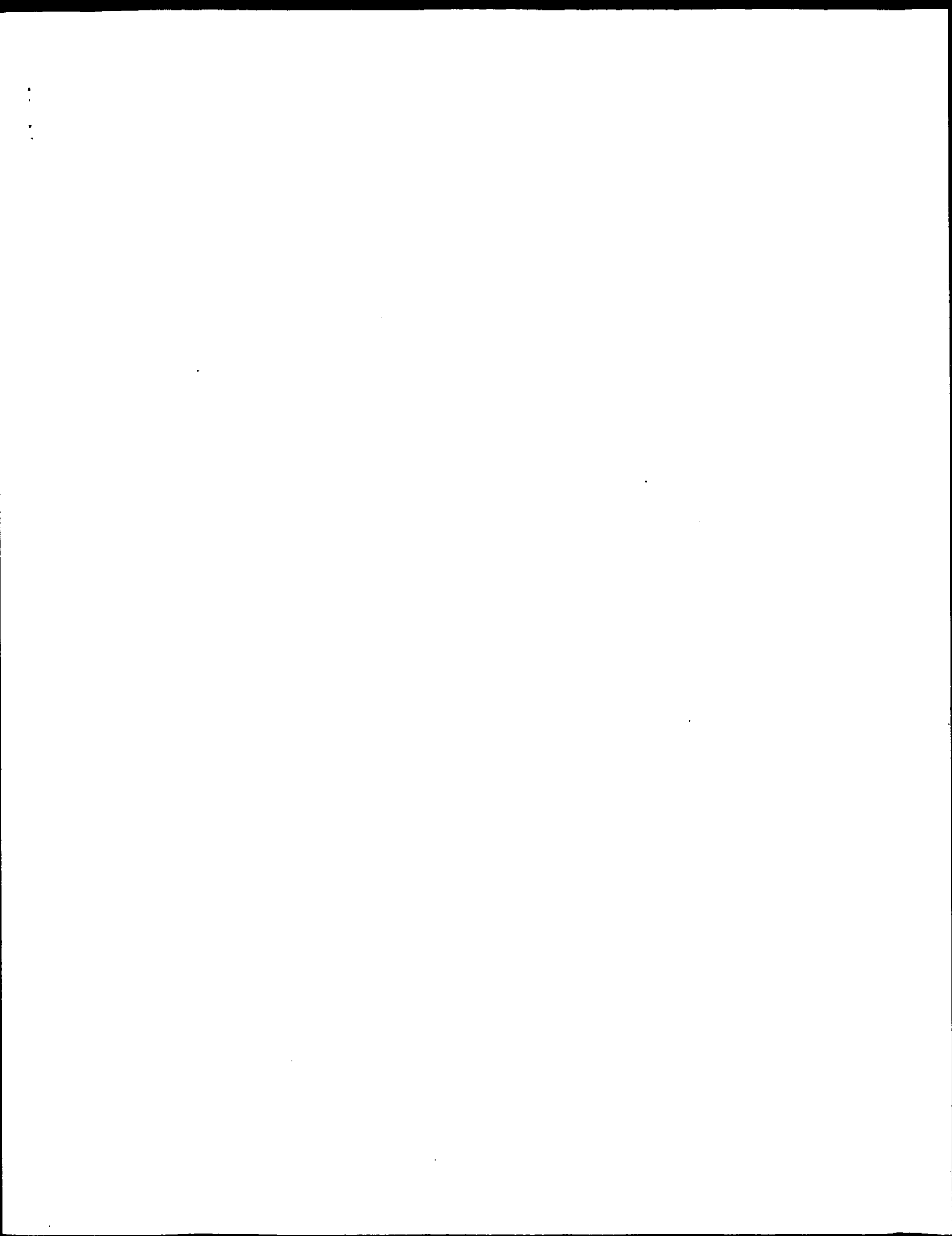
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 Db 492 AGAAGAGCTGCGGAACTTTAAAGCTGGTTCCCTCATCATGATCTCATCTTGT 551  
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 Db 612 AGACATAGACGATACCTTACCTGCTCACTGGAGCTGGAGACATCTCTCTCTGA 671  
 QY 278 CTCTGCTTTTGGGCTGTTATGACATTCATGAGTGGGTTTGAAGAAATTAATGCA 337  
 Db 672 CCTTCCCTTCTGGGCTTACAGCGGGCAAGCTCGGATCTTGGTGTCCACTTTTGA 731  
 QY 338 AATATCTTACGCTTGTACACACTAACTTTGTCTGGAATGCAATTTGGCTGTGA 397  
 Db 732 AGCTCATCTTTGCCATCTTACAAATGAGCTTCTTCAATGAGATCTCTACTTCTTGA 791  
 QY 398 TCAGCATAGACAGATATGT-----GGCAGTAACTAAAGTCCCAAGCAATGAG 445  
 Db 792 TCAGCATTGAACCGCTTACGCTGATCGATCGAGCTGTCTCAGCTCACCGCAGCTGCC 851  
 QY 446 GAGTGGGAAACCATGCTGATCATCTGTTTCTGTCTGATGCTGCTCACTTCTGCA 505  
 Db 852 GCGTCTTCTCATACAGAGAGCTGCTGTGGGATCTGATACTAGCCACAGGCTCT 911  
 QY 506 GCATACCCAGCTGTTTATTTATACAGTAATGACAAATGCTAGGAGCATTCCTATTC 565  
 Db 912 CCATCCAGAGCTCTCTGTAACAGTGAACCTCCAGAGAGACAGAGAGAGATGCGAT 971  
 QY 566 CCGGCTACTAGACATCAATCAATGAAGATGATTAATGCTAG-----AGATCTGCA 619  
 Db 972 GCTCTCTATCAAGAGCATGTGAGGCTTTATACCATCAGGTGGCCAGATGTGGA 1031  
 QY 620 TTGATTTGTAGTACCTTTCTTATTTATGAGGCTGTCTACTTTATCAACAGAGAAC 679  
 Db 1032 TGGGCTTTGTGCTCCCGCTGCGGATGAGCTTGTATCTGTCAATCCACACC 1091  
 QY 680 TCATGAGATGCGCAAACTTTAAATATCTCCAGCCCTTAAAGTTGTGCTCAGTGTGA 739  
 Db 1092 TGTCTCAGGACAGCAACTTTGAGCGCAACAGGCTCATAGGTATCATGCTGTGTG 1151  
 QY 740 TGGTTTCACTGCTCACTGCTTAACTTAACTTGAATGTCAAGTTCTGCGAGCCATAGA 799  
 Db 1152 TGGTCTTCAATGCTTTCAGCTGCTGCTTCAATGAGGTGCTGCGCAGACGTTGCCA 1211  
 QY 800 TCATCTACTCCCTGATCACAGCTGCAACATGACATGACAAAGCATGCTCAGTCAAG 859  
 Db 1212 ACTTCAACATCACAGTATACCTGTGAGCTCAGTAAGCACTCAACATGCTCTGAGAG 1271  
 QY 860 TCACAGAAAGCATGCACTTTTCAACAGTGGCTCAACCCATTCCTTATGTTTATG 919  
 Db 1272 TCACCTTACAGCTGCTGCTGCTGCTGCTCAACCTTTCTTGTGACGCTTATG 1331  
 QY 920 GAGCATCTTCAAAAATCACTGTTATGAAAGTGGCCAAAGAAATATGAGTCTGAG 974  
 Db 1332 GCGTCAAGTTCCGCAACGATCTTCAACCTTCAAGAACCTGGGCTGCTCAG 1386

RESULT 39  
 ARI07241 1900 bp DNA linear PAT 14-FEB-2001  
 LOCUS ARI07241  
 DEFINITION Sequence 18 from patent US 6107475.  
 ACCESSION ARI07241  
 VERSION ARI07241.1 GI:12821771  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.













QY 301 GCACTTATGGGTTTATAGGAAAAATATGCAAAATACCTTACGCTTGTACACA 360  
 DB 301 GCACTTATGGGTTTATAGGAAAAATATGCAAAATACCTTACGCTTGTACACA 360  
 QY 361 CTAACTTGTCTGTGGAATGAGTCTTGTGTTATGATACAGATATATGAGCA 420  
 DB 361 CTAACTTGTCTGTGGAATGAGTCTTGTGTTATGATACAGATATATGAGCA 420  
 QY 421 GTAATTAAGTCCCGACCAATGAGAGTGGAAAAACATGCTGATCATCTGTTCTGT 480  
 DB 421 GTAATTAAGTCCCGACCAATGAGAGTGGAAAAACATGCTGATCATCTGTTCTGT 480  
 QY 481 GTCTGATGCTGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 540  
 DB 481 GTCTGATGCTGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 540  
 QY 541 AATGCTAGTGCATTTCCATTTTCCCGCTACCTAGGAAATCATCAATGAAGATGATT 600  
 DB 541 AATGCTAGTGCATTTCCATTTTCCCGCTACCTAGGAAATCATCAATGAAGATGATT 600  
 QY 601 CAAATGCTAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 DB 601 CAAATGCTAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 QY 661 TTTATGACAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
 DB 661 TTTATGACAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
 QY 721 GTTGTGCTCAGTGTGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
 DB 721 GTTGTGCTCAGTGTGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
 QY 781 TTGTGCGAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
 DB 781 TTGTGCGAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
 QY 841 ATGACATGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 DB 841 ATGACATGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 QY 901 ATGCTTATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 DB 901 ATGCTTATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 QY 961 TATGCTGCTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020  
 DB 961 TATGCTGCTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020  
 QY 1021 CCTACAGAGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
 DB 1021 CCTACAGAGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
 QY 1081 GATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 DB 1081 GATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 QY 1141 AAAAAAM 1147  
 DB 1141 AAAAAAM 1147

RESULT 2  
 AA290528  
 ID AA290528 standard; cDNA, 1232 BP.  
 XX AA290528;  
 AC  
 XX  
 DT 05-JUN-2000 (first entry)  
 XX  
 DE Human BGCKr protein encoding cDNA.  
 XX  
 KW BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;  
 cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;

KW anti-allergic; antiviral; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 70..1122  
 FT /\*tag= a  
 FT /note= "the coding sequence is specifically claimed for"  
 PA  
 PN W09952945-A2.  
 PD 21-OCT-1999.  
 XX  
 XX 16-APR-1999; 99WO-US08395.  
 PE  
 XX 16-APR-1999; 98US-0061753.  
 PR 16-APR-1999; 99US-0061753.  
 XX  
 XX (MILL-) MILLENIDUM PHARM INC.  
 PA  
 PI Gonzalo JA, Gutierrez-Ramos JC;  
 DR MPI, 1999-620375/53.  
 DR P-PSDB; AAY57290.  
 PT  
 PT New nucleic acid encoding human BGCKr receptor, used e.g. for  
 PT modulating inflammation and tumor growth  
 XX  
 PS Claim 2; Fig 2A-B; 123pp; English.  
 XX  
 CC The invention relates to a human BGCKr protein, a G-protein coupled  
 CC receptor. The BGCKr protein can be expressed by standard recombinant  
 CC methodology. BGCKr are receptor proteins possibly involved in modulation  
 CC of proinflammatory or stimulatory functions of chemokines; cell  
 CC proliferation, migration, adhesion and targeting, and exocytosis. The  
 CC BGCKr nucleic acids and derived proteins (or their variants), antibodies  
 CC and modulators are potentially useful for modulating inflammation;  
 CC chemotactic activity of leucocytes; angiogenesis; cell proliferation;  
 CC tumor growth; allergic reactions and entry of human immune deficiency  
 CC virus into cells, for therapeutic or prophylactic purposes. They are also  
 CC used for diagnosis and in drug-screening assays. The present sequence  
 CC represents the cDNA encoding the full-length human BGCKr protein.  
 XX  
 SQ Sequence 1232 BP; 365 A; 267 C; 240 G; 360 T; 0 other;

Query Match 99.4%; Score 1140.2; DB 20; Length 1232;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1142; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGCTTTGGAAACAGAACAGTCAAGATTTATTTATGAGAAAAATGAATGATGCG 60  
 DB 70 ATGGCTTTGGAAACAGAACAGTCAAGATTTATTTATGAGAAAAATGAATGATGCG 129  
 QY 61 ACTTAGACATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120  
 DB 130 ACTTAGACATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 189  
 QY 121 AAGTTTCTCCCTGATTTCTTCAATAGTTTGTGATTTGATGATGATGATGATGAT 180  
 DB 190 AAGTTTCTCCCTGATTTCTTCAATAGTTTGTGATTTGATGATGATGATGATGAT 249  
 QY 181 ATGTAAGTGGCAATTTATGCTTATTTCAAGAAACAGAAACCAAAACATGATGATC 240  
 DB 250 ATGTAAGTGGCAATTTATGCTTATTTCAAGAAACAGAAACCAAAACATGATGATC 309  
 QY 241 CTGAATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 DB 310 CTGAATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 369  
 QY 301 GCACTTATGAGTGGTTTATGAGAAAAATATGATGCAAAATATCTTACGCTTTGACACA 360  
 DB 370 GCACTTATGAGTGGTTTATGAGAAAAATATGATGCAAAATATCTTACGCTTTGACACA 429

QY 361 CTAACCTTGTCTCTGAGATGCAAGTTCTGGCTGTATCAGCATAGACAGATATGTGGCA 420  
 DB 430 CTAACCTTGTCTCTGAGATGCAAGTTCTGGCTGTATCAGCATAGACAGATATGTGGCA 489  
 QY 421 GTAACCTAAGTCCCGAGCAATCAGAGTGGGAAACCATGCTGATCATCTGTTCTGT 480  
 DB 490 GTAACCTAAGTCCCGAGCAATCAGAGTGGGAAACCATGCTGATCATCTGTTCTGT 549  
 QY 481 GTCTGAGATGGCTGATCTGCTGAGATACCCGAGCTGGTTTTTTTATACAGTAATAGAC 540  
 DB 550 GTCTGAGATGGCTGATCTGCTGAGATACCCGAGCTGGTTTTTTTATACAGTAATAGAC 609  
 QY 541 AATGCTAGTGCATTTCCCATTTTCCCGCTACCTAGAAATCATATGAAGATGATT 600  
 DB 610 AATGCTAGTGCATTTCCCATTTTCCCGCTACCTAGAAATCATATGAAGATGATT 669  
 QY 601 CAATGCTAGAGATCTGATTTGGATTTGTATGATACCTTTCTTATATAGGGGGTGTCTAC 660  
 DB 670 CAATGCTAGAGATCTGATTTGGATTTGTATGATACCTTTCTTATATAGGGGGTGTCTAC 729  
 QY 661 TTTATCAGAGAGACATCATATGATGCAAAATTAATATCTGACCCCTAATAA 720  
 DB 730 TTTATCAGAGAGACATCATATGATGCAAAATTAATATCTGACCCCTAATAA 789  
 QY 721 GTTCTGCTCAAGTGTATATGTTTTCATTTGTCATGCACTGCTTATTAACATTTGCAAG 780  
 DB 790 GTTCTGCTCAAGTGTATATGTTTTCATTTGTCATGCACTGCTTATTAACATTTGCAAG 849  
 QY 781 TTTCGCGAGGCAATGATCATATCTACTCCCTGATCACCGCTGCAACATGAGCAACCG 840  
 DB 850 TTTCGCGAGGCAATGATCATATCTACTCCCTGATCACCGCTGCAACATGAGCAACCG 909  
 QY 841 ATGACATCCGCAATCCAGTCAAGAGAGATGCACTCTTTCACAGCTGCTCAACCA 900  
 DB 910 ATGACATCCGCAATCCAGTCAAGAGAGATGCACTCTTTCACAGCTGCTCAACCA 969  
 QY 901 ATCTTTATGTTTATGAGAGATCTTTCAAAAATCTATGAAAGTGGCCAAAGAA 960  
 DB 970 ATCTTTATGTTTATGAGAGATCTTTCAAAAATCTATGAAAGTGGCCAAAGAA 1029  
 QY 961 TATGGGTCCTGAGAGAGACAGACAAAGTGTGAGAGATTTCTTTATCTGAGGCT 1020  
 DB 1030 TATGGGTCCTGAGAGAGACAGACAAAGTGTGAGAGATTTCTTTATCTGAGGCT 1089  
 QY 1021 CCTACAGAGCCAAACAGTACTTTTAAAGTTAAAGTTAAAGTCTGCTCTTTGCTTG 1080  
 DB 1090 CCTACAGAGCCAAACAGTACTTTTAAAGTTAAAGTTAAAGTCTGCTCTTTGCTTG 1149  
 QY 1081 GATACATATGATGATGCTTTCCCTCAAAATTAATATCTGCTTATTTGAAAAAAA 1140  
 DB 1150 GATACATATGATGATGCTTTCCCTCAAAATTAATATCTGCTTATTTGAAAAAAA 1209  
 QY 1141 AAAAAA 1147  
 DB 1210 AAAAAA 1216  
 RESULT 3  
 AAF57686  
 ID AAF57686 strand; DNA; 1147 BP.  
 AC AAF57686;  
 XX  
 DT 29-JUN-2001 (first entry)  
 XX  
 DE Human chemokine receptor CCX CKR preliminary nucleotide sequence.  
 XX  
 KM Chemokine receptor; CCX CKR; chemokine; ELK; SLK; TECK; modulator;  
 KW antiinflammatory; immunosuppressive; cytostatic; antiallergic; human;  
 XX immunostimulant; gene therapy; ds.  
 OS Homo sapiens.  
 XX

PN W0200127146-A2.  
 PD 19-APR-2001.  
 XX  
 PF 10-OCT-2000; 2000WO-US28067.  
 XX  
 PR 12-OCT-1999; 99US-0159015.  
 PR 13-OCT-1999; 99US-0159210.  
 PR 20-DEC-1999; 99US-0172979.  
 PR 28-DEC-1999; 99US-0173389.  
 PR 03-MAR-2000; 2000US-0186626.  
 XX  
 PA (CHEM-) CHEMOCENTRIX INC.  
 XX  
 PI Gosling J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;  
 DR WPI; 2001-281975/29.  
 XX  
 PT Isolated or recombinant chemokine receptor (designated CCX CKR)  
 PT polypeptide (PI) or its fragment, useful for identifying CCX CKR  
 PT modulators which can be used in the treatment of inflammation, allergy,  
 PT an autoimmune disease or cancer -  
 XX  
 PS Claim 7; Page -; 72pp; English.  
 XX  
 CC The invention relates to an isolated or recombinant chemokine receptor  
 CC designated CCX CKR) polypeptide which binds to chemokines such as ELK,  
 CC SLK or TECK. The CCX CKR polypeptide is useful for identifying CCX CKR  
 CC modulators. An agent that modulates the activity or expression of CCX CKR  
 CC in a cell or tissue in the mammal is useful in the treatment of a CCX CKR  
 CC mediated condition such as inflammation, allergy, an autoimmune disease,  
 CC graft rejection, cancer, an infectious disease or an immunosuppressive  
 CC disease. The present sequence represents a preliminary DNA sequence of  
 CC the human CCX CKR coding sequence. This sequence differs from the CCX  
 CC CKR encoding DNA (AAF57685) at the following positions: 47, 64, 78,  
 CC 120, 131, 545, 571 and 574.  
 CC Note: the present sequence is not provided in the specification; it has  
 CC been created from the CCX CKR coding sequence with the information  
 CC provided.  
 XX  
 SQ Sequence 1147 BP; 342 A; 244 C; 225 G; 335 T; 1 other;  
 Query Match 98.8%; Score 1133.8; DB 22; Length 1147;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 1139; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 ATGCTTTGGAACGAAACCAAGTCAACGATTTATTTATGAGAAATGAATGCG 60  
 DB 1 ATGCTTTGGAACGAAACCAAGTCAACGATTTATTTATGAGAAATGAATGCG 60  
 QY 61 ACTATGACTACAGTCAATATGAACTGATCTGTATCAAAAGATGTCAAGAAATTTGCC 120  
 DB 61 ACTATGACTACAGTCAATATGAACTGATCTGTATCAAAAGATGTCAAGAAATTTGCC 120  
 QY 121 AAAGTTTCTCCCTGATTTCTCAAAATGTTTGTGCTGATTTGAGGCAATTTCC 180  
 DB 121 AAAGTTTCTCCCTGATTTCTCAAAATGTTTGTGCTGATTTGAGGCAATTTCC 180  
 QY 181 ATGCTAGTGCATTTATGCTATTTACAAAGAACAGAAACCAAAACAGATGTATC 240  
 DB 181 ATGCTAGTGCATTTATGCTATTTACAAAGAACAGAAACCAAAACAGATGTATC 240  
 QY 241 CTGAATTTGGCTGAGAGATTTACTCTTCTATCTGCTGCTTTTGGGCTGTAAAT 300  
 DB 241 CTGAATTTGGCTGAGAGATTTACTCTTCTATCTGCTGCTTTTGGGCTGTAAAT 300  
 QY 301 GCAATTCATGGGTGGTTTATGAGAAATATGTCAAAATTAATCTTCACTTTGTAACA 360  
 DB 301 GCAATTCATGGGTGGTTTATGAGAAATATGTCAAAATTAATCTTCACTTTGTAACA 360  
 QY 361 CTAACCTTGTCTCTGAGATGCAAGTTTGGCTGTATCAGCATAGACAGATATGTGGCA 420  
 DB 361 CTAACCTTGTCTCTGAGATGCAAGTTTGGCTGTATCAGCATAGACAGATATGTGGCA 420

QY 421 GTAATAAGTCCCGACCAATGAGAGTGGGAAACCATGCTGATCATCTGTTCTGT 480  
 DB 421 GTAATAAGTCCCGACCAATGAGAGTGGGAAACCATGCTGATCATCTGTTCTGT 480  
 QY 481 GTCTGAGTGGCTGCTGATCTGCTGAGATACCCAGCTGGTCTTTTATACAGTAATGAC 540  
 DB 481 GTCTGAGTGGCTGCTGATCTGCTGAGATACCCAGCTGGTCTTTTATACAGTAATGAC 540  
 QY 541 AATGCTAGTGCATCTCCATCTTCCCGCTACCTAGGAAATCATCAATGAAAGCATTTGATT 600  
 DB 541 AATGCTAGTGCATCTCCATCTTCCCGCTACCTAGGAAATCATCAATGAAAGCATTTGATT 600  
 QY 601 CAAATGCTAGATCTGATGATTTGATGATACCTTTCTTATATAGGGGGTGTCTAC 660  
 DB 601 CAAATGCTAGATCTGATGATTTGATGATACCTTTCTTATATAGGGGGTGTCTAC 660  
 QY 661 TTTATCAAGAGAGACATCATGATGAGATGCAAAATTAATCTCGACCCCTTAAA 720  
 DB 661 TTTATCAAGAGAGACATCATGATGAGATGCAAAATTAATCTCGACCCCTTAAA 720  
 QY 721 GTTCTGCTCAGTCTGTTATGATTTTCAATGCTCACTCACTGCTTATTAACATTTGCAAG 780  
 DB 721 GTTCTGCTCAGTCTGTTATGATTTTCAATGCTCACTCACTGCTTATTAACATTTGCAAG 780  
 QY 781 TTCTGCGAGCGCATAGACATCATCTCTCTGATCAACAGCTGCAACATGAGCAACGC 840  
 DB 781 TTCTGCGAGCGCATAGACATCATCTCTCTGATCAACAGCTGCAACATGAGCAACGC 840  
 QY 841 ATGACATCGGCATCGAATGAGAGAGATCGCATCTTTTCAAGCTGCTTCAACCA 900  
 DB 841 ATGACATCGGCATCGAATGAGAGAGATCGCATCTTTTCAAGCTGCTTCAACCA 900  
 QY 901 ATCTTTATGTTTATGAGAGCATCTTTCAAAAATTAAGTAAAGTGGCCAAAGAA 960  
 DB 901 ATCTTTATGTTTATGAGAGCATCTTTCAAAAATTAAGTAAAGTGGCCAAAGAA 960  
 QY 961 TATGGGTCTGGAAGAGCAGAGCAAAAGTGGAGGTTCTTTGATTTGAGAGGT 1020  
 DB 961 TATGGGTCTGGAAGAGCAGAGCAAAAGTGGAGGTTCTTTGATTTGAGAGGT 1020  
 QY 1021 CCTCAGAGCGCAACAGACTTTTGAATTAAGTAAAGTAAAGTGGCTTGTGCTTG 1080  
 DB 1021 CCTCAGAGCGCAACAGACTTTTGAATTAAGTAAAGTAAAGTGGCTTGTGCTTG 1080  
 QY 1081 GATACATATGATGATGCTTTCCCTCAATTAACATCTGCTTATTTGAAAAAAA 1140  
 DB 1081 GATACATATGATGATGCTTTCCCTCAATTAACATCTGCTTATTTGAAAAAAA 1140  
 QY 1141 AAAAAA 1147  
 DB 1141 AAAAAA 1147  
 RESULT 4  
 AAX61288  
 ID AAX61288 standard; cDNA, 1660 BP.  
 AAX61288;  
 29-JUL-1999 (first entry)  
 Human signal peptide-containing protein encoding cDNA SP-16.  
 Human; signal peptide-containing protein; SP; cell proliferation;  
 cancer; neuronal disorder; immune response; detection; ss.  
 Homo sapiens.  
 Key Location/Qualifiers  
 CDS 24..1076  
 FT /\*tag= a  
 XX

PN W09924463-A2.  
 XX 20-MAY-1999.  
 XX 04-NOV-1998; 98WO-US23578.  
 PF 07-NOV-1997; 97US-0966316.  
 PR (INCY-) INCYTE PHARM INC.  
 PA Au-Young J, Lal P, Mathur P, Murry LE, Reddy R;  
 PI WPI, 1999-337694/28.  
 DR P-PSDB; AAY17435.  
 XX CDNA clones encoding signal peptide-containing proteins  
 PS Claim 4; Fig 1; 83pp; English.  
 CC The present sequence represents a human cDNA clone encoding a signal  
 CC peptide-containing protein (SP). SP proteins can be used to stimulate  
 CC cell proliferation or to treat or prevent cancer. SP antagonists are  
 CC also used to treat or prevent cancer, and also for treating or  
 CC preventing neuronal disorders or immune responses. Polynucleotide  
 CC sequences complementary to the SP-encoding polynucleotides are useful  
 CC for the detection of SP-encoding nucleic acid molecules in biological  
 CC samples.  
 XX Sequence 1660 BP; 539 A; 320 C; 328 G; 473 T; 0 other;  
 SQ  
 Query Match 98.8%; Score 1133.6; DB 20; Length 1660;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1136; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ATGGCTTTGGAACAGACCAAGCAACAGATTTATTTATGAGAAATGAATGATGGC 60  
 DB 24 ATGGCTTTGGAACAGACCAAGCAACAGATTTATTTATGAGAAATGAATGATGGC 83  
 QY 61 ACTTATGACTAGACATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120  
 DB 84 ACTTATGACTAGACATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 143  
 QY 121 AAGTTTCTCTCTGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180  
 DB 144 AAGTTTCTCTCTGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 203  
 QY 181 ATGGTATGGCAATTTATGCTATTTACAGAAACAGAGAACCAACAGATGATGATC 240  
 DB 204 ATGGTATGGCAATTTATGCTATTTACAGAAACAGAGAACCAACAGATGATGATC 263  
 QY 241 CTGAATTTGGCTGTAGCAATTTACTCTTCTTATGATGATGATGATGATGATGATGATGAT 300  
 DB 264 CTGAATTTGGCTGTAGCAATTTACTCTTCTTATGATGATGATGATGATGATGATGATGAT 323  
 QY 301 GCAATTCATGAGTGGGTTTATGAGAAATTAATGCGAAATTAATGAGCTTGTACACA 360  
 DB 324 GCAATTCATGAGTGGGTTTATGAGAAATTAATGCGAAATTAATGAGCTTGTACACA 383  
 QY 361 CTAACTTTGTCTCTGAAATGAGCTTTGCTTGTATGATGATGATGATGATGATGATGATGAT 420  
 DB 384 CTAACTTTGTCTCTGAAATGAGCTTTGCTTGTATGATGATGATGATGATGATGATGATGAT 443  
 QY 421 GTAATAAGTCCCGACCAATGAGAGTGGGAAACCATGCTGATCATCTGTTCTGT 480  
 DB 444 GTAATAAGTCCCGACCAATGAGAGTGGGAAACCATGCTGATCATCTGTTCTGT 503  
 QY 481 GTCTGAGTGGCTGCTGATCTGCTGAGATACCCAGCTGGTCTTTTATACAGTAATGAC 540  
 DB 504 GTCTGAGTGGCTGCTGATCTGCTGAGATACCCAGCTGGTCTTTTATACAGTAATGAC 563  
 QY 541 AATGCTAGTGCATCTCCATCTTCCCGCTACCTAGGAAATCATCAATGAAAGCATTTGATT 600  
 DB 564 AATGCTAGTGCATCTCCATCTTCCCGCTACCTAGGAAATCATCAATGAAAGCATTTGATT 623

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QY 601 CAAATGCTAGAGATCTGCATTTGATGATACCTTTCTTATTTATGGGGGTGTCTAC 660
Db 624 CAAATGCTAGAGATCTGCATTTGATGATACCTTTCTTATTTATGGGGGTGTCTAC 663
QY 661 TTTATACAGAGACAGACATCATGAAGTGCACCAACTTAAATATCTGACCCCTTAAA 720
Db 684 TTTATACAGAGACAGACATCATGAAGTGCACCAACTTAAATATCTGACCCCTTAAA 743
QY 721 GTTCTGCTCAGTCTGTTATAGTTTCTGATCTGCTGCTTATTAACATTTGTAAG 780
Db 744 GTTCTGCTCAGTCTGTTATAGTTTCTGATCTGCTGCTTATTAACATTTGTAAG 803
QY 781 TTTCTGCGAGCAGATGACATCATCTACTCTCTGATCAGCTGCAACATGAGCAACGC 840
Db 804 TTTCTGCGAGCAGATGACATCATCTACTCTCTGATCAGCTGCAACATGAGCAACGC 863
QY 841 ATGACATGCGCAGATGACATCATCTACTCTCTGATCAGCTGCAACATGAGCAACGC 900
Db 864 ATGACATGCGCAGATGACATCATCTACTCTCTGATCAGCTGCAACATGAGCAACGC 923
QY 901 ATCTTATGTTTATGAGAGATCTTTCAAAAACCTAAGTGAAGTGGCCAGAAA 960
Db 924 ATCTTATGTTTATGAGAGATCTTTCAAAAACCTAAGTGAAGTGGCCAGAAA 983
QY 961 TATGGTCTCGAGAGACAGACAAAGTGTGAGAGATTTCTTTTGAATCTGAGGT 1020
Db 984 TATGGTCTCGAGAGACAGACAAAGTGTGAGAGATTTCTTTTGAATCTGAGGT 1043
QY 1021 CCGACAGAGCAACCGATCTTTTATGATTTAAAGTAAACCTGCTGCTTTTCTTG 1080
Db 1044 CCGACAGAGCAACCGATCTTTTATGATTTAAAGTAAACCTGCTGCTTTTCTTG 1103
QY 1081 GATACATATGATGATGCTTTCCCTCAATAAATCAATGCTGCTTATTCGAAAAA 1140
Db 1104 GATACATATGATGATGCTTTCCCTCAATAAATCAATGCTGCTTATTCGAAAAA 1163

RESULT 5
AAH77721
ID AAH77721 standard; cDNA, 1839 BP.
AC AAH77721;
XX
DT 13-NOV-2001 (first entry)
DE Consensus cDNA sequence of human chemokine receptor CCR11.
XX
KW Human; chemokine receptor; CCR11; G protein coupled receptor;
KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
KW asthma; angiogenesis; atherosclerosis vascular association disease;
KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
KW left ventricular diastolic dysfunction; migraine; preterm labour;
KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;
KW myocardial infarction; congestive heart failure; endometriosis;
KW vasospasm; retinopathy; neuropathy; pulmonary vascular disease; ss.
XX
OS Homo sapiens.
XX
PN WO20016598-A2.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US07073.
XX
PR 03-MAR-2000; 2000US-0186928.
XX
PR 03-MAR-2000; 2000US-0187231.
XX
PA (ICOS-) ICOS CORP.
XX
PI Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;
XX
DR WPI; 2001-541918/60.

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XX
PT An isolated polynucleotide encoding the chemokine receptor CCR11.
PT useful for treating rheumatoid arthritis, inflammatory bowel disease,
PT asthma, angiogenesis, atherosclerosis, cardiac arrhythmias, Raynaud's
PT phenomenon and migraine.
PS Example 1; Page 104-105; 110pp; English.
XX
CC The present sequence represents a consensus cDNA sequence of human
CC chemokine receptor CCR11. CCR11 is a member of the G protein coupled
CC receptor family. A CCR11 polypeptide, its inhibitor, an antibody, or
CC other modulator of CCR11 expression or biological activity, is useful
CC for treating many inflammatory diseases, for example, rheumatoid
CC arthritis, inflammatory bowel disease, and asthma. They are also
CC useful for treating angiogenesis, atherosclerosis vascular association
CC diseases which may include but are not limited to hypertension, angina
CC pectoris, cardiac arrhythmias, left ventricular diastolic dysfunction,
CC Raynaud's phenomenon, migraine, preterm labour, oesophageal spasm,
CC ischaemic stroke, subarachnoid haemorrhage, myocardial infarction,
CC congestive heart failure, endometriosis, vasospasm, retinopathy,
CC neuropathy, or pulmonary vascular disease.
SQ Sequence 1839 BP; 594 A; 355 C; 353 G; 537 T; 0 other;

Query Match          98.8%; Score 1133.6; DB 22; Length 1839;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGCTTTGGAAACGAAACCACTCAACGATTTATTTATGAGAAATGAATGATGC 60
Db 264 ATGGCTTTGGAAACGAAACCACTCAACGATTTATTTATGAGAAATGAATGATGC 323
QY 61 ACTTATGACTCAGTCAATATGAACTGATCTGATCAAGAGATGACAGAAATTTGCA 120
Db 324 ACTTATGACTCAGTCAATATGAACTGATCTGATCAAGAGATGACAGAAATTTGCA 383
QY 121 AAAGTTTCTCCTGTAATTCCTCAAAATAGTTTGTCAATGAGACTTGAGCAATTC 180
Db 384 AAAGTTTCTCCTGTAATTCCTCAAAATAGTTTGTCAATGAGACTTGAGCAATTC 443
QY 181 ATGATGAGGGAATTTATGCTATTTAACAAGAACAGAAACCAAAACAGATGTGATC 240
Db 444 ATGATGAGGGAATTTATGCTATTTAACAAGAACAGAAACCAAAACAGATGTGATC 503
QY 241 CTGAATTTGGCTGAGAGATTTACTCTCTATTCACCTGCTTTTGGGCTGTTAAT 300
Db 504 CTGAATTTGGCTGAGAGATTTACTCTCTATTCACCTGCTTTTGGGCTGTTAAT 563
QY 301 GCACTTCAATGGGTGGTGTATGAGGAAATATATGCAAAATATCTTACGCTTGAC 360
Db 564 GCACTTCAATGGGTGGTGTATGAGGAAATATATGCAAAATATCTTACGCTTGAC 623
QY 361 CTAACTTTGCTCTGGAATGCACTTTCGCTTGATGATGATACAGATATGTGGCA 420
Db 624 CTAACTTTGCTCTGGAATGCACTTTCGCTTGATGATGATACAGATATGTGGCA 683
QY 421 GTAACATAAGTCCCAAGCAGATCAGAGTGGGAAACCAATGCTGATCATCTGTTCT 480
Db 684 GTAACATAAGTCCCAAGCAGATCAGAGTGGGAAACCAATGCTGATCATCTGTTCT 743
QY 481 GTCTGATGCTGCTCATCTTGTGAGCATACCCAGCTGGTTTTTATACAGTAATG 540
Db 744 GTCTGATGCTGCTCATCTTGTGAGCATACCCAGCTGGTTTTTATACAGTAATG 803
QY 541 AATGCTAGGTGATGCTCATCTTCCCGGCTGCTAGGAAACATGAAAGATGATG 600
Db 804 AATGCTAGGTGATGCTCATCTTCCCGGCTGCTAGGAAACATGAAAGATGATG 863
QY 601 CAAATGCTAGAGATCTGCATTTGATGATACCTTTCTTATTTATGGGGGTGTCTAC 660
Db 864 CAAATGCTAGAGATCTGCATTTGATGATACCTTTCTTATTTATGGGGGTGTCTAC 923
QY 661 TTTATACAGAGACAGACATCATGAAGTGCACCAACTTAAATATCTGACCCCTTAAA 720

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DB 924 TTTATACAGACAGACATGAGATGCCAAATTAATCTGACCCCTAAAA 983  
 QY 721 GTTCTGCTCAGCTCGTTATAGTTTTCATTTGTCATCTCACTGCTTTATTAACATTGTCAAG 780  
 DB 984 GTTCTGCTCAGCTCGTTATAGTTTTCATTTGTCATCTCACTGCTTTATTAACATTGTCAAG 1043  
 QY 781 TTTCTGCCAGCCATTAACATCTCTCTCCGATGACCAAGCTGCAACATGAGCAAGCC 840  
 DB 1044 TTTCTGCCAGCCATTAACATCTCTCTCCGATGACCAAGCTGCAACATGAGCAAGCC 1103  
 QY 841 ATGAGACATGCGCATTCACAGTACAGAAAGCATGCACTCTTTTACAGCTGCTTCAACCA 900  
 DB 1104 ATGAGACATGCGCATTCACAGTACAGAAAGCATGCACTCTTTTACAGCTGCTTCAACCA 1163  
 QY 901 ATCTTTTATGTTTATGAGAGCATCTTTCAAAAATGCTATGAAAGTGCCCAAGAA 960  
 DB 1164 ATCTTTTATGTTTATGAGAGCATCTTTCAAAAATGCTATGAAAGTGCCCAAGAA 1223  
 QY 961 TATGAGCTTGGAGAGACAGACAAAGTGAGAGAGTTCTTTTATGTTGAGGGT 1020  
 DB 1224 TATGAGCTTGGAGAGACAGACAAAGTGAGAGAGTTCTTTTATGTTGAGGGT 1283  
 QY 1021 CCTACAGAGCCAAACAGTACTTTTATGATTTAAAGTAAAGTCTCTGCTTTTCTTG 1080  
 DB 1284 CCTACAGAGCCAAACAGTACTTTTATGATTTAAAGTAAAGTCTCTGCTTTTCTTG 1343  
 QY 1081 GATACATATGATGATGCTTTTCCCTCAATTAACATCTGCTTATCTGAAAAA 1140  
 DB 1344 GATACATATGATGATGCTTTTCCCTCAATTAACATCTGCTTATCTGAAAAA 1403

## RESULT 6

AAH77722 standard; DNA; 1925 BP.

AAH77722;

13-NOV-2001 (first entry)

Genomic clone of human chemokine receptor CCR11.

Human; chemokine receptor; CCR11; G protein coupled receptor;  
 inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;  
 asthma; angiodysplasia; arteriosclerosis vascular association disease;  
 hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;  
 left ventricular diastolic dysfunction; migraine; preterm labour;  
 oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;  
 myocardial infarction; congestive heart failure; endometritis;  
 vasospasm; retinopathy; nephropathy; pulmonary vascular disease; ss.

Homo sapiens.

WO200166598-A2.

13-SEP-2001.

05-MAR-2001; 2001WO-US07073.

03-MAR-2000; 2000US-0186928.

03-MAR-2000; 2000US-0187231.

(ICOS-) ICOS CORP.

Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;

WPI; 2001-541918/60.

An isolated polynucleotide encoding the chemokine receptor CCR11,  
 useful for treating rheumatoid arthritis, inflammatory bowel disease,  
 asthma, angiodysplasia, arteriosclerosis, cardiac arrhythmias, Raynaud's  
 phenomenon and migraine.

Example 1; Page 105-106; 110pp; English.

The present sequence represents a genomic clone of human chemokine  
 receptor CCR11. CCR11 is a member of the G protein coupled  
 receptor family. A CCR11 polypeptide, its inhibitor, an antibody, or  
 other modulator of CCR11 expression or biological activity, is useful  
 for treating many inflammatory diseases, for example, rheumatoid  
 arthritis, inflammatory bowel disease, and asthma. They are also  
 useful for treating angiodysplasia, arteriosclerosis vascular association  
 diseases which may include but are not limited to hypertension, angina  
 pectoris, cardiac arrhythmias, left ventricular diastolic dysfunction,  
 Raynaud's phenomenon, migraine, preterm labour, oesophageal spasm,  
 ischaemic stroke, subarachnoid haemorrhage, myocardial infarction,  
 congestive heart failure, endometritis, vasospasm, retinopathy,  
 nephropathy, or pulmonary vascular disease.

Sequence 1925 BP; 623 A; 368 C; 363 G; 571 T; 0 other;

Query Match 98.8%; Score 1133.6; DB 22; Length 1925;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1136; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCTTTGGAAAGCAACAGTCAACAGATTAATTAATGAGAAATGATGCG 60  
 DB 264 ATGCTTTGGAAAGCAACAGTCAACAGATTAATTAATGAGAAATGATGCG 323  
 QY 61 ACTTATGACTACAGTCAATTAATGAACTGATCTGATCAAGAAAGTGCAGAAATTGCA 120  
 DB 324 ACTTATGACTACAGTCAATTAATGAACTGATCTGATCAAGAAAGTGCAGAAATTGCA 383  
 QY 121 AAAGTTTCTGCTGCTGATTTCTCTCAATTAATTTGCTGATTTGCACTTGGCAATTC 180  
 DB 384 AAAGTTTCTGCTGCTGATTTCTCTCAATTAATTTGCTGATTTGCACTTGGCAATTC 443  
 QY 181 ATGATAGGCAATTTATGAGCAATTAATTAATGAGAAAGCAAGAAAGATGATGATC 240  
 DB 444 ATGATAGGCAATTTATGAGCAATTTATGAGCAATTTATGAGAAAGCAAGAAAGATGATGATC 503  
 QY 241 CTGAATTTGGCTGATGAGATTTACTCTCTTATTAATGATGCTGCTTTTGGCTGAT 300  
 DB 504 CTGAATTTGGCTGATGAGATTTACTCTCTTATTAATGATGCTGCTTTTGGCTGAT 563  
 QY 301 GCAATTCATGCTGCTGATTTAGGAAATTAATGAGCAATTAATGAGCAATTTAGCA 360  
 DB 564 GCAATTCATGCTGCTGATTTAGGAAATTAATGAGCAATTTAGCAATTTAGCA 623  
 QY 361 CTAATCTTGTCTCTGAGATGATTTGCTGCTGATTTAGCAATTTAGCAATTTAGCA 420  
 DB 624 CTAATCTTGTCTCTGAGATGATTTGCTGCTGATTTAGCAATTTAGCAATTTAGCA 683  
 QY 421 GTTACTAAAGTCCCAAGCAATCAGAGTGGAAAAACATGCTGATCATCTGTTCTGT 480  
 DB 684 GTTACTAAAGTCCCAAGCAATCAGAGTGGAAAAACATGCTGATCATCTGTTCTGT 743  
 QY 481 GTTGTGATGCTGCTGATTTGCTGAGCATTTCCCAAGCTGTTTATTAAGTAATGAC 540  
 DB 744 GTTGTGATGCTGCTGATTTGCTGAGCATTTCCCAAGCTGTTTATTAAGTAATGAC 803  
 QY 541 AATGCTAGTGCATTTCCCAATTTTCCCGCTACTAGAAACATCAATGAAAGCATGATT 600  
 DB 804 AATGCTAGTGCATTTCCCAATTTTCCCGCTACTAGAAACATCAATGAAAGCATGATT 863  
 QY 601 CAATGCTAGAGATCTGCAATTTGATGATGATGATGATGATGATGATGATGATGATG 660  
 DB 864 CAATGCTAGAGATCTGCAATTTGATGATGATGATGATGATGATGATGATGATGATG 923  
 QY 661 TTTATACAGCAAGACATCTCATGAAAGTCCCAACATTTAAATTTCTGAGCCCTAAAA 720  
 DB 924 TTTATACAGCAAGACATCTCATGAAAGTCCCAACATTTAAATTTCTGAGCCCTAAAA 983  
 QY 721 GTTCTGCTCAGCTCGTTATAGTTTTCATTTGTCATCTCACTGCTTTATTAACATTGTCAAG 780  
 DB 984 GTTCTGCTCAGCTCGTTATAGTTTTCATTTGTCATCTCACTGCTTTATTAACATTGTCAAG 1043



QY 781 TTTCGCCGAGCCATAGACATCATCTACTCCTGTATCCAGCTGCAACATGAGCAACGC 840  
 Db 1044 TTTCGCCGAGCCATAGACATCATCTACTCCTGTATCCAGCTGCAACATGAGCAACGC 1103  
 QY 841 ATGACATATGCGCATTCAGAGTACAGAGAAAGCATGCCACTCTTTTCCAGCTGCTTACCCCA 900  
 Db 1104 ATGACATATGCGCATTCAGAGTACAGAGAAAGCATGCCACTCTTTTCCAGCTGCTTACCCCA 1163  
 QY 901 ATCCCTTATGTTTTATGAGAGCATCTTTTCAAAACTACGTTATGAAGTGGCCAGAAA 960  
 Db 1164 ATCCCTTATGTTTTATGAGAGCATCTTTTCAAAACTACGTTATGAAGTGGCCAGAAA 1223  
 QY 961 TATGGCTCTTGAAGAGACAGAGACAAAGTGTGAGAGAGTTTCTTTTGAATTCGAGGT 1020  
 Db 1224 TATGGCTCTTGAAGAGACAGAGACAAAGTGTGAGAGAGTTTCTTTTGAATTCGAGGT 1283  
 QY 1021 CCTACAGAGCCACACGACTCTTTTGAAGTTAAAGTAAAGTGTGCTTGTGCTTGTG 1080  
 Db 1284 CCTACAGAGCCACACGACTCTTTTGAAGTTAAAGTAAAGTGTGCTTGTGCTTGTG 1343  
 QY 1081 GATACATATGATGATGATGCTTCCCTCAATTAATAACATCTGCTTATTCGAAAAA 1140  
 Db 1344 GATACATATGATGATGATGCTTCCCTCAATTAATAACATCTGCTTATTCGAAAAA 1403

RESULT 7  
 AAX22557  
 ID AAX22557 standard; cDNA; 2407 BP.

AC AAX22557;

DT 24-MAY-1999 (first entry)

XX Human HFI041 cDNA.

DE HFI041: G-coupled receptor; disease susceptibility; diagnosis; immunise;  
 KM treatment; FFI041 protein; gene therapy; immune response; vaccine; HIV-2;  
 KM inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;  
 KM diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;  
 KM hypotension; hypertension; urinary retention; osteoporosis; allergy;  
 KM angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;  
 KM benign prostatic hypertrophy; psychotic disorder; neurological disorder;  
 KM anxiety; manic depression; delirium; dementia; severe mental retardation;  
 KM dyskinnesia; Huntington's disease; Gilles de la Tourette's syndrome;  
 KM linkage analysis; gene mapping; human; ss.

OS Homo sapiens.

XX Key Location/Qualifiers  
 FT CDS 249..1301  
 FT /tag= a  
 FT /product= "HFI041"

PN EP899332-A2.

PD 03-MAR-1999.

PF 17-FEB-1998; 98EP-0301170.

PR 27-OCT-1997; 97US-0962922.

PR 15-AUG-1997; 97US-0055895.

PA (SMK) SMITHKLINE BEECHAM CORP.

PI Ellis CE;

DR MPI: 1999-144803/13.

DR P-PSDB; AAM93169.

XX New G-coupled receptor (HFI041) polypeptide and polynucleotide -  
 PT useful as diagnostic reagents and for prevention and treatment of  
 PT cancer, HIV infections and Parkinson's disease

XX Claim 2; Page 21-22; 27p; English.

PS This sequence encodes a G-coupled receptor, HFI041 which is useful for  
 CC diagnosing susceptibility to disease by detecting mutations in the  
 CC HFI041 gene, and can diagnose diseases associated with HFI041 protein  
 CC imbalance by determining HFI041 polypeptide expression levels. Agonists  
 CC and antagonists of the protein can be used in treatment to activate  
 CC (agonist) or inhibit (antagonist) HFI041 activity, in addition to direct  
 CC administration of antisense sequences to prevent expression, or HFI041  
 CC polynucleotides to treat conditions associated with a lack of FFI041  
 CC protein. Gene therapy may also be used to affect endogenous HFI041  
 CC polypeptide expression. HFI041 antibodies are useful for inducing an  
 CC immune response to immunise and prevent disease, and for isolating  
 CC HFI041 clones or purifying the polypeptides by affinity chromatography.  
 CC HFI041 polypeptides can be administered directly or as a vaccine to  
 CC inoculate against disease. Diseases diagnosed, prevented and treated  
 CC include bacterial, fungal, protozoan and viral infections, particularly  
 CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's  
 CC disease; acute heart failure; hypotension; hypertension; urinary  
 CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;  
 CC asthma; allergies; benign prostatic hypertrophy; and psychotic and  
 CC neurological disorders, including anxiety, schizophrenia, manic  
 CC depression, delirium, dementia, severe mental retardation and dyskinesias  
 CC such as Huntington's disease or Gilles de la Tourette's syndrome. The  
 CC HFI041 polypeptide is also useful for mapping the gene to a chromosome,  
 CC allowing gene inheritance to be studied through linkage analysis.

XX Sequence 2407 BP; 820 A; 453 C; 428 G; 706 T; 0 other;

XX Query Match 98.8%; Score 1133.6; DB 20; Length 2407;

XX Best Local Similarity 99.6%; Pred. No. 0;

XX Matches 1136; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCTTTGGAACGAGACAGCTCAACAGATTATATATGAGAAATGAATGAATGCG 60  
 Db 249 ATGCTTTGGAACGAGACAGCTCAACAGATTATATATGAGAAATGAATGAATGCG 308  
 QY 61 ACTTATGACTACAGTCAATATGAATGATCTGTATCAAGAGATGTCAGAGATTGCA 120  
 Db 309 ACTTATGACTACAGTCAATATGAATGATCTGTATCAAGAGATGTCAGAGATTGCA 368  
 QY 121 AAAGTTTCTTCCCTGTTATCTTCAATATGTTTGTCAITGGACTTGCAGCAATTC 180  
 Db 369 AAAGTTTCTTCCCTGTTATCTTCAATATGTTTGTCAITGGACTTGCAGCAATTC 428  
 QY 181 ATGGATGAGCAATTTATGCTTATTAACAAGAAACAGAAACAGATGATGATC 240  
 Db 429 ATGGATGAGCAATTTATGCTTATTAACAAGAAACAGAAACAGATGATGATC 488  
 QY 241 CTGAATTTGGCTGTAGAGATTACTCTTCTATTTCACTGTGCTTTTGGGCTGTAT 300  
 Db 489 CTGAATTTGGCTGTAGAGATTACTCTTCTATTTCACTGTGCTTTTGGGCTGTAT 548  
 QY 301 GCAAGTTATGGGTTTATGAGAAATATATGCAAAATTAATTCAAGCTTGATCACA 360  
 Db 549 GCAAGTTATGGGTTTATGAGAAATATATGCAAAATTAATTCAAGCTTGATCACA 608  
 QY 361 CTAAAGTTTGTCTGGAATGAGCTTCTGGCTTGTATGCAATGATGATGATGATG 420  
 Db 609 CTAAAGTTTGTCTGGAATGAGCTTCTGGCTTGTATGCAATGATGATGATGATG 668  
 QY 421 GTAACTAAAGTCCCAAGCAATGAGAGTGGGAAACCATGTGATGATCTGTTCTGT 480  
 Db 669 GTAACTAAAGTCCCAAGCAATGAGAGTGGGAAACCATGTGATGATCTGTTCTGT 728  
 QY 481 GTCTGATGCTGTCATCTTGTGAGATACCCAGCTGTTTATACAGTAATGAC 540  
 Db 729 GTCTGATGCTGTCATCTTGTGAGATACCCAGCTGTTTATACAGTAATGAC 788  
 QY 541 AATGCTAGTGAATGCAATTTTCCCGCTACTGTGGAACATCAATGAAGATGATT 600  
 Db 789 AATGCTAGTGAATGCAATTTTCCCGCTACTGTGGAACATCAATGAAGATGATT 848





QY 841 ATGACATGCGCATTCAGAGTCAAGAAAGATCGACCTCTTTTCAAGCTGCTCAACCA 900  
 DB 850 ATGACATGCGCATTCAGAGTCAAGAAAGATCGACCTCTTTTCAAGCTGCTCAACCA 909  
 QY 901 ATCTTTATGTTTTTATGAGGAGCATCTTTCAAAAACGTTATGAAAGTGGCCAAAGAA 960  
 DB 910 ATCTTTATGTTTTTATGAGGAGCATCTTTCAAAAACGTTATGAAAGTGGCCAAAGAA 969  
 QY 961 TATGGGCTCTGAGAGACAGACAGAAAGTGTGAGAGAGTTCTTTTGAATCTGAGGGT 1020  
 DB 970 TATGGGCTCTGAGAGACAGACAGAAAGTGTGAGAGAGTTCTTTTGAATCTGAGGGT 1029  
 QY 1021 CTTCAGAGCCACACGACTCTTTTGAATTTAAAGTAAACGTCCTGCTTTTGGTTG 1080  
 DB 1030 CTTCAGAGCCACACGACTCTTTTGAATTTAAAGTAAACGTCCTGCTTTTGGTTG 1089  
 QY 1081 GATCATATGATATGATGCTTTCCCTCAATTAACATCTGCTTATTTCTGAAAAA 1140  
 DB 1090 GATCATATGATATGATGCTTTCCCTCAATTAACATCTGCTTATTTCTGAAAAA 1149  
 QY 1141 A 1141  
 DB 1150 A 1150

RESULT 9  
 AAS98075 standard; DNA; 1800 BP.  
 ID AAS98075  
 AC AAS98075;  
 XX  
 DT 12-MAR-2002 (first entry)  
 DE Human DNA for potential G protein-coupled receptor #32.  
 XX  
 XX Human: G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor;  
 KM Alzheimer's disease; amyotrophic lateral sclerosis; asthma;  
 KM atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy;  
 KM chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;  
 KM depression; epilepsy; macular degeneration; lymphoma; melanoma;  
 KM multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;  
 KM psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;  
 KM tuberculous; cognition disorder; memory disorder; anorexia;  
 KM hormonal release disorder; cardiovascular activity disorder;  
 KM pain perception disorder; obesity; diabetes; obesity;  
 KM diabetes; hyperlipidaemia; stroke; gene therapy.  
 OS Homo sapiens.  
 XX  
 XX WO200185791-A1.  
 PN 15-NOV-2001.  
 PD 11-MAY-2001; 2001WO-US15332.  
 PF 11-MAY-2000; 2000US-203217P.  
 PR 18-MAY-2000; 2000US-205945P.  
 XX  
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
 PA Brown JP, Miller M, Burner G, Fabre-Suver C, Pritchard D;  
 PI WPI; 2002-066595/09.  
 DR Novel G protein-coupled receptor polypeptides including galanin  
 PT receptor polypeptides useful for identifying modulators that are useful  
 PT for treating Alzheimer's disease, psoriasis, melanoma, multiple  
 PT sclerosis, stroke  
 PS Disclosure; Page 134-135; 144pp; English.  
 XX The invention relates to an isolated polypeptide encoded by a  
 CC nucleic acid molecule that is at least 80% identical to the G

CC protein-coupled (GPCR) polynucleotides included in the specification.  
 CC Also included are probes based on the GPCR sequences (including  
 CC antisense probes), a host cell comprising an expression vector comprising  
 CC the GPCR sequence, antibodies raised against the polypeptides,  
 CC and methods of identifying modulators of the polypeptides. The  
 CC function as modulators, activators, repressors, agonists or antagonists  
 CC of the novel GPCR polypeptides including the GAL4 polypeptide. The  
 CC antibodies and nucleic acid probes as described above can be used to  
 CC detect the presence of the polypeptides and nucleic acids and are used to  
 CC diagnose a variety of diseases or disorders in which GPCRs are involved  
 CC e.g., Alzheimer's disease, amyotrophic lateral sclerosis, asthma,  
 CC atherosclerosis, basal cell carcinoma, breast carcinoma, cardiomyopathy,  
 CC chondrosarcoma, chronic obstructive pulmonary disease, Crohn's disease,  
 CC depression, epilepsy, macular degeneration, lymphoma, melanoma,  
 CC multiple sclerosis, osteoarthritis, osteoporosis, Parkinson's disease,  
 CC psoriasis, rheumatoid arthritis, schizophrenia, ulcerative colitis,  
 CC tuberculous and many other diseases listed in the specification. The  
 CC probes and antibodies are also useful for diagnosing cognition and memory  
 CC disorders, anorexia, hormonal release disorders, cardiovascular activity  
 CC disorders, pain perception disorders, obesity, diabetes, Alzheimer's  
 CC disease. Preferably, compounds that decrease or increase  
 CC the expression of galanin receptor (GAL4) can be used to treat obesity,  
 CC diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is  
 CC useful for treating the above mentioned disorders by gene therapy  
 CC techniques. The present sequence is a novel GPCR polynucleotide of the  
 CC invention.  
 CC  
 XX Sequence 1800 BP; 579 A; 345 C; 341 G; 535 T; 0 other;  
 QY  
 Query Match 98.7%; Score 1132; DB 24; Length 1800;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1135; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 ATGCTTTGGAGAACAGACCACTCAACGATATATATGAGAAATGAATGAATGCG 60  
 DB 41 ATGCTTTGGAGAACAGACCACTCAACGATATATATGAGAAATGAATGAATGCG 100  
 QY 61 ACTTATGACTCAGCATATATGATGATCTGTATCAAGAAAGTGCAGAAATTTGCA 120  
 DB 101 ACTTATGACTCAGCATATATGATGATCTGTATCAAGAAAGTGCAGAAATTTGCA 160  
 QY 121 AAAGTTTCTCCCTGTATTTCTGCAAAATGTTTGTCAATGAGCTTGACGCAATTC 180  
 DB 161 AAAGTTTCTCCCTGTATTTCTGCAAAATGTTTGTCAATGAGCTTGACGCAATTC 220  
 QY 181 ATGCTAGTGGCAATTTATGCTATTTACAGAAAGAACCAAAACAGATGTGTATATC 240  
 DB 221 ATGCTAGTGGCAATTTATGCTATTTACAGAAAGAACCAAAACAGATGTGTATATC 280  
 QY 241 CTGAATTTGGCTGAGAGATTTACTCTTCTATTTACTGCTTTTGGGCTGTATAT 300  
 DB 281 CTGAATTTGGCTGAGAGATTTACTCTTCTATTTACTGCTTTTGGGCTGTATAT 340  
 QY 301 GCAATTTGGGCTGAGAGATTTTAAAGAAATATATGCAAAATTAATCTGAGCTTTGAC 360  
 DB 341 GCAATTTGGGCTGAGAGATTTTAAAGAAATATATGCAAAATTAATCTGAGCTTTGAC 400  
 QY 361 CTAAACTTTGCTCTGAGAAAGCACTTTCTGCTGTATGAGCAATATATGAGCA 420  
 DB 401 CTAAACTTTGCTCTGAGAAAGCACTTTCTGCTGTATGAGCAATATATGAGCA 460  
 QY 421 GTAACATAAGTCCCAACCAATCAGAGTGGGAAACCATGCTGATCATCTTTCTGT 480  
 DB 461 GTAACATAAGTCCCAACCAATCAGAGTGGGAAACCATGCTGATCATCTTTCTGT 520  
 QY 481 GTCTGATGCTGCTGATCTTCTGAGCAATCCCAAGCTGTTTTTTATACAGTAATGAC 540  
 DB 521 GTCTGATGCTGCTGATCTTCTGAGCAATCCCAAGCTGTTTTTTATACAGTAATGAC 580  
 QY 541 AATGCTAGTGCATTTCCATTTTCCCGCTACTAGAGAACATCAATGAAGATTTGAT 600  
 DB 581 AATGCTAGTGCATTTCCATTTTCCCGCTACTAGAGAACATCAATGAAGATTTGAT 640



Db 744 TTTATCAGACAGACAGACCTATGAAAGTCCAAAACATTAATATCTCGACCCCTTAAAA 803  
 Qy 721 GTTGTGCTCAGACAGTCTTATATAGTTTTCATTTGCTCACTCACTGCTTAAACATTTGCAAG 780  
 Db 804 GTTGTGCTCAGACAGTCTTATATAGTTTTCATTTGCTCACTCACTGCTTAAACATTTGCAAG 863  
 Qy 781 TTTGTGCGAGCCATAGACATATCTCTCTGATCAGCTGCAACATGAGCAAAAGCC 840  
 Db 864 TTTGTGCGAGCCATAGACATATCTCTCTGATCAGCTGCAACATGAGCAAAAGCC 923  
 Qy 841 ATGACATCGGCATCGACATGACAGAAAGCATGCTTTCAGCTGCTCAACCCA 900  
 Db 924 ATGACATCGGCATCGACATGACAGAAAGCATGCTTTCAGCTGCTCAACCCA 983  
 Qy 901 ATCTTTATGTTTTTATGAGAGCATCTTTCAAAAACATGTTATGAAAGTGGCCAAAGAA 960  
 Db 984 ATCTTTATGTTTTTATGAGAGCATCTTTCAAAAACATGTTATGAAAGTGGCCAAAGAA 1043  
 Qy 961 TATGGGTCCTGAGAGACAGACAGAAAGTGTGAGAGATTTCTTTGATTTGAGGGT 1020  
 Db 1044 TATGGGTCCTGAGAGACAGACAGAAAGTGTGAGAGATTTCTTTGATTTGAGGGT 1103  
 Qy 1021 CCTACAGAGCCACAGACATCTTTAGCATTTAAAGTAAAGTCTGCTTGGCTTGG 1080  
 Db 1104 CCTACAGAGCCACAGACATCTTTAGCATTTAAAGTAAAGTCTGCTTGGCTTGG 1163  
 Qy 1081 GATACATATGATGATGATGCTTCCCTCAAAATAAACATGCTCTTATTTGAAAAAAA 1140  
 Db 1164 GATACATATGATGATGATGCTTCCCTCAAAATAAACATGCTCTTATTTGAAAAA 1223

RESULT 11  
 AAX22558 standard; cDNA; 2156 BP.  
 AAX22558;  
 24-MAY-1999 (first entry)

Human HPIA041 cDNA.  
 HPIA041; G-coupled receptor; disease susceptibility; diagnosis; immunise; treatment; F10A41 protein; gene therapy; immune response; vaccine; HIV-2; inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer; diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; allergy; angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia; benign prostatic hypertrophy; psychotic disorder; neurological disorder; anxiety; manic depression; delirium; dementia; severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; linkage analysis; gene mapping; human; ss.  
 Homo sapiens.  
 EP899332-A2.  
 03-MAR-1999.  
 17-FEB-1998; 98BP-0301170.  
 27-OCT-1997; 97US-0962822.  
 15-AUG-1997; 97US-0055895.  
 (SMK) SMITHKLINE BEECHAM CORP.  
 Ellis CE;  
 WPI, 1999-144803/13.  
 P-PSDB; AAW93170.  
 New G-coupled receptor (HPIA041) polypeptide and polynucleotide - useful as diagnostic reagents and for prevention and treatment of cancer, HIV infections and Parkinson's disease

XX Disclosure; Page 24; 27p; English.  
 PS This sequence encodes a G-coupled receptor, HPIA041 which is useful for  
 CC diagnosing susceptibility to diseases by detecting mutations in the  
 CC HPIA041 gene, and can diagnose diseases associated with HPIA041 protein  
 CC imbalance by determining HPIA041 polypeptide expression levels. Agonists  
 CC and antagonists of the protein can be used in treatment to activate  
 CC (agonist) or inhibit (antagonist) HPIA041 activity, in addition to direct  
 CC administration of antisense sequences to prevent expression, or HPIA041  
 CC polynucleotides to treat conditions associated with a lack of HPIA041  
 CC protein. Gene therapy may also be used to affect endogenous HPIA041  
 CC polypeptide expression. HPIA041 antibodies are useful for inducing an  
 CC immune response to immunise and prevent disease, and for isolating  
 CC HPIA041 clones or purifying the polypeptides by affinity chromatography.  
 CC HPIA041 polypeptides can be administered directly or as a vaccine to  
 CC inoculate against disease. Diseases diagnosed, prevented and treated  
 CC include bacterial, fungal, protozoan and viral infections, particularly  
 CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's  
 CC disease; acute heart failure; hypotension; hypertension; urinary  
 CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;  
 CC asthma; allergies; benign prostatic hypertrophy; and psychotic and  
 CC neurological disorders, including anxiety, schizophrenia, manic  
 CC depression, delirium, dementia, severe mental retardation and dyskinesias  
 CC such as Huntington's disease or Gilles de la Tourette's syndrome. The  
 CC HPIA041 polypeptide is also useful for mapping the gene to a chromosome,  
 CC allowing gene inheritance to be studied through linkage analysis.  
 XX Sequence 2156 BP; 726 A; 399 C; 367 G; 664 T; 0 other;

Query Match 98.6%; Score 1130.6; DB 20; Length 2156;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1133; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCTTGGAAAGACAGACAGATTTATATAGGAAATGAAATGAGACT 63  
 Db 1 GCTTGGAAAGACAGACAGATTTATATATAGGAAATGAAATGAGACT 60  
 Qy 64 TATGACTACAGTCAATATGAACTGATCTGATCAAAAGATGACAGAAATTTGCAAA 123  
 Db 61 TATGACTACAGTCAATATGAACTGATCTGATCAAAAGATGACAGAAATTTGCAAA 120  
 Qy 124 GTTTTCTCTCCCTGATTTCTCAATAGTTTCTCATTTGAGACTTGGACATTCATG 183  
 Db 121 GTTTTCTCTCCCTGATTTCTCAATAGTTTCTCATTTGAGACTTGGACATTCATG 180  
 Qy 184 GAGAGGCAATTTTGGCTATTATCAAGAAACAGAAACCAACAGATGTCATCTG 243  
 Db 181 GAGAGGCAATTTTGGCTATTATCAAGAAACAGAAACCAACAGATGTCATCTG 240  
 Qy 244 AATTTGGCTGAGAGATTTACTCTCTTATTCACCTGCTTTTGGGCTGTTAATGCA 303  
 Db 241 AATTTGGCTGAGAGATTTACTCTCTTATTCACCTGCTTTTGGGCTGTTAATGCA 300  
 Qy 304 GTTCATGGGTTGGTTTATGAGAAATATATGCAAAATTAATTCAGCTTGTACACACT 363  
 Db 301 GTTCATGGGTTGGTTTATGAGAAATATATGCAAAATTAATTCAGCTTGTACACACT 360  
 Qy 364 AACTTTGCTCTGAAATGAGATTTCTGCTTGTATGCAATAGATTTGAGGAGTA 423  
 Db 361 AACTTTGCTCTGAAATGAGATTTCTGCTTGTATGCAATAGATTTGAGGAGTA 420  
 Qy 424 ACTAAAGTCCCAAGCCATGAGAGTGGGAAACCAATGCTGATCATCTGTTCTGTGTC 483  
 Db 421 ACTAAAGTCCCAAGCCATGAGAGTGGGAAACCAATGCTGATCATCTGTTCTGTGTC 480  
 Qy 484 TGAATGCTGCTCATCTTCTGAGCATACCCAGCTGTTTATACAGTAATGACAAAT 543  
 Db 481 TGAATGCTGCTCATCTTCTGAGCATACCCAGCTGTTTATACAGTAATGACAAAT 540  
 Qy 544 GCTAGGTGCAATTCATTTTCCCGCTACTAGGAACATCAATGAAGATGATTTCA 603  
 Db 541 GCTAGGTGCAATTCATTTTCCCGCTACTAGGAACATCAATGAAGATGATTTCA 600



Db 768 CAAATGCTAGAGATCTGACATTTGTTAGTACCTTTCTTATTTATGAGGGGTGCTTAC 827  
 Qy 661 TTATTCACAGAGACACTCATGAAAGTGGCAAAATTAAATATCTCCAGCCCTTAAA 720  
 Db 828 TTATTCACAGAGACACTCATGAAAGTGGCAAAATTAAATATCTCCAGCCCTTAAA 887  
 Qy 721 GTTCTGCTCAGAGTCTTATAGTTTTCATTTGTCATCTCACTGCTTAAATTTGTCAG 780  
 Db 888 GTTCTGCTCAGAGTCTTATAGTTTTCATTTGTCATCTCACTGCTTAAATTTGTCAG 947  
 Qy 781 TTTCGCGAGGACATGACATCTACTCTCTGATTCACAGCTGCAACATGAGCAAAAGC 840  
 Db 948 TTTCGCGAGGACATGACATCTACTCTCTGATTCACAGCTGCAACATGAGCAAAAGC 1007  
 Qy 841 ATGACATCCGCTCATTCAGATTCAGAAAGATCCGCTTTTCAAGCTGCTCAACCCA 900  
 Db 1008 ATGACATCCGCTCATTCAGATTCAGAAAGATCCGCTTTTCAAGCTGCTCAACCCA 1067  
 Qy 901 ATCTTTATGTTTATGAGAGATCTTTCAAAAATGATGAAAGTGGCCAAAGAA 960  
 Db 1068 ATCTTTATGTTTATGAGAGATCTTTCAAAAATGATGAAAGTGGCCAAAGAA 1127  
 Qy 961 TATGGGCTCGAGAGACAGAGCAAAAGTGGAGAGGTTGCTTTGATTTGAGGGT 1020  
 Db 1128 TATGGGCTCGAGAGACAGAGCAAAAGTGGAGAGGTTGCTTTGATTTGAGGGT 1187  
 Qy 1021 CCTACAGAGCAACAGTACTTTTATGATTTAAAGTAAAGTCTGCTGCTTTGCTTG 1080  
 Db 1188 CCTACAGAGCAACAGTACTTTTATGATTTAAAGTAAAGTCTGCTGCTTTGCTTG 1247  
 Qy 1081 GATTCATATGATGATGCTTTCCCTCAAAATTAATCAATCTGCTTATTTGAAAAAAA 1140  
 Db 1248 GATTCATATGATGATGCTTTCCCTCAAAATTAATCAATCTGCTTATTTGAAAAAAA 1307

RESULT 13  
 AAS14572  
 ID AAS14572 standard; cDNA; 1113 BP.  
 AC AAS14572;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Human cDNA encoding G protein-coupled receptor, GPCR, 2389.  
 XX  
 KW Human; ss; GPCR; G protein-coupled receptor; 2389; cardiant;  
 KW antithrombotic; analgesic; cytoprotective; antiangiogenic;  
 KW cardiovascular disorder; angiogenesis-related disorder;  
 KW neural disorder; pain response disorder; inflammatory disorder;  
 KW atherosclerosis; angina pectoris; myocardial infarction;  
 KW ischaemic heart disease; sudden cardiac death; obesity;  
 KW hypertensive heart disease; diabetes; prostate cancer-related pain.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..1053  
 FT CDS /tag= a  
 FT /product= "GPCR2398"  
 FT /note= "This region is specifically claimed in  
 claim 2"

WO200164882-A2.  
 07-SEP-2001.  
 28-FEB-2001; 2001WO-US06543.  
 29-FEB-2000; 2000US-186059P.  
 (MILL-) MILLENNIUM PHARM INC.  
 Glucksmann MA, Galvin KM, Siles-Santiago I;

XX  
 DR WPI: 2001-589866/66.  
 DR P-PSDB; AAU08994.  
 XX  
 PT Novel G protein coupled receptors and nucleic acids encoding them, for  
 FT identifying agents for the treatment of cardiac disorders  
 PS  
 XX  
 PS  
 XX  
 CC The invention relates to novel human G protein-coupled receptors (GPCR)  
 CC named 1983, 52881, 2399, 45449, 50289 and 52872. The novel GPCRs and  
 CC nucleic acids encoding them are useful for identifying agents for the  
 CC treatment of cardiovascular disorders, angiogenesis-related disorders,  
 CC neural disorders, pain response disorders and inflammatory disorders  
 CC e.g. atherosclerosis, angina pectoris and myocardial infarction,  
 CC ischaemic heart disease, sudden cardiac death, hypertensive heart  
 CC disease, diabetes, prostate cancer-related pain, diabetes and obesity.  
 CC The present sequence encodes GPCR 2398.  
 XX  
 SQ Sequence 1113 BP; 325 A; 239 C; 220 G; 329 T; 0 other;

Query Match 97.0%; Score 1113; DB 22; Length 1113;  
 Best Local Similarity 100.0%; Pred. No. 9, 8e-314;  
 Matches 1113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTTTGGAACAGAACAGTCAACAGATTTATTTATGAGAAATGAAATGAGGC 60  
 Db 1 ATGCTTTGGAACAGAACAGTCAACAGATTTATTTATGAGAAATGAAATGAGGC 60  
 Qy 61 ACTTATGACATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120  
 Db 61 ACTTATGACATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120  
 Qy 121 AAAGTTTCCCTCCCTGATTTCTGCAAAATGTTTCTGCAATGAGACTTGAGGCAATTC 180  
 Db 121 AAAGTTTCCCTCCCTGATTTCTGCAAAATGTTTCTGCAATGAGACTTGAGGCAATTC 180  
 Qy 181 ATGAGTATGCAATTTATGCTTATTTACAGAAACAGAAACAGAAACAGATGATGATC 240  
 Db 181 ATGAGTATGCAATTTATGCTTATTTACAGAAACAGAAACAGAAACAGATGATGATC 240  
 Qy 241 CTGAATTTGCTGATGAGATTTATCTCTTATTTATCTGCTGCTTTTGGGCTGTTAAT 300  
 Db 241 CTGAATTTGCTGATGAGATTTATCTCTTATTTATCTGCTGCTTTTGGGCTGTTAAT 300  
 Qy 301 GCAATGATGAGGATGATTTAGGAAATATGCAAAATTAATCTTACAGCTTGTACACA 360  
 Db 301 GCAATGATGAGGATGATTTAGGAAATATGCAAAATTAATCTTACAGCTTGTACACA 360  
 Qy 361 CTAAATCTTGTCTGCAATGATGATTTCTGCTTGTATGATGATGATGATGATGATGAT 420  
 Db 361 CTAAATCTTGTCTGCAATGATGATTTCTGCTTGTATGATGATGATGATGATGATGAT 420  
 Qy 421 GTAATCTAAAGTCCCGACCAATCAGAGTGGGAAACCATGCTGATCATCTGTTCTGT 480  
 Db 421 GTAATCTAAAGTCCCGACCAATCAGAGTGGGAAACCATGCTGATCATCTGTTCTGT 480  
 Qy 481 GTCTGATGAGGCTGATCTGCTGAGCATCCCGAGTGGTTTATTAAGTAATGATGAT 540  
 Db 481 GTCTGATGAGGCTGATCTGCTGAGCATCCCGAGTGGTTTATTAAGTAATGATGAT 540  
 Qy 541 AATGCTAGTGCATTTCCATTTTCCCGCTACCTAGCAACATCAATGAAAGATGAT 600  
 Db 541 AATGCTAGTGCATTTCCATTTTCCCGCTACCTAGCAACATCAATGAAAGATGAT 600  
 Qy 601 CAAATGCTAGAGATCTGATGATTTGATGATCCCTTTCTTATTTATGAGGGGTGCTAC 660  
 Db 601 CAAATGCTAGAGATCTGATGATTTGATGATCCCTTTCTTATTTATGAGGGGTGCTAC 660  
 Qy 661 TTATTCACAGAGACACTCATGAAAGTGGCAAAATTAAATATCTCCAGCCCTTAAA 720  
 Db 661 TTATTCACAGAGACACTCATGAAAGTGGCAAAATTAAATATCTCCAGCCCTTAAA 720

QY 721 GTTCTGCTCAGTCGTTATAGTTTTCATTTGTCACCTCAATGCTTATTAACATTGTCAG 780  
 DB 721 GTTCTGCTCAGTCGTTATAGTTTTCATTTGTCACCTCAATGCTTATTAACATTGTCAG 780  
 QY 781 TTTCGCCGAGCCATAGACATCATCTACTCCCTGATCCAGCTGCAACATGAGCAAAAGC 840  
 DB 781 TTTCGCCGAGCCATAGACATCATCTACTCCCTGATCCAGCTGCAACATGAGCAAAAGC 840  
 QY 841 ATGACATCCGCTCAGTCACAGAAAGATGGCACTCTTTTCAACGCGCCCTCAACCCA 900  
 DB 841 ATGACATCCGCTCAGTCACAGAAAGATGGCACTCTTTTCAACGCGCCCTCAACCCA 900  
 QY 901 ATCTTTATGTTTATAGGGAGCATCTTTCAAAAATACGTTATGAAAGTGGCCAAAGAA 960  
 DB 901 ATCTTTATGTTTATAGGGAGCATCTTTCAAAAATACGTTATGAAAGTGGCCAAAGAA 960  
 QY 961 TATGGGTCTGAGAGAGACAGAGCAAAAGTGGAGAGTTTCTTTTGAATTCGAGGGT 1020  
 DB 961 TATGGGTCTGAGAGAGACAGAGCAAAAGTGGAGAGTTTCTTTTGAATTCGAGGGT 1020  
 QY 1021 CTTACAGAGCCACCATGACTTTTATGATTTAAAGTAAAGTAAAGTCTGCTTTGCTTG 1080  
 DB 1021 CTTACAGAGCCACCATGACTTTTATGATTTAAAGTAAAGTAAAGTCTGCTTTGCTTG 1080  
 QY 1081 GATACATATGATGATGCTTTCCCTCAATTA 1113  
 DB 1081 GATACATATGATGATGCTTTCCCTCAATTA 1113

## RESULT 14

AAH77720 standard; cDNA; 1150 BP.

AAH77720;

13-NOV-2001 (first entry)

Nucleotide sequence of human chemokine receptor CCR11 cDNA clone.

Human; chemokine receptor; CCR11; G protein coupled receptor;  
 inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;  
 asthma; angiodenesis; arteriosclerosis; vascular association disease;  
 hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;  
 left ventricular diastolic dysfunction; migraine; preterm labour;  
 oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;  
 myocardial infarction; congestive heart failure; endometriosis;  
 vasospasm; retinopathy; nephropathy; pulmonary vascular disease; ss.

Homo sapiens.

W0200166598-A2.

13-SEP-2001.

05-MAR-2001; 2001WO-US07073.

03-MAR-2000; 2000US-0186928.

03-MAR-2000; 2000US-0187231.

(ICOS-) ICOS CORP.

Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;

WPI; 2001-541918/60.

An isolated polynucleotide encoding the chemokine receptor CCR11,  
 useful for treating rheumatoid arthritis, inflammatory bowel disease,  
 asthma, angiodenesis, arteriosclerosis, cardiac arrhythmias, Raynaud's  
 phenomenon and migraine -

Example 1; Page 103-104; 110pp; English.

AAH77715-20 represent cDNA clones of human chemokine receptor CCR11.

CC CCR11 is a member of the G protein coupled receptor family. A CCR11  
 polypeptide, its inhibitor, an antibody, or other modulator of CCR11  
 expression or biological activity, is useful for treating many  
 inflammatory diseases, for example, rheumatoid arthritis, inflammatory  
 bowel disease, and asthma. They are also useful for treating  
 angiodenesis, arteriosclerosis, vascular association diseases which may  
 include but are not limited to hypertension, angina pectoris, cardiac  
 arrhythmias, left ventricular diastolic dysfunction, Raynaud's  
 phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic  
 stroke, subarachnoid haemorrhage, myocardial infarction, congestive  
 heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or  
 pulmonary vascular disease.

Sequence 1150 BP; 335 A; 246 C; 232 G; 337 T; 0 other;

Query Match 95.1%; Score 1090.6; DB 22; Length 1150;  
 Best Local Similarity 99.6%; Pred. No. 3,36-307;  
 Matches 1093; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 44 AAAATGAATGATGAGCACTTATGACTACAGTCAATATGAATGATCTGATCAAGAG 103  
 DB 1 AAAATGAATGATGAGCACTTATGACTACAGTCAATATGAATGATCTGATCAAGAG 60  
 QY 104 ATGCAAGAAATTTGCAAAAGTTTCTCCCTGATTTCTGCAATATGATTTGCTATG 163  
 DB 61 ATGCAAGAAATTTGCAAAAGTTTCTCCCTGATTTCTGCAATATGATTTGCTATG 120  
 QY 164 GACTTGAGGCAATTTCCATGGAGTGGCAATTTATGCTTATTAAGAAAGAGAACCA 223  
 DB 121 GACTTGAGGCAATTTCCATGGAGTGGCAATTTATGCTTATTAAGAAAGAGAACCA 180  
 QY 224 AAACAGATGTATGATCTGAAATTTGGCTGTAGAGATTTACTCTTATTAATCTGCTG 283  
 DB 181 AAACAGATGTATGATCTGAAATTTGGCTGTAGAGATTTACTCTTATTAATCTGCTG 240  
 QY 284 CTTTGGGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 343  
 DB 241 CTTTGGGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
 QY 344 CTTGAGCCTTTGACACACTAACTTTGCTCTGAGATGCAATTTCTGCTGTATGACCA 403  
 DB 301 CTTGAGCCTTTGACACACTAACTTTGCTCTGAGATGCAATTTCTGCTGTATGACCA 360  
 QY 404 TAGACAGATGTATGAGCACTTAAAGTCCAGCAATGAGATGAGGAAACCATGCT 463  
 DB 361 TAGACAGATGTATGAGCACTTAAAGTCCAGCAATGAGATGAGGAAACCATGCT 420  
 QY 464 GGATCATCTGTTTCTGCTGAGTGGCTGCAATGCTGCTGAGCATGCCAGCTGGTT 523  
 DB 421 GGATCATCTGTTTCTGCTGAGTGGCTGCAATGCTGCTGAGCATGCCAGCTGGTT 480  
 QY 524 TTATACAGTAATGACATGCTAGTGATTCGATTTTCCCGCTACCTAGAACAT 583  
 DB 481 TTATACAGTAATGACATGCTAGTGATTCGATTTTCCCGCTACCTAGAACAT 540  
 QY 584 CAATGAAGCATTTGATTAAGTCTAGATCTGATTTGATTTGATGATTTGATTTGATTT 643  
 DB 541 CAATGAAGCATTTGATTAAGTCTAGATCTGATTTGATTTGATTTGATTTGATTTGATTT 600  
 QY 644 TTATGGGGGTGCTCTTATCAAGCAAGGACATGATGAAGATGCAACATTTAAA 703  
 DB 601 TTATGGGGGTGCTCTTATCAAGCAAGGACATGATGAAGATGCAACATTTAAA 660  
 QY 704 TATCTGAGCCCTAAAGTTTCTGCTCAGAGTGGTATATGATTTTCTGCTCAATGCTG 763  
 DB 661 TATCTGAGCCCTAAAGTTTCTGCTCAGAGTGGTATATGATTTTCTGCTCAATGCTG 720  
 QY 764 CTTATTAACATTTGCAAGTTTCTGCTCAGAGTGGTATATGATTTTCTGCTCAATGCTG 823  
 DB 721 CTTATTAACATTTGCAAGTTTCTGCTCAGAGTGGTATATGATTTTCTGCTCAATGCTG 780  
 QY 824 GCAACATGAGCAAGCATGAGCATGCAAGTCAAGTCAAGAAAGCATGCACTTTTC 883



Db 781 GCACATGAGCAAGCATGACATCCCAATCCAACTGACAGAAAGCATGCACTTTTC 840  
QY 884 ACAGCTGCTCAACCCATCCTTATGTTTATGAGAGATCTTAAAGACAGCTTA 943  
Db 841 ACAGCTGCTCAACCCATCCTTATGTTTATGAGAGATCTTAAAGACAGCTTA 900  
QY 944 TGAAGTGGCCAGAAATATGGTCTCGAGAGACAGACAAAGTGTGAGAGTTTC 1003  
Db 901 TGAAGTGGCCAGAAATATGGTCTCGAGAGACAGACAAAGTGTGAGAGTTTC 960  
QY 1004 CTTTGTATTCGAGGGTCTTACAGAGCCAACTACTTTTACATTTAAAGTAAACT 1063  
Db 961 CTTTGTATTCGAGGGTCTTACAGAGCCAACTACTTTTACATTTAAAGTAAACT 1020  
QY 1064 GCTTCGCTTTTGGTTGGATATCATATGAATGATGCTTCCCTCAATAAATCAATCGCC 1123  
Db 1021 GCTTCGCTTTTGGTTGGATATCATATGAATGATGCTTCCCTCAATAAATCAATCGCA 1080  
QY 1124 TTATTTGAAAAAATAA 1140  
Db 1081 TTATTTGAAAACTCAA 1097

## RESULT 15

AAZ90527 standard; cDNA; 1130 BP.

AAZ90527;

05-JUN-2000 (first entry)

Human BGCKr partial cDNA sequence.

XX BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;  
XX cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;  
XX anti-allergic; antiviral; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 19..1020

FT /-tag= a

PN WO952945-A2.

PD 21-OCT-1999.

PF 16-APR-1999; 99WO-US08395.

PR 16-APR-1998; 98US-0061753.

PR 16-APR-1999; 99US-0061753.

PA (MILL-) MILLENIUM PHARM INC.

PI Gonzalo JA, Gutierrez-Ramos JC;

DR WPI; 1999-620375/53.

DR P-PSDB; AAY57289.

XX New nucleic acid encoding human BGCKr receptor, used e.g. for  
XX modulating inflammation and tumor growth  
XX  
XX Example 1; Fig 1A-B; 123bp; English.

XX The invention relates to a human BGCKr protein, a G-protein coupled  
XX receptor. The BGCKr protein can be expressed by standard recombinant  
XX methodology. BGCKr are receptor proteins possibly involved in modulation  
XX of proinflammatory or stimulatory functions of chemokines; cell  
XX proliferation, migration, adhesion and targeting, and exocytosis. The  
XX BGCKr nucleic acids and derived proteins (or their variants), antibodies  
XX and modulators are potentially useful for modulating inflammation;  
XX chemotactant activity of leucocytes; angiogenesis; cell proliferation;  
XX tumor growth; allergic reactions and entry of human immune deficiency

CC virus into cells, for therapeutic or prophylactic purposes. They are also  
CC used for diagnosis and in drug-screening assays. The present sequence  
CC represents the cDNA sequence of a partial human BGCKr clone.  
XX  
SQ Sequence 1130 BP; 331 A; 251 C; 222 G; 326 T; 0 other;

Query Match 95.0%; Score 1090.2; DB 20; Length 1130;  
Best Local Similarity 99.5%; Pred. No. 4.3e-307;  
Matches 1092; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 51 AATGATGACCTTATGACTAGTCAATATGAACTGATCTGATCAAGAAAGTGTGAG 110  
Db 18 AATGATGACCTTATGACTAGTCAATATGAACTGATCTGATCAAGAAAGTGTGAG 77  
QY 111 AGAATTTGCAAAAGTTTCCCTGATATTCCTACAAATAGTTTTCGATGGAATTGC 170  
Db 78 AGAATTTGCAAAAGTTTCCCTGATATTCCTACAAATAGTTTTCGATGGAATTGC 137  
QY 171 AGGCAATTCATGGTAGTGGCAATTTATGCTTATTAAGAAAGAGAAACCAAAAGCA 230  
Db 138 AGGCAATTCATGGTAGTGGCAATTTATGCTTATTAAGAAAGAGAAACCAAAAGCA 197  
QY 231 TGTGTACATCTGAAATTTGGCTGAGCAATTTATCTCTTATTAATCTGCTTTTGG 290  
Db 198 TGTGTACATCTGAAATTTGGCTGAGCAATTTATCTCTTATTAATCTGCTTTTGG 257  
QY 291 GGCCTTATGACAGTTCAATGGTGGTTTAAAGGAAATATGTCAAATTAATTTACG 350  
Db 258 GGCCTTATGACAGTTCAATGGTGGTTTAAAGGAAATATGTCAAATTAATTTACG 317  
QY 351 CTTGTACACACTTAACTTTGCTCTGGAATGCAATTTCTGGCTTGTATGACATAGACAG 410  
Db 318 CTTGTACACACTTAACTTTGCTCTGGAATGCAATTTCTGGCTTGTATGACATAGACAG 377  
QY 411 ATATGTGCAATTAATAAGTCCCAAGCAATGCAAGTGTGGAAGAAACCAATGCTGATCAT 470  
Db 378 ATATGTGCAATTAATAAGTCCCAAGCAATGCAAGTGTGGAAGAAACCAATGCTGATCAT 437  
QY 471 CTGTTTCTGTGTGAGATGGTGCATCTTGTGAGATGATCCCAAGCTGTTTATATAC 530  
Db 438 CTGTTTCTGTGTGAGATGGTGCATCTTGTGAGATGATCCCAAGCTGTTTATATAC 497  
QY 531 AGTAATGACAAATGCTAGTGCATTTCCCATTTTCCCGCTACCTAGAAACATCAATGAA 590  
Db 498 AGTAATGACAAATGCTAGTGCATTTCCCATTTTCCCGCTACCTAGAAACATCAATGAA 557  
QY 591 AGCATTTGTTAAATGCTAGATGTCATTTGATTTGATGATCCTTTTATATGAG 650  
Db 558 AGCATTTGTTAAATGCTAGATGTCATTTGATTTGATGATCCTTTTATATGAG 617  
QY 651 GGTGTGCTACTTTATCAAGAGAGAGACATCATGAAGATGCCAAACCTTAATATCTCG 710  
Db 618 GGTGTGCTACTTTATCAAGAGAGAGACATCATGAAGATGCCAAACCTTAATATCTCG 677  
QY 711 ACCCTTAAAGTTTGTCTCAAGTGTGTTATGATTTTATGATGCTACCTACCTGCTTAA 770  
Db 678 ACCCTTAAAGTTTGTCTCAAGTGTGTTATGATTTTATGATGCTACCTACCTGCTTAA 737  
QY 771 CATGTGAAGTTTGTGCGAGACCATGACATCATCTACTCCCTGATACACGCTGCAACAT 830  
Db 738 CATGTGAAGTTTGTGCGAGACCATGACATCATCTACTCCCTGATACACGCTGCAACAT 797  
QY 831 GAGCAAGCATGAGATGCGCATCCCAAGTCAAGAGAGAGATGCACTGTTACAGCTG 890  
Db 798 GAGCAAGCATGAGATGCGCATCCCAAGTCAAGAGAGAGATGCACTGTTACAGCTG 857  
QY 891 CTTGACCCCAATCTTTATGTTTATGAGAGATCTTTCAAAACTACGTTATGAAGT 950  
Db 858 CTTGACCCCAATCTTTATGTTTATGAGAGATCTTTCAAAACTACGTTATGAAGT 917  
QY 951 GGCCAAAGAAATATGGTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1010  
Db 918 GGCCAAAGAAATATGGTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 977



QY 1011 TTCTGAGGCTCTACAGAGCAACAGTACTTTTACATTTTAAAGTAAACTGCTTCG 1070  
 DB 978 TTCTGAGGCTCTACAGAGCAACAGTACTTTTACATTTTAAAGTAAACTGCTTCG 1037  
 QY 1071 CTTTTCGTTGATACATATGATGCTTTCCCTCCAAATATAATCATCTGCTTATTC 1130  
 DB 1038 CTTTTCGTTGATACATATGATGCTTTCCCTCCAAATATAATCATCTGCTTATTC 1097  
 QY 1131 GAAAAAATATAATATAAT 1147  
 DB 1098 GAAACTCAAAAAA 1114

RESULT 16  
 AAH77711  
 ID AAH77711 standard; DNA; 1053 BP.

XX AAH77711;  
 XX  
 DT 13-NOV-2001 (first entry)  
 XX

DE Nucleotide sequence of human chemokine receptor CCR11.  
 XX  
 XX Human; chemokine receptor; CCR11; G protein coupled receptor;  
 KM inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;  
 KM asthma; angiogenesis; atherosclerosis vascular association disease;  
 KM hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;  
 KM left ventricular diastolic dysfunction; migraine; preterm labour;  
 KM oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;  
 KM myocardial infarction; congestive heart failure; endometriosiis;  
 KM vasospasm; retinopathy; neuropathy; pulmonary vascular disease; ss.  
 XX

OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1053  
 FT /tag= a  
 FT /product= "chemokine receptor CCR11"

XX  
 PN MO200166598-A2.  
 XX  
 PD 13-SEP-2001.  
 XX  
 PF 05-MAR-2001; 2001MO-US07073.  
 XX  
 PR 03-MAR-2000; 2000US-0186928.  
 PR 03-MAR-2000; 2000US-0187231.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Gray PW, Schweickart VL, Epp A, Raport CI, Chantry D, Steiner B;  
 XX  
 XX WPI; 2001-541918/60.  
 DR P-PSDB; AAG67237.  
 XX  
 PT An isolated polynucleotide encoding the chemokine receptor CCR11,  
 PT useful for treating rheumatoid arthritis, inflammatory bowel disease,  
 PT asthma, angiogenesis, atherosclerosis, cardiac arrhythmias, Raynaud's  
 PT phenomenon and migraine -  
 XX  
 PS Claim 1; Page 94-95; 110pp; English.

CC The present sequence encodes the human chemokine receptor CCR11. CCR11  
 CC is a member of the G protein coupled receptor family. A CCR11  
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11  
 CC expression or biological activity, is useful for treating many  
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory  
 CC bowel disease, and asthma. They are also useful for treating  
 CC angiogenesis, atherosclerosis vascular association diseases which may  
 CC include but are not limited to hypertension, angina pectoris, cardiac  
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's  
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic

CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive  
 CC heart failure, endometriosiis, vasospasm, retinopathy, neuropathy, or  
 CC pulmonary vascular disease.  
 XX

SQ Sequence 1053 BP; 308 A; 226 C; 210 G; 309 T; 0 other;

Query Match 91.8%; Score 1053; DB 22; Length 1053;  
 Best local Similarity 100.0%; Pred. No. 2.8e-296;  
 Matches 1053; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTTTGGAACAGAACCAAGTCAAGTATATATATGAGAAATGAATGATGCG 60  
 DB 1 ATGGCTTTGGAACAGAACCAAGTCAAGTATATATATATGAGAAATGAATGATGCG 60

QY 61 ACTATGACCTACGATCAATATGAACTGATCTGATCAAGAAGATGTCAGAGATTTGCA 120  
 DB 61 ACTATGACCTACGATCAATATGAACTGATCTGATCAAGAAGATGTCAGAGATTTGCA 120

QY 121 AAAGTTTCTCCCTGATTCCTCACAATAGTTTGTCAATGGACTTGGACGCAATTCC 180  
 DB 121 AAAGTTTCTCCCTGATTCCTCACAATAGTTTGTCAATGGACTTGGACGCAATTCC 180

QY 181 ATGATGAGCAATTTATGCTATTAACAAGAAACAGAACCAAGATGTTGATATC 240  
 DB 181 ATGATGAGCAATTTATGCTATTAACAAGAAACAGAACCAAGATGTTGATATC 240

QY 241 CTGAATTTGGCTGATGACAGATTTTACTCTTATTCATCTGCTTTTGGGCTGTTAAT 300  
 DB 241 CTGAATTTGGCTGATGACAGATTTTACTCTTATTCATCTGCTTTTGGGCTGTTAAT 300

QY 301 GCAGTTCAATGGGTGGGTTTAAAGGAAATAATGTCAAAATTAATCTGACCTGTACACA 360  
 DB 301 GCAGTTCAATGGGTGGGTTTAAAGGAAATAATGTCAAAATTAATCTGACCTGTACACA 360

QY 361 CTAAACTTTGCTCTGGAATGCAATTTCTGCTGTATTCAGCATATGCAATATGTCGA 420  
 DB 361 CTAAACTTTGCTCTGGAATGCAATTTCTGCTGTATTCAGCATATGCAATATGTCGA 420

QY 421 GTAACCTAAAGTCCCGACAGCAATCAGAGTGGGAAACCAATGTCATCTGTTCTGT 480  
 DB 421 GTAACCTAAAGTCCCGACAGCAATCAGAGTGGGAAACCAATGTCATCTGTTCTGT 480

QY 481 GTCTGATGCTGTCATCTGCTGAGCATACCCGAGCTGTTTTTATACAGTAAATGAC 540  
 DB 481 GTCTGATGCTGTCATCTGCTGAGCATACCCGAGCTGTTTTTATACAGTAAATGAC 540

QY 541 AATGCTAGTGCATTTCCCATTTTCCCGCTACCTAGAAACATCAATGAAGAAGCATTTGATT 600  
 DB 541 AATGCTAGTGCATTTCCCATTTTCCCGCTACCTAGAAACATCAATGAAGAAGCATTTGATT 600

QY 601 CAATAGCTAGAGATCTGATGATTTGTATGATACCTTTCTTATATGAGGAGTGTGTAC 660  
 DB 601 CAATAGCTAGAGATCTGATGATTTGTATGATACCTTTCTTATATGAGGAGTGTGTAC 660

QY 661 TTTATCAAGCAAGACATCATAGATGCAAAACATTAATATCTGACCCCTTAAAA 720  
 DB 661 TTTATCAAGCAAGACATCATAGATGCAAAACATTAATATCTGACCCCTTAAAA 720

QY 721 TTTATCAAGCAAGACATCATAGATGCAAAACATTAATATCTGACCCCTTAAAA 720  
 DB 721 TTTATCAAGCAAGACATCATAGATGCAAAACATTAATATCTGACCCCTTAAAA 720

QY 721 GTTCTGCTCAGATGCTGTTATGTTTCAATGTCATGCTAATGCTTATTAACATTTGTAAG 780  
 DB 721 GTTCTGCTCAGATGCTGTTATGTTTCAATGTCATGCTAATGCTTATTAACATTTGTAAG 780

QY 781 TTCTGCGAGGCAATAGACATATCTACTCTCTGATCAAGCTGCAACATAGCAAAAGCG 840  
 DB 781 TTCTGCGAGGCAATAGACATATCTACTCTCTGATCAAGCTGCAACATAGCAAAAGCG 840

QY 841 ATGACATGCGCATTCACAGTACAGAAAGATGCACTTTTCAAGCTGCTCAACCA 900  
 DB 841 ATGACATGCGCATTCACAGTACAGAAAGATGCACTTTTCAAGCTGCTCAACCA 900

QY 901 ATCTTTATGTTTATGAGGAGCATCTTTTCAAAAACATACGTTATGAAGTGGCCAAAGAA 960  
 DB 901 ATCTTTATGTTTATGAGGAGCATCTTTTCAAAAACATACGTTATGAAGTGGCCAAAGAA 960

QY 961 TATGGCTCTGGAGAGACAGACAAAGTGTGAGAGAGTTCTCTTTGATTCTGAGGCT 1020  
 CC TATGGCTCTGGAGAGAGACAGACAAAGTGTGAGAGAGTTCTCTTTGATTCTGAGGCT 1020  
 Db 961 TATGGCTCTGGAGAGAGACAGACAAAGTGTGAGAGAGTTCTCTTTGATTCTGAGGCT 1020

QY 1021 CCTACAGAGCCACACAGTACTTTTGTAGCATTTTA 1053  
 CC CCTACAGAGCCACACAGTACTTTTGTAGCATTTTA 1053  
 Db 1021 CCTACAGAGCCACACAGTACTTTTGTAGCATTTTA 1053

RESULT 17  
 AAS98091/c  
 ID AAS98091 standard; DNA; 1059 BP.  
 XX  
 AC AAS98091;  
 XX  
 DT 12-MAR-2002 (first entry)  
 DT  
 XX  
 DE Human DNA for potential G protein-coupled receptor #48.  
 XX

Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor;  
 KW Alzheimer's disease; amyotrophic lateral sclerosis; asthma;  
 KW atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy;  
 KW chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;  
 KW depression; epilepsy; macular degeneration; lymphoma; melanoma;  
 KW multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;  
 KW psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;  
 KW tuberculous; cognition disorder; memory disorder; anorexia;  
 KW hormonal release disorder; cardiovascular activity disorder;  
 KW pain perception disorder; obesity; diabetes; obesity;  
 KW diabetes; hyperlipidaemia; stroke; gene therapy.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200185791-A1.  
 PN  
 XX 15-NOV-2001.  
 PD  
 XX  
 PF 11-MAY-2001; 2001WO-US15332.  
 XX  
 XX 11-MAY-2000; 2000US-203217P.  
 PR 18-MAY-2000; 2000US-205945P.  
 XX  
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
 PA  
 XX Brown JP, Miller M, Burner G, Fabre-Suver C, Pritchard D;  
 PI  
 XX WPI; 2002-066595/09.  
 DR  
 XX Novel G protein-coupled receptor polypeptides including galanin  
 PT receptor polypeptides useful for identifying modulators that are useful  
 PT for treating Alzheimer's disease, psoriasis, melanoma, multiple  
 PT sclerosis, stroke  
 PT  
 XX  
 PS Claim 2; Page 75; 144p; English.  
 PS  
 XX The invention relates to an isolated polypeptide encoded by a  
 CC nucleic acid molecule that is at least 80% identical to the G  
 CC protein-coupled (GPCR) polynucleotides included in the specification.  
 CC Also included are probes based on the GPCR sequences (including  
 CC antisense probes), a host cell comprising an expression vector comprising  
 CC the GPCR sequence, antibodies raised against the polypeptides,  
 CC and methods of identifying modulators of the polypeptides. The  
 CC polypeptides are useful for identifying modulator compounds which  
 CC function as modulators, activators, repressors, agonists or antagonists  
 CC of the novel GPCR polypeptides including the GAL4 polypeptide. The  
 CC antibodies and nucleic acid probes as described above can be used to  
 CC detect the presence of diseases or disorders in which GPCRs are involved  
 CC e.g., Alzheimer's disease, amyotrophic lateral sclerosis, asthma,  
 CC atherosclerosis, basal cell carcinoma, breast carcinoma, cardiomyopathy,  
 CC chondrosarcoma, chronic obstructive pulmonary disease, Crohn's disease,  
 CC depression, epilepsy, macular degeneration, lymphoma, melanoma.

CC multiple sclerosis, osteoarthritis, osteoporosis, Parkinson's disease,  
 CC psoriasis, rheumatoid arthritis, schizophrenia, ulcerative colitis,  
 CC tuberculous and many other diseases listed in the specification. The  
 CC probes and antibodies are also useful for diagnosing cognition and memory  
 CC disorders, anorexia, hormonal release disorder, obesity, diabetes, Alzheimer's  
 CC disease. Preferably, compounds that decrease or increase  
 CC the expression of galanin receptor (GAL4) can be used to treat obesity,  
 CC diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is  
 CC useful for treating the above mentioned disorders by gene therapy  
 CC techniques. The present sequence is a novel GPCR polynucleotide of the  
 CC invention.  
 CC  
 XX  
 XX Sequence 1059 BP; 310 A; 213 C; 228 G; 308 T; 0 other;  
 SQ

Query Match 91.5%; Score 1050; DB 24; Length 1059;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-25;  
 Matches 1050; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTTTGGAAACAGACACAGTCAACAGATTATTTATGAGAAATGAAATGATGATGC 60  
 Db 1050 ATGGCTTTGGAAACAGACACAGTCAACAGATTATTTATGAGAAATGAAATGATGATGC 991

QY 61 ACTTATGACTCAAGTCAATATGAACTGATCTGTATCAAAAGATGTCAGAAATTGCA 120  
 Db 990 ACTTATGACTCAAGTCAATATGAACTGATCTGTATCAAAAGATGTCAGAAATTGCA 931

QY 121 AAAGTTTCTCCCTGATATCTCTCAATAGTTTCGATATGAGCTTGACGCAATTC 180  
 Db 930 AAAGTTTCTCCCTGATATCTCTCAATAGTTTCGATATGAGCTTGACGCAATTC 871

QY 181 ATGGTAGTGGCAATTTATGCTATTACAAGAAACAGACACAAACAGATGTATATC 240  
 Db 870 ATGGTAGTGGCAATTTATGCTATTACAAGAAACAGACACAAACAGATGTATATC 811

QY 241 CTGAATTTGGCTGTAGACAGATTACTCTCTTATTAATCACTTGCTTTTGGCTGTAT 300  
 Db 810 CTGAATTTGGCTGTAGACAGATTACTCTCTTATTAATCACTTGCTTTTGGCTGTAT 751

QY 301 GCAGTTCATGGGGGGGTTTATGAGAAATATGTCAAATTAATCTTGACCTTGACACA 360  
 Db 750 GCAGTTCATGGGGGGGTTTATGAGAAATATGTCAAATTAATCTTGACCTTGACACA 691

QY 361 CTAACTTTTCTCTGAGATGAGATTCTGCTTGTATCAGCATAGACAGATATGAGCA 420  
 Db 690 CTAACTTTTCTCTGAGATGAGATTCTGCTTGTATCAGCATAGACAGATATGAGCA 631

QY 421 GTTACTTAAAGTCCCAAGCCATCAGAGTGGGAAACCATGCTGATCTGTTTCGT 480  
 Db 630 GTTACTTAAAGTCCCAAGCCATCAGAGTGGGAAACCATGCTGATCTGTTTCGT 571

QY 481 GTCTGATGAGCTGCAATCTTGCTGAGCATACCCAGCTGTTTATTAAGTAATGAC 540  
 Db 570 GTCTGATGAGCTGCAATCTTGCTGAGCATACCCAGCTGTTTATTAAGTAATGAC 511

QY 541 AATGCTAGGTGATTCCTCCATTTTCCCGCTACTAGGAACATCAATGAAGCATTTGAT 600  
 Db 510 AATGCTAGGTGATTCCTCCATTTTCCCGCTACTAGGAACATCAATGAAGCATTTGAT 451

QY 601 CAAATCTAGAGATCTGCATTTGATTTGATGATCTTTTATTAATGAGGGTGTGCTAC 660  
 Db 450 CAAATCTAGAGATCTGCATTTGATTTGATGATCTTTTATTAATGAGGGTGTGCTAC 391

QY 661 TTATACAGCAAGGACATCACTGAAAGATGCCAAACATTAATAATCTGACCCCTAAA 720  
 Db 390 TTATACAGCAAGGACATCACTGAAAGATGCCAAACATTAATAATCTGACCCCTAAA 331

QY 721 GTTCTGCTCAGTCTGTTATGTTTCTTATGCTCAATGCTCTTATACATTTGCAAG 780  
 Db 330 GTTCTGCTCAGTCTGTTATGTTTCTTATGCTCAATGCTCTTATACATTTGCAAG 271

QY 781 TTGTGCGAGCCATAGACATCATCTACTCCCTGATCAGCTGCAACATGAGCAAGCC 840

DB 270 TTCTGCCGAGCCATAGCATCATCTCTCCCTGATCATGACAGTGAACATGACAAAGC 211  
 QY 841 ATGACATGCGCCATCCAGTCAAGAAAGCATGCACTCTTTACAGCTGCTCAACCCA 900  
 DB 210 ATGACATGCGCCATCCAGTCAAGAAAGCATGCACTCTTTACAGCTGCTCAACCCA 151  
 QY 901 ATCTTTATGTTTTTATGAGAGCATCTTTCAAAAACGATTAAGAGGCGCAAGAA 960  
 DB 150 ATCTTTATGTTTTTATGAGAGCATCTTTCAAAAACGATTAAGAGGCGCAAGAA 91  
 QY 961 TATGAGTCTGAG 1020  
 DB 90 TATGAGTCTGAG 31  
 QY 1021 CCTACAGAGCCAAACGATCTTTTACATT 1050  
 DB 30 CCTACAGAGCCAAACGATCTTTTACATT 1  
 RESULT 18  
 AAD01128 standard; cDNA, 1053 BP.  
 AAD01128;  
 AC AAD01128;  
 XX 02-NOV-2000 (first entry)  
 DE Human orphan G protein-coupled receptor hPPRI cDNA.  
 XX Human orphan G protein-coupled receptor; GPCR; hPPRI; drug screening;  
 KM transmembrane receptor; expressed sequence tag; EST; signal cascade; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1053  
 FT /tag= a  
 FT /product= "hPPRI"  
 FT /note= "Human orphan G protein-coupled receptor"  
 PN W0200031258-A2.  
 PD 02-JUN-2000.  
 PF 13-OCT-1999; 99MO-US23687.  
 XX 20-NOV-1998; 98US-0109213.  
 PR 16-FEB-1999; 99US-0120416.  
 PR 26-FEB-1999; 99US-0121852.  
 PR 12-MAR-1999; 99US-0123946.  
 PR 12-MAR-1999; 99US-0123949.  
 PR 28-MAY-1999; 99US-0136436.  
 PR 28-MAY-1999; 99US-0136437.  
 PR 28-MAY-1999; 99US-0136439.  
 PR 28-MAY-1999; 99US-0136567.  
 PR 28-MAY-1999; 99US-0137127.  
 PR 28-MAY-1999; 99US-0137131.  
 PR 29-JUN-1999; 99US-0141448.  
 PR 29-SEP-1999; 99US-0156555.  
 PR 29-SEP-1999; 99US-0156633.  
 PR 29-SEP-1999; 99US-0156634.  
 PR 29-SEP-1999; 99US-0156653.  
 PR 01-OCT-1999; 99US-0157280.  
 PR 01-OCT-1999; 99US-0157281.  
 PR 01-OCT-1999; 99US-0157282.  
 PR 01-OCT-1999; 99US-0157293.  
 PR 01-OCT-1999; 99US-0157294.  
 PR 12-OCT-1999; 99US-0416760.  
 PR 12-OCT-1999; 99US-0417044.  
 XX  
 PA (AREN-) ARENA PHARM INC.  
 XX Chen R, Dang HT, Liaw CW, Lin I,

XX WPI: 2000-40068/34.  
 DR P-PSDB; AAY71301.  
 XX Novel human orphan G protein-coupled receptors and the encoding cDNAs  
 FT for use in the identification of G protein-coupled receptor agonists -  
 PS Claim 41; Page 68-69; 102pp; English.  
 CC The present sequence is a cDNA encoding hPPRI, an endogenous human  
 CC orphan G protein-coupled receptor (GPCR), expressed in the pituitary  
 CC gland, heart, salivary gland, small intestine and testis. The hPPRI cDNA  
 CC was identified using EST (expressed sequence tag) A359504 and 238667 as  
 CC a probe. The orphan GPCR of the invention, like all GPCRs has seven  
 CC transmembrane alpha helices with an extracellular N-terminus and an  
 CC intracellular C-terminus. However, no endogenous ligands has yet been  
 CC identified for the proteins of the invention. The orphan GPCRs may be  
 CC used in the identification of their endogenous ligands, and to screen  
 CC potential GPCR agonists and antagonists for use as pharmaceutical agents.  
 CC The proteins may also be used in the study of GPCR-mediated signalling  
 CC cascades, and to elucidate their precise role in normal and diseased  
 CC human conditions. Nucleic acid encoding human orphan GPCRs may be used  
 CC for tissue localisation expression analysis to provide information about  
 CC their function in healthy and pathological states.  
 CC  
 SQ Sequence 1053 BP; 306 A; 226 C; 211 G; 310 T; 0 other;

Query Match 91.0%; Score 1043.4; DB 21; Length 1053;

Best Local Similarity 99.4%; Pred. No. 1.8e-293; Matches 1047; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGGCTTTGGACAGAACCCAGTCAAGATTTATTTATGAGAAATGAAATGAATGGC 60  
 DB 1 ATGGCTTTGGACAGAACCCAGTCAAGATTTATTTATGAGAAATGAAATGAATGGC 60  
 QY 61 ACTTATGATTAAGTCAATATGATCTGATCAAAAGAGTGAAGATTGCA 120  
 DB 61 ACTTATGATTAAGTCAATATGATCTGATCAAAAGAGTGAAGATTGCA 120  
 QY 121 AAAGTTTCTCCCTGATATCTCTCAAAATGTTTGTATTTGATTTGCAAGCAATTCC 180  
 DB 121 AAAGTTTCTCCCTGATATCTCTCAAAATGTTTGTATTTGATTTGCAAGCAATTCC 180  
 QY 181 ATGTAGTGGCAATTTATGCTTATTAAGAAACAGAGAACCAAAACAGATGTGATTC 240  
 DB 181 ATGTAGTGGCAATTTATGCTTATTAAGAAACAGAGAACCAAAACAGATGTGATTC 240  
 QY 241 CTGAATTTGGCTGTAGCAATTTACTCTTATTAACCTGCTTTTGGCTGTAT 300  
 DB 241 CTGAATTTGGCTGTAGCAATTTACTCTTATTAACCTGCTTTTGGCTGTAT 300  
 QY 301 GCAGTTCATGGGTGGTTTAAAGAAATATATGCAAAATTAATCTTACCTTTGACCA 360  
 DB 301 GCAGTTCATGGGTGGTTTAAAGAAATATATGCAAAATTAATCTTACCTTTGACCA 360  
 QY 361 CTAACTTTGTCTCTGGAATGCAATTTCTGCTTGTATAGATAGACAGATATGCGCA 420  
 DB 361 CTAACTTTGTCTCTGGAATGCAATTTCTGCTTGTATAGATAGACAGATATGCGCA 420  
 QY 421 GTAACTTAAGTCCCAAGCAATCAGAGTGGGAAACCAATGCTGATCATCTGTTCTGT 480  
 DB 421 GTAACTTAAGTCCCAAGCAATCAGAGTGGGAAACCAATGCTGATCATCTGTTCTGT 480  
 QY 481 GTCTGATGCGTCCCATCTTTGCGAGCATACCCAGCTGGTTTTTATACAGTAATGAC 540  
 DB 481 GTCTGATGCGTCCCATCTTTGCGAGCATACCCAGCTGGTTTTTATACAGTAATGAC 540  
 QY 541 AATGCTAGGTGCAATTTTCCCGCTTACCTAGAGAAATCAATGAATCAATGAT 600  
 DB 541 AATGCTAGGTGCAATTTTCCCGCTTACCTAGAGAAATCAATGAATCAATGAT 600  
 QY 601 CAATGCTAGAGATCTGCAATGATTTGATAGACCTTTCTTATTAATGAGGGTGTCTAC 660

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Db 601 CAATGCTAGAGATCTGATTTGGATTGTAGTACCCTTTCTTATTTATGAGGGGTGCTAC 660
Qy 661 TTATCAGAGCAGACACTCATGAAGATGCCAATTAATAATCTGACCCCTTAAA 720
Db 661 TTATCAGAGCAGACACTCATGAAGATGCCAATTAATAATCTGACCCCTTAAA 720
Qy 721 GTTGTGCTCAGAGTGTATAGTTTTCATTTGCTACTCACTCACTGCTTATATGATGTCAG 780
Db 721 GTTGTGCTCAGAGTGTATAGTTTTCATTTGCTACTCACTCACTGCTTATATGATGTCAG 780
Qy 781 TTGCGCCGAGCATGAGATATCTACTCCCTGATCAGACCTGACATGACGAAACGC 840
Db 781 TTGCGCCGAGCATGAGATATCTACTCCCTGATCAGACCTGACATGACGAAACGC 840
Qy 841 ATGACATGCGCATTCACATGACAGAAAGCATGCGACTCTTTCACAGCTGCTCAACCA 900
Db 841 ATGACATGCGCATTCACATGACAGAAAGCATGCGACTCTTTCACAGCTGCTCAACCA 900
Qy 901 ATCTTTATGTTTTTATGAGAGCATCTTTCAAAAAGTATGAAAGTGCCCAAGAAA 960
Db 901 ATCTTTATGTTTTTATGAGAGCATCTTTCAAAAAGTATGAAAGTGCCCAAGAAA 960
Qy 961 TATGGTCTGAGAGAGCAGAGCAAAAGTGAGAGAGTCTCTTTGATTCGAGGGT 1020
Db 961 TATGGTCTGAGAGAGCAGAGCAAAAGTGAGAGAGTCTCTTTGATTCGAGGGT 1020
Qy 1021 CCTACAGAGCCACAGTACTTTTATGATTTAA 1053
Db 1021 CCTACAGAGCCACAGTACTTTTATGATTTAA 1053

```

RESULT 19  
 AAA46029  
 ID AAA46029 standard; cDNA; 1053 BP.

```

XX AAA46029;
XX
XX 22-AUG-2000 (first entry)
XX
XX Human G protein coupled receptor hppr1 encoding cDNA seq ID NO:23.
XX
XX Human; G protein coupled receptor; GPCR; transmembrane receptor;
XX identification; agonist; screening; therapeutic; pharmaceutical;
XX mutant; ss.
XX
XX Homo sapiens.
XX
XX PN MO200022131-A2.
XX
XX 20-APR-2000.
XX
XX 13-OCT-1999; 99MO-US24065.
XX
XX
XX 13-OCT-1998; 98US-0170496.
XX 12-NOV-1998; 98US-0108029.
XX 20-NOV-1998; 98US-0109213.
XX 27-NOV-1998; 98US-0110060.
XX 16-FEB-1999; 99US-0120416.
XX 26-FEB-1999; 99US-0121852.
XX 12-MAR-1999; 99US-0123944.
XX 12-MAR-1999; 99US-0123945.
XX 12-MAR-1999; 99US-0123946.
XX 12-MAR-1999; 99US-0123948.
XX 12-MAR-1999; 99US-0123949.
XX 28-MAY-1999; 99US-0136436.
XX 28-MAY-1999; 99US-0136437.
XX 28-MAY-1999; 99US-0136439.
XX 28-MAY-1999; 99US-0137127.
XX 28-MAY-1999; 99US-0137131.
XX 28-MAY-1999; 99US-0137567.
XX 30-JUN-1999; 99US-0141448.
XX 27-AUG-1999; 99US-0151114.

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PR 03-SEP-1999; 99US-0152524.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156555.
PR 29-SEP-1999; 99US-0156634.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Behan DP, Lehmann-Brinsma K, Chalmers DT, Chen R, Dang HT;
XX Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX
XX WPI; 2000-317986/27.
XX
XX P-PSDB; AAB02835.
XX
XX Non-endogenous, human G protein-coupled receptors for screening
XX receptor, inverse or partial agonists useful as therapeutic agents
XX
XX Example 1; Page 98-99; 187pp; English.
XX
XX
XX The present invention describes transmembrane receptors, preferably
XX human G protein coupled receptors (GPCR), for which the endogenous
XX ligand is unknown (orphan GPCR receptors). More specifically the present
XX invention relates to non-endogenous, constitutively activated versions
XX of a human GPCR. These non-endogenous human GPCRs can be useful for
XX the direct identification of candidate compounds as receptors agonists,
XX inverse agonists or partial agonists for use as pharmaceutical agents.
XX AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
XX the exemplification of the present invention.
XX
XX Sequence 1053 BP; 306 A; 226 C; 211 G; 310 T; 0 other;

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Query Match 91.0%; Score 1043.4; DB 21; Length 1053;  
 Best Local Similarity 99.4%; Pred. No. 1.8e-293;  
 Matches 1047; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy 1 ATGGCTTTGGAACAGACACAGTCAACAGATTTATTTGAGAAATGAATGAATGCC 60
Db 1 ATGGCTTTGGAACAGACACAGTCAACAGATTTATTTATGAGAAATGAATGAATGCC 60
Qy 61 ACTTATGACTACAGTCAATATGAACTGATCTGTATCAAAAGAGTGCAGAAATTTGCA 120
Db 61 ACTTATGACTACAGTCAATATGAAATGATCTGTATCAAAAGAGTGCAGAAATTTGCA 120
Qy 121 AAAGTTTTCCTCCCTGTATTCCTCAGATATGTTTTCGTCATTTGAGCACTTGAGCAATTC 180
Db 121 AAAGTTTTCCTCCCTGTATTCCTCAGATATGTTTTCGTCATTTGAGCACTTGAGCAATTC 180
Qy 181 ATGTAAGTGGCAATTTATGCTATTTACAGAAACAGAGAACCAACAGATGTATCATC 240
Db 181 ATGTAAGTGGCAATTTATGCTATTTACAGAAACAGAGAACCAACAGATGTATCATC 240
Qy 241 CTGAATTTGGCTGTAGCAGATTTACTCCTTATTCACCTGCTTTTGGGCTGTAAAT 300
Db 241 CTGAATTTGGCTGTAGCAGATTTACTCCTTATTCACCTGCTTTTGGGCTGTAAAT 300
Qy 301 GCAGTTCAATGAGTGGTTTATGAGAAATAATGTGCAAAATTAACCTTGACCTGTACACA 360
Db 301 GCAGTTCAATGAGTGGTTTATGAGAAATAATGTGCAAAATTAACCTTGACCTGTACACA 360
Qy 361 CTAAACTTTGTCTCTGGAATGCACTTTCTGCTGTATCAGATAGACAGATATGTGCA 420
Db 361 CTAAACTTTGTCTCTGGAATGCACTTTCTGCTGTATCAGATAGACAGATATGTGCA 420
Qy 421 GTAACTAAAGTCCAGCAGATCAGAGTGGGAAACCAAGCTGGATCATCTGTTTGT 480
Db 421 GTAACTAAAGTCCAGCAGATCAGAGTGGGAAACCAAGCTGGATCATCTGTTTGT 480
Qy 481 GTCTGATGCTGCGCATCTTCTGAGCATACCCAGCTGTTTTTTATACAGTAAATGAC 540
Db 481 GTCTGATGCTGCGCATCTTCTGAGCATACCCAGCTGTTTTTTATACAGTAAATGAC 540
Qy 541 AATGCTAGTGCATTTCCATTTTCCCGCTGCTAGGAAATCAATCAATGAAGATGATT 600
Db 541 AATGCTAGTGCATTTCCATTTTCCCGCTGCTAGGAAATCAATCAATGAAGATGATT 600

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Db 482 ACTTATACAGCAGGAGCACTCATGAGATGCCAAATTAATATCTGACCCCTAA 541
Qy 719 AAGTTCTGCTACAGTGCCTTATGTTTTCATTGTCACTCAACTGCCCTATTAATGTCA 778
Db 542 AAGTTCTGCTACAGTGCCTTATGTTTTCATTGTCACTCAACTGCCCTATTAATGTCA 601
Qy 779 AGTTCTGCGAGCCATAGACATCATCTACCTCCGATCACCAGCTGCACATGAGCAAC 838
Db 602 AGTTCTGCGAGCCATAGACATCATCTACCTCCGATCACCAGCTGCACATGAGCAAC 661
Qy 839 GCATGAGCATGCGCATCCAGTCCAGAGAACATCGACTCTTTCACAGCTGCTCAAC 938
Db 662 GCATGAGCATGCGCATCCAGTCCAGAGAACATCGACTCTTTCACAGCTGCTCAAC 721
Qy 899 CAATCCTTTATGTTTATGAGGACATCTTCAAAAACAGTATGAAAGTGCCAAAG 958
Db 722 CAATCCTTTATGTTTATGAGGACATCTTCAAAAACAGTATGAAAGTGCCAAAG 781
Qy 959 AATATGGGTCCTGAGAGAGACAGACAAAGTGTGAGAGAGTTCTTTTGAATCTGAGG 1018
Db 782 AATATGGGTCCTGAGAGAGACAGACAAAGTGTGAGAGAGTTCTTTTGAATCTGAGG 841
Qy 1019 GTCTACAGAGCCAGCACTTTCATGCACTTAAAGTAAATGCTGCTGCTTTTGTCT 1078
Db 842 GTCTACAGAGCCAGCACTTTCATGCACTTAAAGTAAATGCTGCTGCTTTTGTCT 901
Qy 1079 TGGATACATATGATGATGATGCTTCCCTCAAAATAAACATCTGCTTATCTGAAAAA 1138
Db 902 TGGATACATATGATGATGATGCTTCCCTCAAAATAAACATCTGCTTATCTGAAAAA 961
Qy 1139 AA 1140
Db 962 AA 963

RESULT 21
AAH77715
ID AAH77715 standard; cDNA; 1388 BP.
XX
AC AAH77715;
XX
DT 13-NOV-2001 (first entry)
XX
DE Nucleotide sequence of human chemokine receptor CCR11 cDNA clone.
XX
KW Human; chemokine receptor; CCR11; G protein coupled receptor;
KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
KW asthma; angiodenesis; atherosclerosis vascular association disease;
KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
KW left ventricular diastolic dysfunction; migraine; preterm labour;
KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;
KW myocardial infarction; congestive heart failure; endometriosis;
KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease; ss.
XX
OS Homo sapiens.
XX
PN WO200166598-A2.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US07073.
XX
PR 03-MAR-2000; 2000US-0186928.
XX
PR 03-MAR-2000; 2000US-0187231.
XX
PA (ICOS-) ICOS CORP.
XX
PI Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B,
DR WPI; 2001-541918/60.
XX
PT An isolated polynucleotide encoding the chemokine receptor CCR11,

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PT useful for treating rheumatoid arthritis, inflammatory bowel disease,
PT asthma, angiodenesis, atherosclerosis, cardiac arrhythmias, Raynaud's
PT phenomenon and migraine -
XX
PS Example 1; Page 101-102; 110pp; English.
XX
CC AAH77715-20 represent cDNA clones of human chemokine receptor CCR11.
CC CCR11 is a member of the G protein coupled receptor family. A CCR11
CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11
CC expression or biological activity, is useful for treating many
CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory
CC bowel disease, and asthma. They are also useful for treating
CC angiodenesis, atherosclerosis vascular association diseases which may
CC include but are not limited to hypertension, angina pectoris, cardiac
CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's
CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic
CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive
CC heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or
CC pulmonary vascular disease.
XX
SQ Sequence 1388 BP; 447 A; 270 C; 274 G; 397 T; 0 other;

Query Match      81.9%; Score 939.2; DB 22; Length 1388;
Best Local Similarity 99.2%; Pred. No. 4.7e-263;
Matches 944; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 189 GGCATTTATGCTTATCAAGAAACAGAGAACCAACAGATGTCATCTGAAATTT 248
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Qy 249 GGCTGTAGCATTTACTCTCTTCTTATTCATCTGCTTTTGGCTGTGAATGCAATTCA 308
Db 61 GGCTGTAGCATTTACTCTCTTCTTATTCATCTGCTTTTGGCTGTGAATGCAATTCA 120
Qy 309 TGGGTGGGTTTAAAGGAAATATGTCAAATTAATCTGACCTGTATACACATTAATCT 368
Db 121 TGGGTGGGTTTAAAGGAAATATGTCAAATTAATCTGACCTGTATACACATTAATCT 180
Qy 369 TGTCTCTGAAATGCAATTTCTGCTTGTATCAGATAGACATATGTCAGATTAATTA 428
Db 181 TGTCTCTGAAATGCAATTTCTGCTTGTATCAGATAGACATATGTCAGATTAATTA 240
Qy 429 AGTCCCAAGCCATATCAGAGATGAGGAAACCAATGCTGATCATCTGTTTCTGTGAT 488
Db 241 TGTCCCAAGCCATATCAGAGATGAGGAAACCAATGCTGATCATCTGTTTCTGTGAT 300
Qy 489 GGGTGGCATCTTGTGAGCATATCCCAAGCTGTTTATATACATTAATACATATGCTAG 548
Db 301 GGGTGGCATCTTGTGAGCATATCCCAAGCTGTTTATATACATTAATACATATGCTAG 360
Qy 549 GTGATTTCCATTTTCCCGCTACTAGGAAATCAATGAAAGCATTTGAAATGCT 608
Db 361 GTGATTTCCATTTTCCCGCTACTAGGAAATCAATGAAAGCATTTGAAATGCT 420
Qy 609 AGAGATCTGCAATTTGATGATACCTTTCTTATATGAGGGGTGCTACTTATAC 668
Db 421 AGAGATCTGCAATTTGATGATACCTTTCTTATATGAGGGGTGCTACTTATAC 480
Qy 669 AGCAAGGACATCTATGAAGATGCCAAACATTAATATCTGACCCCTAAAGTCTGCT 728
Db 481 AGCAAGGACATCTATGAAGATGCCAAACATTAATATCTGACCCCTAAAGTCTGCT 540
Qy 729 CACAGTGGTATAGTTTTCATTTGTCACTCAATGCTTATATGATGTCAGAGTTCGCC 788
Db 541 CACAGTGGTATAGTTTTCATTTGTCACTCAATGCTTATATGATGTCAGAGTTCGCC 600
Qy 789 AGCCATAGACATCATCTACCTGATCACCAGCTGCAATAGAGCAAGCATGAGCAT 848
Db 601 AGCCATAGACATCATCTACCTGATCACCAGCTGCAATAGAGCAAGCATGAGCAT 660
Qy 849 CGCCATCAAGTACAGAAAGCATGCACTTTTCAAGCTGCTCAACCCATCTCTTA 908
Db 661 CGCCATCAAGTACAGAAAGCATGCACTTTTCAAGCTGCTCAACCCATCTCTTA 720

```

QY 909 TGTATTATGAGGACATCTTCAAAAACTACGTATGAAGTGGCCAGAAATATGGGTC 968  
 Db 721 TGTATTATGAGGACATCTTCAAAAACTACGTATGAAGTGGCCAGAAATATGGGTC 780  
 QY 969 CTGAGAGAGACAGACAGAAAGTGTGAGAGATTCTTTGATTCTGAGGGCTTACAGA 1028  
 Db 781 CTGAGAGAGACAGACAGAAAGTGTGAGAGATTCTTTGATTCTGAGGGCTTACAGA 840  
 QY 1029 GCCAACCACTACTTTTATGCACTTTAAAGTTAAACCTGCTGCTTTTGTGATGATACATA 1088  
 Db 841 GCCAACCACTACTTTTATGCACTTTAAAGTTAAACCTGCTGCTTTTGTGATGATACATA 900  
 QY 1089 TGAATGATGCTTTCCCTCAAAATTAACATCTGCTATTTCTGAAAAAAA 1140  
 Db 901 TGAATGATGCTTTCCCTCAAAATTAACATCTGCTATTTCTGAAACTCAA 952

RESULT 22  
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 ID AAH77712 standard; DNA; 2059 BP.  
 XX  
 AC AAH77712;  
 XX  
 DT 13-NOV-2001 (first entry)  
 XX  
 DE Nucleotide sequence of bovine chemokine receptor CCR11.  
 XX  
 XX Human; chemokine receptor; CCR11; G protein coupled receptor;  
 KM inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;  
 KM asthma; angiogenesis; atherosclerosis vascular association disease;  
 KM hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;  
 KM left ventricular diastolic dysfunction; migraine; preterm labour;  
 KM oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;  
 KM myocardial infarction; congestive heart failure; endometriosis;  
 KM vasospasm; retinopathy; nephropathy; pulmonary vascular disease; ss.  
 XX  
 OS Bos sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 481..1533  
 FT /\*tag= a  
 FT /product= "chemokine receptor CCR11"  
 XX  
 PN MO200166598-A2.  
 XX  
 XX 13-SEP-2001.  
 PD  
 XX  
 PF 05-MAR-2001; 2001WO-US07073.  
 XX  
 PR 03-MAR-2000; 2000US-0186928.  
 PR 03-MAR-2000; 2000US-0187231.  
 XX  
 PA (ICOS-) ICOS CORP.  
 PI Gray PM, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;  
 XX  
 XX WPI: 2001-541918/60.  
 DR P-PSDB; AAG67238.  
 XX  
 XX An isolated polynucleotide encoding the chemokine receptor CCR11,  
 PT useful for treating rheumatoid arthritis, inflammatory bowel disease,  
 PT asthma, angiogenesis, atherosclerosis, cardiac arrhythmias, Raynaud's  
 PT phenomenon and migraine -  
 XX  
 XX Example 1; Page 97-99, 110pp; English.  
 PS  
 XX The present sequence encodes the bovine chemokine receptor CCR11. CCR11  
 CC is a member of the G protein coupled receptor family. A CCR11  
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11  
 CC expression or biological activity, is useful for treating many  
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory  
 CC bowel disease, and asthma. They are also useful for treating

CC angiogenesis, atherosclerosis vascular association diseases which may  
 CC include but are not limited to hypertension, angina pectoris, cardiac  
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's  
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic  
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive  
 CC heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or  
 CC pulmonary vascular disease.  
 CC  
 SQ Sequence 2059 BP; 720 A; 366 C; 345 G; 628 T; 0 other;  
 Query Match 77.2%; Score 886; DB 22; Length 2059;  
 Best Local Similarity 87.4%; Pred. No. 1.8e-247;  
 Matches 970; Conservative 0; Mismatches 140; Indels 0; Gaps 0;  
 QY 1 ATGCTTTGGAACAGAACAGTCAACAGATATTATTAATGAGAAATGAATGAATGAC 60  
 Db 481 ATGCTTTGGAATACACACAGTCAACAGATATTATTAATGAGAAATGAATGAATGAC 540  
 QY 61 ACTTATGACTACAGTCAATATGACTGATCTGTATCAAAAGAGATGAGAAATTTGCA 120  
 Db 541 ACTCATGACTATGACTACAGTATGAGATGATCTGTATCAAAAGAGATGAGAAATTTGCA 600  
 QY 121 AAAGTTTCCCTCCCTGATATCCCTCAATAGTTTTCATTTGCTTGGACTTGCAGCAATTCC 180  
 Db 601 AAAGTTTCTTACTCTGCTCTTTCATCAATAGCTTTCAATGACTTGCAGCAATTCC 660  
 QY 181 ATGCTATGAGGCAATTTATGCTTATTAACAGAAACAGAACCAAAACGATGTGTACATC 240  
 Db 661 ACTGATAGGAGCAATTTATGCTTATTAACAGAAACAGAACCAAAACGATGTGTACATC 720  
 QY 241 CTGAATTTGGCTGTGACAGATTTACTCTTCAATCACTGCTTTTGGGCTGTAT 300  
 Db 721 CTGAATTTGGGAGTGGCGGATTTATCTTCAATCACTGCTTTTGGGCTGTAT 780  
 QY 301 GGAGTTCAATGGGTGGGTTTAAAGGAAATTAATGTGCAAAATTAATCACTTGCCTTGTACACA 360  
 Db 781 GGAGTTCAATGGGTGGGTTTAAAGGAAATTAATGTGCAAAATTAATCACTTGCCTTGTACACA 840  
 QY 361 CTAAATCTTGTCTCTGGAATGACATTTCTGCTGTATACAGATACAGATATGTGCA 420  
 Db 841 GTCAATTTTGTCTCTGGAATGACATTTCTGCTGTATACAGATACAGATATGTGCA 900  
 QY 421 GTTACTTAAGTCCCGACCAATCAGAGTGGGAAACCATGTGATCATCTGTTCTGT 480  
 Db 901 GTTACTTAAGTCCCGACCAATCAGAGTGGGAAACCATGTGATCATCTGTTCTGT 960  
 QY 481 GTCTGATGGCTGCACTCTTGTGAGACATACCCAGCTGTTTATTAACAGTAATGAC 540  
 Db 961 GTCTGATGGCTGCACTCTTGTGAGATACCCAGCTGTTTATTAACAGTAATGAC 1020  
 QY 541 AATGCTAGGTGATTCCTCATTTTCCCGGCTACCTAGAACATCAATGAAGATTGAT 600  
 Db 1021 AATGCTAGGTGATTCCTCATTTTCCCGGCTACCTAGAACATCAATGAAGATTGAT 1080  
 QY 601 CAATGCTAGATCTGCAATTTGATTTAGTACCTTTCTTATATGAGGAGTGTGCTAC 660  
 Db 1081 CAATGCTAGATCTGCAATTTGATTTAGTACCTTTCTTATATGAGGAGTGTGCTAC 1140  
 QY 661 TTTATCAGACAGAACACTCATGAAGATGCCAAACATTAATAATCTGCAGCCCTAATA 720  
 Db 1141 TTTATCAGACAGAACACTCATGAAGATGCCAAACATTAATAATCTGCAGCCCTAATA 1200  
 QY 721 GTTCTGCTACAGTGTGTTATGATTTTCAATTTGCACTCAACGCTTTATTAACATTTGTCAAG 780  
 Db 1201 GTTCTGCTACAGTGTGTTATGATTTTCAATTTGCACTCAACGCTTTATTAACATTTGTCAAG 1260  
 QY 781 TTTCTGCGAGCATTAACATCAATCTACTCCCTGATACAGCTGCAACATGAGCAAGC 840  
 Db 1261 TTTCTGCGAGCATTAACATCAATCTACTCCCTGATACAGCTGCAACATGAGCAAGC 1320  
 QY 841 ATGACATGCGCATTCACAGATGCAAGAAAGCATGCACTTTTCAAGCTGCTCAACCA 900  
 Db 1321 ATGACATGCGCATTCACAGATGCAAGAAAGCATGCACTTTTCAAGCTGCTCAACCC 1380







XX DE Human expressed polynucleotide SEQ ID NO 24.  
XX KM Human; nootropic; neuroprotective; cytoskeletal; dermatological; viroinide;  
KM immunosuppressive; antineoplastic; anti-HIV; antibacterial; vulnery;  
KM antiparkinsonian; antisticking; antiaemic; antiarrhythmic; cancer;  
KM antineumatic; hepatocytic; cerebroprotective; antiinflammatory;  
KM antiallergic; antidiabetic; anticancer; anticonvulsant; antifungal;  
KM antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
KM neurological disease; infection; nephrotoxic; gene therapy; vaccine;  
ss.  
XX Homo sapiens.  
XX OS  
XX PN WO200155387-A1.  
XX PD  
XX 02-AUG-2001.  
XX PF  
XX 17-JAN-2001; 2001WO-US01310.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
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PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
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PR 14-JUL-2000; 2000US-0218290.  
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PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
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PR 02-OCT-2000; 2000US-0236802.  
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PR 13-OCT-2000; 2000US-0238935.  
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PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
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PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
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PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
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PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.

PR 05-DEC-2000; 2000US-0251988.  
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 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX WPI; 2001-465573/50.  
 DR P-PSDB; AAM99949.  
 XX  
 XX  
 XX  
 PT Isolated digestive system associated polypeptide for treating,  
 PT preventing and/or propping disorders related to the digestive system  
 PT including digestive system cancers and also for testing and detection  
 PT e.g. diagnosis -  
 XX  
 XX  
 PS Claim 1; SEQ ID NO 24; 509pp + Sequence listing; English.  
 XX  
 CC The invention relates to novel genes (AA199548-AA199604) and proteins  
 CC (AAM99936-AAM99984) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;  
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasitic infections.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIP0 at ftp.wip0.int/pub/published\_pot\_sequences.  
 CC  
 XX  
 SO Sequence 828 BP; 251 A; 188 C; 154 G; 235 T; 0 other;  
 Query Match 71.2%; Score 816.2; DB 22; Length 828;  
 Best Local Similarity 99.4%; Pred. No. 2.5e-227;  
 Matches 818; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 325 AAATAATGCAAAATTAACCTTGACACACTAACTTGTCTGTGAGATGAG 384  
 DB 1 AAATAATGCAAAATTAACCTTGACACACTAACTTGTCTGTGAGATGAG 60  
 QY 385 TTTCGGCTTGATCAAGATAGACAGATATGAGCACTAACTTGTGAGATGAG 444  
 DB 61 TTTCGGCTTGATCAAGATAGACAGATATGAGCACTAACTTGTGAGATGAG 120  
 QY 445 GGAGTGGGAAAACCATGCTGATCATCTGTTGTGTGTGAGATGAGCTGCTGCTG 504  
 DB 121 GGAGTGGGAAAACCATGCTGATCATCTGTTGTGTGTGAGATGAGCTGCTGCTG 180  
 QY 505 AGCATACCCAGCTGCTTTTATACAGTAATGACATGCTGAGTCCCATTTTC 564  
 DB 181 AGCATACCCAGCTGCTTTTATACAGTAATGACATGCTGAGTCCCATTTTC 240  
 QY 565 CCCCCTACCTAGGAACATCAATGAAGCAATTGATCAATGCTAGAGATGCAATTGGA 624  
 DB 241 CCCCCTACCTAGGAACATCAATGAAGCAATTGATCAATGCTAGAGATGCAATTGGA 300  
 QY 625 TTGTGATGACCTTTTCTTATATGAGGGGTGTGCTACTTTATCAGACAGACACTCATG 684  
 DB 301 TTGTGATGACCTTTTCTTATATGAGGGGTGTGCTACTTTATCAGACAGACACTCATG 360

QY 685 AAGATGCCAAACATTAATAATCTGACCCCTAAAGTCTGCTACAGTGTATAGTT 744  
 DB 361 AAGATGCCAAACATTAATAATCTGACCCCTAAAGTCTGCTACAGTGTATAGTT 420  
 QY 745 TTCAATGTCACCTCAACCTGCTTATTAACATTTGCAAGTTCTGCGGACCATAGATCATC 804  
 DB 421 TTCAATGTCACCTCAACCTGCTTATTAACATTTGCAAGTTCTGCGGACCATAGATCATC 480  
 QY 805 TACTCCCTGATACCAAGCTGCAACATGAGCAAAAGCATGACATGCGCATCAAGTACA 864  
 DB 481 TACTCCCTGATACCAAGCTGCAACATGAGCAAAAGCATGACATGCGCATCAAGTACA 540  
 QY 865 GAAAGCATGCACTCTTTCACAGGCTGCAACCAATCTTATGTTTTATGAGGAGCA 924  
 DB 541 GAAAGCATGCACTCTTTCACAGGCTGCAACCAATCTTATGTTTTATGAGGAGCA 600  
 QY 925 TCTTTCAAAAATACGTTATGAAAGTGCCAAAGAAATATGGGTCTGAGAGACAGAGA 984  
 DB 601 TCTTTCAAAAATACGTTATGAAAGTGCCAAAGAAATATGGGTCTGAGAGACAGAGA 660  
 QY 985 CAAAGTGTGAGAGAGTTTCTTTTGTATTTGAGGGTCTCTACAGAGCCAACTGATCTTTT 1044  
 DB 661 CAAAGTGTGAGAGAGTTTCTTTTGTATTTGAGGGTCTCTACAGAGCCAACTGATCTTTT 720  
 QY 1045 AGCATTTAAGGTAAACATGCTGCTGCTTTGCTTGATACATGATGATGCTTTCCC 1104  
 DB 721 AGCATTTAAGGTAAACATGCTGCTGCTTTGCTTGATACATGATGATGCTTTCCC 780  
 QY 1105 CTCAAAATTAACATCTGCTTATTTCTGAAAAAATTAATTAATTAATTAATTAATTAAT 1147  
 DB 781 CTCAAAATTAACATCTGCTTATTTCTGAAAAAATTAATTAATTAATTAATTAATTAAT 823  
 RESULT 25  
 AAH77719  
 ID AAH77719 standard; CDNA; 797 BP.  
 XX  
 AC AAH77719;  
 XX  
 DT 13-NOV-2001 (first entry)  
 XX  
 DE Nucleotide sequence of human chemokine receptor CCR11 cDNA clone.  
 XX  
 KW Human; chemokine receptor; CCR11; G protein coupled receptor;  
 KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;  
 KW asthma; angiogenesis; arteriosclerosis vasculature association disease;  
 KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;  
 KW left ventricular diastolic dysfunction; migraine; preterm labour;  
 KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;  
 KW myocardial infarction; congestive heart failure; endometriosis;  
 KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN M020016598-A2.  
 XX  
 PD 13-SEP-2001.  
 XX  
 XX 05-MAR-2001; 2001WO-US07073.  
 XX  
 PR 03-MAR-2000; 2000US-0186928.  
 PR 03-MAR-2000; 2000US-0187231.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;  
 XX WPI; 2001-541918/60.  
 DR  
 XX  
 PT An isolated polynucleotide encoding the chemokine receptor CCR11,  
 PT useful for treating rheumatoid arthritis, inflammatory bowel disease,  
 PT asthma, angiogenesis, arteriosclerosis, cardiac arrhythmias, Raynaud's

phenomenon and migraine -

XX Example 1; Page 103; 110bp; English.

PS AAH7715-20 represent cDNA clones of human chemokine receptor CCR11.  
 CC CCR11 is a member of the G protein coupled receptor family. A CCR11  
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11  
 CC expression or biological activity, is useful for treating many  
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory  
 CC bowel disease, and asthma. They are also useful for treating  
 CC angiogenesis, atherosclerosis vascular association diseases which may  
 CC include but are not limited to hypertension, angina pectoris, cardiac  
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's  
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic  
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive  
 CC heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or  
 CC pulmonary vascular disease.

SQ Sequence 797 BP; 230 A; 168 C; 155 G; 244 T; 0 other;

Query Match 69.5%; Score 797; DB 22; Length 797;

Best Local Similarity 100.0%; Pred. No. 9.7e-22; Mismatches 0; Gaps 0;

Matches 797; Conservative 0; Indels 0; Gaps 0;

QY 15 GAACAGTCAAGATTTATTTATGAGGAAATGAAATGAAATGCACTTATGACTACAG 74

Db 1 GAACAGTCAAGATTTATTTATGAGGAAATGAAATGAAATGCACTTATGACTACAG 60

QY 75 TCAATATGAGTATCTGTATCAAGAAAGATGTCAGAGATTTGCAAAAGTTTCTCTCC 134

Db 61 TCAATATGAGTATCTGTATCAAGAAAGATGTCAGAGATTTGCAAAAGTTTCTCTCC 120

QY 135 TGTATCTCTCAATGATTTGTCATTTGCACTTGGCACTTCCAAATTCAGAGTGGCAAT 194

Db 121 TGTATCTCTCAATGATTTGTCATTTGCACTTGGCACTTCCAAATTCAGAGTGGCAAT 180

QY 195 TTATGCTATTATCAAGAAAGAGAAACCAAGATGTGATCTCTGAATTTGGCTGT 254

Db 181 TTATGCTATTATCAAGAAAGAGAAACCAAGATGTGATCTCTGAATTTGGCTGT 240

QY 255 AGCAGATTTACTCTCTTATTTACTCTGCTCTTTTGGGCTGTAAATGAGTTCATGGGTG 314

Db 241 AGCAGATTTACTCTCTTATTTACTCTGCTCTTTTGGGCTGTAAATGAGTTCATGGGTG 300

QY 315 GGTTTTAAAGGAAATTAATGCAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 374

Db 301 GGTTTTAAAGGAAATTAATGCAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 360

QY 375 TGAATGAGTATCTGCTGTATGATGAGATGAGATGATGAGATGAGATGAGATGAGATG 434

Db 361 TGAATGAGTATCTGCTGTATGATGAGATGAGATGATGAGATGAGATGAGATGAGATG 420

QY 435 CAGCAATGAGAGTGGGAAAACCATGCTGATCATCTGTTCTGTCTGTGATGGCTGC 494

Db 421 CAGCAATGAGAGTGGGAAAACCATGCTGATCATCTGTTCTGTCTGTGATGGCTGC 480

QY 495 CATCTTGGTGAACATACCCAGCTGTTTATTAATCAAGAAATGCAATGCAAGTGCAT 554

Db 481 CATCTTGGTGAACATACCCAGCTGTTTATTAATCAAGAAATGCAATGCAAGTGCAT 540

QY 555 TCCCATTTTCCCGCTACTAGAAATCAATGAAGCATTTGATTAATGCTAGAGAT 614

Db 541 TCCCATTTTCCCGCTACTAGAAATCAATGAAGCATTTGATTAATGCTAGAGAT 600

QY 615 CTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 674

Db 601 CTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 660

QY 675 GACACTCATGAGATGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 734

Db 661 GACACTCATGAGATGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720

QY 735 CGTTATAGTTTTCATTTGATCTGATCACTGCTTATTAATTTGCAAGTTCTGCCGAGCAT 794

Db 721 CGTTATAGTTTTCATTTGATCTGATCACTGCTTATTAATTTGCAAGTTCTGCCGAGCAT 780

QY 795 AGACATCATCTACTCCC 811

Db 781 AGACATCATCTACTCCC 797

RESULT 26

AAZ90529

ID AAZ90529 standard; cDNA; 1053 BP.

XX AAZ90529;

XX 05-JUN-2000 (first entry)

XX Mouse BGCR protein encoding cDNA.

XX BGCR protein; G-protein coupled receptor; human; chemokine; exocytosis;

XX cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;

XX anti-allergic; antiviral; ss.

XX Mus sp.

XX Key Location/Qualifiers

XX CDS 1..1053

XX /tag= a

XX MO9952945-A2.

XX 21-OCT-1999.

XX 16-APR-1999; 99WO-US08395.

XX 16-APR-1998; 98US-0061753.

XX 16-APR-1999; 99US-0061753.

XX (MILL-) MILLENIUM PHARM INC.

XX Gonzalo JA, Gutierrez-Ramos JC;

XX WPI; 1999-620375/53.

XX P-PSDB; AAY57291.

XX New nucleic acid encoding human BGCR receptor, used e.g. for

XX modulating inflammation and tumor growth

XX Disclosure; Fig 3; 123pp; English.

XX The invention relates to a human BGCR protein, a G-protein coupled

XX receptor. The BGCR protein can be expressed by standard recombinant

XX methodology. BGCR are receptor proteins possibly involved in modulation

XX of proinflammatory or stimulatory functions of chemokines; cell

XX proliferation, migration, adhesion and targeting, and exocytosis. The

XX BGCR nucleic acids and derived proteins (or their variants), antibodies

XX and modulators are potentially useful for modulating inflammation;

XX chemotactic activity of leucocytes; angiogenesis; cell proliferation;

XX tumor growth; allergic reactions and entry of human immune deficiency

XX virus into cells, for therapeutic or prophylactic purposes. They are also

XX used for diagnosis and in drug-screening assays. The present sequence

XX represents the cDNA encoding the mouse BGCR protein.

XX Sequence 1053 BP; 261 A; 274 C; 253 G; 264 T; 1 other;

SQ

Query Match 67.0%; Score 768.8; DB 20; Length 1053;

Best Local Similarity 83.1%; Pred. No. 1.8e-213;

Matches 875; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 1 ATGGCTTTGAAAGAAACCAAGTCAAGATTTATTTATGAGGAAATGAATGATGCG 60

Db 1 ATGGCTTTGAAAGTGAACCAAGTCAAGATTTATTTATGAGGAAATGAATGATGATGCG 60

QY 61 ACTTATGACTAAGTGAATGAAATGATGCTGTATCAAGAAAGATGTCAGAAATTTGCA 120



Query Match 56.8%; Score 652; DB 24; Length 660;  
 Best Local Similarity 99.2%; Pred. No. 1,6e-179;  
 Matches 655; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 391 GCTGTATGACATAGACATATGAGAGTAACTAAATCCCGCCCAATCAGAGATG 450  
 DB 1 GCTTGCATAGCATAGACATATGAGAGTAACTAAATCCCGCCCAATCAGAGATG 60  
 QY 451 GGAACCATGCTGATCATCTGTTCTGTGTCTGATGCTGCTGCTCATCTTCTGAGCAT 510  
 DB 61 GGAACCATGCTGATCATCTGTTCTGTGTCTGATGCTGCTGCTCATCTTCTGAGCAT 120  
 QY 511 CCCAGCTGCTTTTATAGATTAAGACAAATGCTGATGCTGCTGCTCATCTTCTGAGCAT 570  
 DB 121 CCCAGCTGCTTTTATAGATTAAGACAAATGCTGATGCTGCTGCTCATCTTCTGAGCAT 180  
 QY 571 TACCTAGAACATCAATGAAAGCATTTGATCAATGCTAGATCTGATGCTGATTTGTA 630  
 DB 181 TACCTAGAACATCAATGAAAGCATTTGATCAATGCTAGATCTGATGCTGATTTGTA 240  
 QY 631 GTACCTTTCTTATATAGAGGGGTGTCTACTTTATCAACAGAGACATCAAGAAATG 690  
 DB 241 GTACCTTTCTTATATAGAGGGGTGTCTACTTTATCAACAGAGACATCAAGAAATG 300  
 QY 691 CCAACATTTAAATATCTGACCCCTAAAGTTCTGCTCAAGTCTTATAGTTTCATT 750  
 DB 301 CCAACATTTAAATATCTGACCCCTAAAGTTCTGCTCAAGTCTTATAGTTTCATT 360  
 QY 751 GTCACTCACTGCTTAAATATCTGACCCCTAAAGTTCTGCTCAAGTCTTATAGTTTCATT 810  
 DB 361 GTCACTCACTGCTTAAATATCTGACCCCTAAAGTTCTGCTCAAGTCTTATAGTTTCATT 420  
 QY 811 CTGATCACCAGCTGACATGACAAAGCATGACATCGCATCCCAAGTCAAGCAAGC 870  
 DB 421 CTGATCACCAGCTGACATGACAAAGCATGACATCGCATCCCAAGTCAAGCAAGC 480  
 QY 871 ATGCACTCTTCAAGTGTGCTCAACCCATCTTATATGTTTATAGAGGATCTTTC 930  
 DB 481 ATGCACTCTTCAAGTGTGCTCAACCCATCTTATATGTTTATAGAGGATCTTTC 540  
 QY 931 AAAAATCTGATTAAGAAAGTGGCCAAAGATATGGGTCTGAGAGACAGAGCAAAAT 990  
 DB 541 AAAAATCTGATTAAGAAAGTGGCCAAAGATATGGGTCTGAGAGACAGAGCAAAAT 600  
 QY 991 GTGAGAGGATTTCTTTGATTTGAGAGGTCTCTACAGAGCCACAGACTTTAGCAT 1050  
 DB 601 GTGAGAGGATTTCTTTGATTTGAGAGGTCTCTACAGAGCCACAGACTTTAGCAT 660

RESULT 28  
 AAH77717  
 ID AAH77717 standard; cDNA; 604 BP.  
 AC AAH77717;  
 XX 13-NOV-2001 (first entry)  
 DE Nucleotide sequence of human chemokine receptor CCR11 cDNA clone.  
 XX Human; chemokine receptor; CCR11; G protein coupled receptor;  
 KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;  
 KW asthma; angiogenesis; atherosclerosis vascular association disease;  
 KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;  
 KW left ventricular diastolic dysfunction; migraine; preterm labour;  
 KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;  
 KW myocardial infarction; congestive heart failure; endometriosis;  
 KW vasospasm; retinopathy; neuropathy; pulmonary vascular disease; ss.  
 OS Homo sapiens.  
 XX WO200166598-A2.  
 PN 13-SEP-2001.  
 PD

XX 05-MAR-2001; 2001WO-US07073.  
 PF 03-MAR-2000; 2000US-0186928.  
 PR 03-MAR-2000; 2000US-0187231.  
 XX (ICOS-) ICOS CORP.  
 XX Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;  
 DR WPI; 2001-541918/60.  
 XX An isolated polynucleotide encoding the chemokine receptor CCR11,  
 PT useful for treating rheumatoid arthritis, inflammatory bowel disease,  
 PT asthma, angiogenesis, atherosclerosis, cardiac arrhythmias, Raynaud's  
 PT phenomenon and migraine -  
 PS Example 1; Page 102; 110pp; English.  
 CC AAH77715-20 represent cDNA clones of human chemokine receptor CCR11.  
 CC CCR11 is a member of the G protein coupled receptor family. A CCR11  
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11  
 CC expression or biological activity, is useful for treating many  
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory  
 CC bowel disease, and asthma. They are also useful for treating  
 CC angiogenesis, atherosclerosis vascular association diseases which may  
 CC include but are not limited to hypertension, angina pectoris, cardiac  
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's  
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic  
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive  
 CC heart failure, endometriosis, vasospasm, retinopathy, neuropathy, or  
 CC pulmonary vascular disease.  
 CC XX  
 SQ Sequence 604 BP; 179 A; 143 C; 109 G; 173 T; 0 other;

Query Match 52.1%; Score 597.6; DB 22; Length 604;  
 Best Local Similarity 99.3%; Pred. No. 1.1e-163;  
 Matches 600; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 537 TGACATGCTAGAGTGCATCCCATTTTCCCGCTACCTAGAGACATCAATGAAGCAT 596  
 DB 1 TGACATGCTAGAGTGCATCCCATTTTCCCGCTACCTAGAGACATCAATGAAGCAT 60  
 QY 597 GATTCATATGCTAGAGATCTGCATTTGATTTGATGATCCCTTTCTTATATAGGGGTG 656  
 DB 61 GATTCATATGCTAGAGATCTGCATTTGATTTGATGATCCCTTTCTTATATAGGGGTG 120  
 QY 657 CTACTTATACAGCAAGAGACATCAATGAAGTGCATTAATAATATCGACCCCT 716  
 DB 121 CTACTTATACAGCAAGAGACATCAATGAAGTGCATTAATAATATCGACCCCT 180  
 QY 717 AAAAGTTCTGCTACAGTGTATTAAGTTTCAATGCTCAATGCTTATATACATTTGT 776  
 DB 181 AAAAGTTCTGCTACAGTGTATTAAGTTTCAATGCTCAATGCTTATATACATTTGT 240  
 QY 777 CAAGTTCTGCGAGCCATATGACATCTACTCCCTGATCACAGTGCAGCAATGAGCA 836  
 DB 241 CAAGTTCTGCGAGCCATATGACATCTACTCCCTGATCACAGTGCAGCAATGAGCA 300  
 QY 837 AGCGATGAGATGCGCATCCCAATGACAGAAAGCATGCACTTTTCAAGCTGCTCA 896  
 DB 301 AGCGATGAGATGCGCATCCCAATGACAGAAAGCATGCACTTTTCAAGCTGCTCA 360  
 QY 897 CCAATCTTTATGTTTATATGAGAGCATTTTCAAAAATCACTGTTATGAAAGTGCAG 956  
 DB 361 CCAATCTTTATGTTTATATGAGAGCATTTTCAAAAATCACTGTTATGAAAGTGCAG 420  
 QY 957 GAAATATGGTCTGAGAGAGACAGAGCAAAATGAGAGGATTTCTTTGATCTGA 1016  
 DB 421 GAAATATGGTCTGAGAGAGACAGAGCAAAATGAGAGGATTTCTTTGATCTGA 480  
 QY 1017 GGGTCTACAGAGCAACAGTACTTTTATGATTTAAAGTAAAGTCTGCTGCTTTTG 1076

Db 481 GGGTCTTACAGACCAACAGTACTTTTACATTTAAAGTAAACCTGCTGCTTTTG 540  
 QY 1077 CTGGATACATATGATGATGCTTCCCTCAATATAAATCTGCTTATTTGAAATA 1136  
 Db 541 CTGGATACATATGATGATGCTTCCCTCAATATAAATCTGCTTATTTGAAACT 600  
 QY 1137 AAAA 1140  
 Db 601 CAAA 604

RESULT 29  
 AAX86675  
 ID AAX86675 standard; DNA; 789 BP.  
 AC AAX86675;  
 XX  
 DT 14-OCT-1999 (first entry)  
 XX  
 DE DNA encoding a seven-pass transmembrane receptor protein fragment.  
 XX  
 KM Seven-pass transmembrane receptor; autoimmune disease;  
 KM white blood cell dysfunction; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..789  
 FT /\*tag= a  
 FT /product= "seven-pass transmembrane receptor  
 FT protein"  
 XX  
 XX WO9933876-A1.  
 XX  
 XX 08-JUL-1999.  
 XX  
 XX 24-DEC-1998; 98WO-JP05886.  
 XX  
 XX 24-DEC-1997; 97JP-0354537.  
 XX  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 XX  
 XX Iehimaru H, Koshio T, Ohno T;  
 XX  
 XX WPI; 1999-493806/41.  
 XX  
 XX P-PSDB; AAY30126.  
 XX  
 XX New seven-pass transmembrane receptor protein useful for treating,  
 XX preventing or diagnosing autoimmune diseases  
 XX  
 XX Claim 16; Page 104-106; 118pp; Japanese.  
 XX  
 XX The present sequence encodes a murine seven-pass transmembrane  
 XX receptor protein fragment. The protein and its DNA can be used to  
 XX screen substances for the diagnosis, prevention and treatment of  
 XX autoimmune diseases, particularly those due to white blood cell  
 XX dysfunction.  
 XX  
 XX Sequence 789 BP; 188 A; 210 C; 185 G; 206 T; 0 other;  
 QY  
 Query Match 51.6%; Score 592.2; DB 20; Length 789;  
 Best Local Similarity 84.4%; Pred. No. 4,6e-162;  
 Matches 666; Conservative 0; Mismatches 123; Indels 0; Gaps 0;  
 QY 262 TTACTCTTCAATTCATCTGCTGCTTTGGGCTGTTAATGACATGAGGGGTTTAA 321  
 Db 1 TTGTACTTCTGATCAGCTGCTCTTTTGGGAGTTAATGACATGAGGATTTCTA 60  
 QY 322 GGGAAATTAATGTCAAATTAATCTGACCTGTACACACTTAACTTGTCTGGAAATG 381  
 Db 61 GGCATAATGATGTCAAAGTACGTGAGCCCTGTACACGCTTAACTTGTCTGGGATG 120  
 QY 382 CAGTTTCTGCTGTATCAGATAGACATATGTCGAGTAATTAAGTCCACGCCAA 441

Db 121 CAGTTCTGCTGTATCAGATAGTACATATATGAGCAATTAACCAACCCCGACCA 180  
 QY 442 TCGAGATGGGAAACCAATGCTGATCATCTGTTCTGTCTGATGCTGCCATCTTG 501  
 Db 181 TCGAGACGGGAGACCCCTGTTGATCATCTGTGTGTGTGATGAGCCCGCATCTTG 240  
 QY 502 CTGAGCATACCCGAGCTGTTTATATACAGTAATGCAATGATAGGATTCCTCCAT 561  
 Db 241 CTGAGCATACCCGAGCTGTTTATATACAGTAATGCAATGATAGGATTCCTCCAT 300  
 QY 562 TTCCCGCTACCTAGGAACATCAATGAAGATGATTCGAATCTGAGATCTGCAAT 621  
 Db 301 TTCCCGCACCACTAGGAACATCCCTGAAGATCATTCATCATCTGGAATTCGGCATC 360  
 QY 622 GGAATTTGATACCTCTTCTTATATGAGGAGTGTGCTACTTATACAGACAGACATC 681  
 Db 361 GGCCTTGTGTGCTGCTTCTCATATGAGGCTGTGCTATGCGCATACCGCCGCGCTC 420  
 QY 682 ATGAGATGCCAAACATTAATAATCTGACCCCTTAAAGTTCTGCTACAGTCTTATA 741  
 Db 421 ATCAATATGCCCAACATTAATAAGTCTGCCCCCTCAGGGTTCCTGCGGTGTGTG 480  
 QY 742 GTTTTCATTTGCTCACTCACTGCTTATAACATTTGCAAGTTCGCGAGCCATAGATC 801  
 Db 481 GTTTTCATTTGCTCACTCACTGCTTATAACATTTGCAAGTTCGCGAGCCATAGATC 540  
 QY 802 ATCTACTCCCTGATACCAAGCTGCAACATGAGCAACGATGAGATGCCATCCAAATC 861  
 Db 541 ATCTACTCCCTGATACCAAGCTGCAACATGAGCAACGATGAGATGCCATCCAAATC 600  
 QY 862 ACAGAAAGCATGCACTCTTTACAGCTGCTCAACCCCATCTTATGTTTATGAGGA 921  
 Db 601 ACAGAGAGCATGCGCTCTTCCACAGCTGCTCAACCCCATCTTATGTTTATGAGGA 660  
 QY 922 GCATCTTTCAAACTACGTTATGAAAGTGGCCAAAGAAATGCGTCTGAGAGACAG 981  
 Db 661 GCCTCTTCAAAACTATATCATGAAAGTGGCCAAAGAAATGATGATCTGAGAGACAG 720  
 QY 982 AGACAAAGTGGAGAGATTTCTTTGATCTGAGGGTCTTACAGGCCAACAGTACT 1041  
 Db 721 AGACAAAGTGGAGAAATTTCTTTGATCTGAGGGTCTTACAGGCCAACAGTACT 780  
 QY 1042 TTTAGCATT 1050  
 Db 781 TTTACATT 789

RESULT 30  
 AA199588/C  
 ID AA199588 standard; cDNA; 821 BP.  
 XX  
 XX AA199588;  
 XX  
 XX 04-JAN-2002 (first entry)  
 XX  
 XX Human expressed polynucleotide SEQ ID NO 51.  
 DE  
 XX Human; noctropic; neuroprotective; cytoskeletal; dermatological; virocidic;  
 KM immunosuppressive; anti-inflamatory; anti-HIV; antibacterial; vulnerary;  
 KM antiparkinsonian; antispasmodic; antianemic; antiarthritic; cancer;  
 KM antineumatic; hepatotropic; cerebroprotective; anti-inflamatory;  
 KM antileptic; antidiabetic; antitumor; anticonvulsant; antifungal;  
 KM antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
 KM neurological disease; infection; neurotropic; gene therapy; vaccine;  
 KM ss.  
 OS Homo sapiens.  
 XX  
 XX WO000155387-A1.  
 XX  
 XX 02-AUG-2001.  
 PD  
 XX

PF 17-JAN-2001; 2001MO-US01310.  
 XX  
 PR 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
 PR 02-MAR-2000; 2000US-0186350.  
 PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 07-JUL-2000; 2000US-0216880.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 11-JUL-2000; 2000US-0217496.  
 PR 14-JUL-2000; 2000US-0218290.  
 PR 26-JUL-2000; 2000US-0220963.  
 PR 26-JUL-2000; 2000US-0220964.  
 PR 14-AUG-2000; 2000US-0224518.  
 PR 14-AUG-2000; 2000US-0224519.  
 PR 14-AUG-2000; 2000US-0225213.  
 PR 14-AUG-2000; 2000US-0225214.  
 PR 14-AUG-2000; 2000US-0225266.  
 PR 14-AUG-2000; 2000US-0225267.  
 PR 14-AUG-2000; 2000US-0225268.  
 PR 14-AUG-2000; 2000US-0225270.  
 PR 14-AUG-2000; 2000US-0225447.  
 PR 14-AUG-2000; 2000US-0225757.  
 PR 14-AUG-2000; 2000US-0225758.  
 PR 14-AUG-2000; 2000US-0225759.  
 PR 18-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226868.  
 PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230439.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0233080.  
 PR 08-SEP-2000; 2000US-0233081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0233397.  
 PR 14-SEP-2000; 2000US-0233398.  
 PR 14-SEP-2000; 2000US-0233399.  
 PR 14-SEP-2000; 2000US-0234400.  
 PR 14-SEP-2000; 2000US-0234401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.  
 PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235484.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 27-SEP-2000; 2000US-0235836.  
 PR 29-SEP-2000; 2000US-0236327.  
 PR 29-SEP-2000; 2000US-0236367.  
 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.

PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240960.  
 PR 20-OCT-2000; 2000US-0241221.  
 PR 20-OCT-2000; 2000US-0241785.  
 PR 20-OCT-2000; 2000US-0241786.  
 PR 20-OCT-2000; 2000US-0241787.  
 PR 20-OCT-2000; 2000US-0241808.  
 PR 20-OCT-2000; 2000US-0241809.  
 PR 20-OCT-2000; 2000US-0241826.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
 PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
 PR 17-NOV-2000; 2000US-0249212.  
 PR 17-NOV-2000; 2000US-0249213.  
 PR 17-NOV-2000; 2000US-0249214.  
 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Barash SC, Ruben SM;  
 PI WPI; 2001-46573/50.  
 XX P-PSDB; AAM99976.  
 DR  
 XX

PT Isolated digestive system associated polypeptide for treating,  
PT preventing and/or proposing disorders related to the digestive system  
PT including digestive system cancers and also for testing and detection  
PT e.g. diagnosis -

XX Claim 1; SEQ ID NO 51; 509bp + Sequence Listing; English.

CC The invention relates to novel genes (AA199548-AA199604) and proteins  
CC (AA199548-AA199604) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;  
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 821 BP; 231 A; 165 C; 188 G; 228 T; 9 other;

Query Match 48.1%; Score 551.8; DB 22; Length 821;  
Best Local Similarity 95.1%; Pred. No. 2,7e-150;  
Matches 597; Conservative 2; Mismatches 24; Indels 5; Gaps 3;

QY 520 GTTTTATACAGTAATGACATGCTAGTGCATTCCTCCATTTCCCGCTCCTAGGA 579  
DB 820 GTGTTTATCNCNTATGACATGCTAGT---CATCCATTTCCCGCTCCTAGGA 765  
QY 580 ACATCAATGAAGGATGATTCATTAATGCTAGATGCTAGTGGATTGATGATCCCTTT 639  
DB 764 ACATCAATGAAGGATGATTCATTAATGCTAGATGCTAGTGGATTGATGATCCCTTT 706  
QY 640 CTATATATGAGGGGCTGCTCTTATACAGGACATCTCATGAAAGATGCCAAACATT 699  
DB 705 CTATATATGAGGGGCTGCTCTTATACAGGACATCTCATGAAAGATGCCAAACATT 646  
QY 700 AAATATCTGACCCCTAAAGATGCTCTACAGTCTGTTATGTTTATGCTACCTCAA 759  
DB 645 AAATATCTGACCCCTAAAGATGCTCTACAGTCTGTTATGTTTATGCTACCTCAA 586  
QY 760 CTGCTTATATACATGCTCAAGTTCTGCGGACCATGACATCATCTACTCCCTGATCAC 819  
DB 585 CTGCTTATATACATGCTCAAGTTCTGCGGACCATGACATCATCTACTCCCTGATCAC 526  
QY 820 AGCTGCAACATGAGCAAGCATGACATGCGCATCAAGTCCAGAAAGCATCGCACATC 879  
DB 525 AGCTGCAACATGAGCAAGCATGACATGCGCATCAAGTCCAGAAAGCATCGCACATC 466  
QY 880 TTTACAGAGCTGCTCAACCCATCTTATGTTTATGAGGACATCTTCAAAAACATC 939  
DB 465 TTTACAGAGCTGCTCAACCCATCTTATGTTTATGAGGACATCTTCAAAAACATC 406  
QY 940 GTTATGAAAGTGGCCAAAGAAATATGAGTCTGAGAAAGACAGAGCAAAAGTGGAGAG 999  
DB 405 GTTATGAAAGTGGCCAAAGAAATATGAGTCTGAGAAAGACAGAGCAAAAGTGGAGAG 346  
QY 1000 TTTCTTATGATCTGAGGGTCTACAGAGCCAAAGATCTTTTGGCTTTTAAAGTAA 1059  
DB 345 TTTCTTATGATCTGAGGGTCTACAGAGCCAAAGATCTTTTGGCTTTTAAAGTAA 286  
QY 1060 AACTGCTGCTGCTTTTGGCTGATACATATGATGCTTTCCCTCAATTAACATC 1119  
DB 285 AACTGCTGCTGCTTTTGGCTGATACATATGATGCTTTCCCTCAATTAACATC 226  
QY 1120 TGCTTATTTCTGAAAAAATAAAAAAAM 1147

DB 225 TGCATTTCTGAACTCAAAAAA 198

RESULT 31

ABA06498/c

ABA06498 standard; cDNA; 821 BP.

10-JAN-2002 (first entry)

Human cDNA SEQ ID NO: 164.

Human; gene therapy; neural disorder; immune system disorder;

muscular disorder; reproductive disorder; gastrointestinal disorder;

pulmonary disorder; cardiovascular disorder; renal disorder;

proliferative disorder; inflammation; ss.

Homo sapiens.

WO200154474-A2.

02-AUG-2001.

17-JAN-2001; 2001WO-US01349.

31-JAN-2000; 2000US-179065P.

04-FEB-2000; 2000US-180628P.

24-FEB-2000; 2000US-184664P.

02-MAR-2000; 2000US-186350P.

16-MAR-2000; 2000US-189874P.

17-MAR-2000; 2000US-190076P.

18-APR-2000; 2000US-198123P.

19-MAY-2000; 2000US-205515P.

07-JUN-2000; 2000US-209467P.

28-JUN-2000; 2000US-214866P.

30-JUN-2000; 2000US-215135P.

07-JUL-2000; 2000US-216647P.

07-JUL-2000; 2000US-216880P.

11-JUL-2000; 2000US-217487P.

11-JUL-2000; 2000US-217496P.

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26-JUL-2000; 2000US-220963P.

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23-AUG-2000; 2000US-227009P.

30-AUG-2000; 2000US-228924P.

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08-SEP-2000; 2000US-231243P.





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Db 345 TTTCCTTTGATTCTGAGGTCCTACAGAGCCAAACGATACCTTTAGATTAAAGTTAA 286  
Qy 1060 AACTGCTCTGCTTTGCTTTGCTTGATACATATGATGATGCTTTCCCTCAATTAACATC 1119  
Db 285 AACTGCTCTGCTTTGCTTTGCTTGATACATATGATGATGCTTTCCCTCAATTAACATC 226  
Qy 1120 TGCCTTATCTGAAAAAAT 1147  
Db 225 TGCAATTATCTGAAACTCAAAAAA 198  
RESULT 32  
AAS28957/c  
ID AAS28957 standard; cDNA; 821 BP.  
XX AAS28957;  
AC  
XX  
XX 21-NOV-2001 (first entry)  
DT  
XX  
DE cDNA encoding for human uterine motility-association polypeptide #22.  
XX  
XX Human; uterine motility-association disorder; uterus; pregnancy;  
KM labour; menstrual cycle; gene therapy; ss.  
XX Homo sapiens.  
OS  
XX  
XX W0200155201-A1.  
XX PD  
XX 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01317.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
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PR 08-DEC-2000; 2000US-0251989.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
  
(HUMA-) HUMAN GENOME SCT INC.  
PA Rosen CA, Barash SC, Ruben SM;  
XX MPI: 2001-451936/48.  
XX P-PSDB; AAUI8361.  
XX  
XX Isolated polypeptide for treating, preventing and/ or prognosing  
PT disorders of the endocrine system such as reproductive disorders,  
PT endocrine cancers and also for testing and detection e.g. diagnosis -  
XX  
XX Claim 1; SEQ ID No 90; 604pp; English.  
PS  
XX  
XX Sequences AAS29511-AAS29736 represent cDNA molecules, which encode the  
CC ascorbic polypeptides of the invention. Endocrine polypeptides and their  
CC associated polynucleotides of the invention are useful in the diagnosis,  
CC treatment and prevention of various types of disorders in e.g. humans,  
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A  
CC pathological condition can be determined by determining the presence or  
CC absence of a mutation in an endocrine polynucleotide. The treatable  
CC disorders include autoimmune diseases such as rheumatoid arthritis,  
CC

hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

Query Match 48.1%; Score 551.8; DB 22; Length 821;  
Best Local Similarity 95.1%; Pred. No. 2,7e-150; Mismatches 24; Indels 5; Gaps 3;  
Matches 597; Conservative 2;

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DB 820 GTGTTTATCAGTAATGACATGCTAGTGCATTCCTCCATTTCCCGCTACTAGGA 765  
QY 580 ACATCAATGAAAGCATTTGATTAATGCTAGATTCGATTTGATGATCCCTTT 639  
DB 764 ACATCAATGAAAGCATTTGATTAATGCTAGATTCGATTTGATGATCCCTTT 706  
QY 640 CTTTATATGAGGCTGTGCTACTTATACAGCAAGACATCAATGAAAGCATTT 699  
DB 705 CTTTATATGAGGCTGTGCTACTTATACAGCAAGACATCAATGAAAGCATTT 646  
QY 700 AAATATATCGACCCCTTAAAGTTCTGCTACAGTCTGTAATGTTTCATTTGCTACTCA 759  
DB 645 AAATATATCGACCCCTTAAAGTTCTGCTACAGTCTGTAATGTTTCATTTGCTACTCA 586  
QY 760 CTGCTTATTAACATTTGCTAGTTCGCTGAGCCATTAACATCTCTCTGATACCC 819  
DB 585 CTGCTTATTAACATTTGCTAGTTCGCTGAGCCATTAACATCTCTCTGATACCC 526  
QY 820 AGCTGCAACATGAGCAACGATGAGACATGCGCATCAAGCAAGCAAGATGCGACTC 879  
DB 525 AGCTGCAACATGAGCAACGATGAGACATGCGCATCAAGCAAGCAAGATGCGACTC 466  
QY 880 TTTACAGCTGCTCAACCAATCTTATGTTTATGAGGAGCATTTCAAAAATAC 939  
DB 465 TTTACAGCTGCTCAACCAATCTTATGTTTATGAGGAGCATTTCAAAAATAC 406  
QY 940 GTTATGAAAGTGGCCAGAAATATGGTCTCTGAGAAAGACAGACAAAGTGTGAGAG 999  
DB 405 GTTATGAAAGTGGCCAGAAATATGGTCTCTGAGAAAGACAGACAAAGTGTGAGAG 346  
QY 1000 TTTCTTTTGAATTCGAGGCTCTACAGAGCAACAGTACTTTTAGCATTTAAAGTAA 1059  
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QY 1060 AACTGCTGCTGCTTTGCTGATACATATGATGATGCTTTCCCTCAATTAATACATC 1119  
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RESULT 34  
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AC AAS30190;  
XX AAS30190;  
XX 21-NOV-2001 (first entry)  
DT  
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XX Human; antiinflammatory; neuroprotective; immunomodulator; vulnery;  
KW Cardiovascular; cytosolic; nephrotoxic; antihaemic; nephritis;  
KW immunosuppressive; kidney disorder; renal failure; hypertension;  
KW cardiovascular disorder; myocardial infarction; blood disorder; anaemia;  
KW blood coagulation disorder; electrolyte imbalance disorder; cancer;  
KW hypotension; hyperkalaemia; neoplastic disorder; nephroma;  
KW autoimmune disease; inflammatory disease; reproductive system disorder;  
KW endocrine disorder; neural activity; neurological disorder;  
KW wound healing; respiratory disorder; ss.  
OS Homo sapiens.  
PN WO20015328-A2.  
PD 02-AUG-2001.  
PF 17-JAN-2001; 2001WO-US01359.  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
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 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
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 PI Rosen CA, Barash SC, Ruben SM;  
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 DR MPI, 2001-488787/53.  
 DR P-PSDB; AAU18669.  
 XX  
 PT New polynucleotides and polypeptides, useful for diagnosing, treating,  
 PT preventing or prognosing e.g. kidney, cardiovascular, blood,  
 PT electrolyte imbalance or neoplastic disorders, autoimmune diseases,  
 PT cancers -  
 XX  
 PS Claim 1; SEQ ID No 36; 506bp; English.  
 XX  
 CC The invention relates to novel nucleic acids and polypeptides useful for  
 CC diagnosing, treating, preventing and/or prognosing disorders related to  
 CC these polypeptides. The polynucleotides are especially useful in the  
 CC diagnosis, prognosis, prevention and/or treatment of diseases which  
 CC include kidney disorders (e.g. renal failure or nephritis),  
 CC cardiovascular disorders (e.g. hypertension or myocardial infarction),  
 CC blood disorders (e.g. anaemia or blood coagulation disorders),  
 CC electrolyte imbalance disorders (e.g. hyponatraemia or hyperkalaemia),  
 CC neoplastic disorders (e.g. nephroma or renal cell cancer), autoimmune  
 CC diseases, cancers, inflammatory diseases, reproductive system  
 CC disorders, endocrine disorders, neural activity and neurological  
 CC disorders, wound healing and respiratory disorders. AAS30165-AAS30251  
 CC represent the novel human renal and cardiovascular-associated nucleic  
 CC acid sequences of the invention. Note: The sequence data for this patent  
 CC did not form part of the invention. The sequence data for this patent  
 CC electronic format directly from WIPO at:  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
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 Best Local Similarity 95.1%; Pred. No. 2; e-150;  
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KW Human; neoplastic disease associated polypeptide; cancer; gene therapy;  
KW hyperproliferative disorder; neural disorder; immune system disorder;  
KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
KW pulmonary disorder; cardiovascular disorder; renal disorder; ss.  
KW neuroprotective; cyostatic; anti inflammatory; vasotropic; ss.  
XX  
OS Homo sapiens.  
XX  
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XX  
PD 02-AUG-2001.  
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 PR 05-JAN-2001; 2001US-0259678.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Rosen CA, Barash SC, Ruben SM;  
 XX  
 PI WPI; 2001-581633/65.  
 XX P-PSDB; AAU87280.  
 DR  
 XX

PT New isolated nucleic acid encoding a protein for diagnosing,  
 PT preventing, treating or ameliorating medical conditions and used as  
 PT food additives or preservatives -

XX Claim 1; SEQ ID No 200; 837bp; English.

XX The invention describes an isolated nucleic acid molecule (I) encoding a  
 CC novel central nervous system protein. (I) and polypeptides (II) encoded  
 CC by (I), are used to treat a medical conditions and in diagnosis of a  
 CC pathological condition. Disorders which are diagnosed or treated include  
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
 CC angiodysplasia, nervous system disorders e.g. Alzheimer's disease and  
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
 CC adenocarcinomas and irritable bowel syndrome, reproductive system  
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
 CC leukaemia, disorders involving neovascularisation e.g. malignancies,  
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
 CC acute kidney failure and blood related disorders e.g. myocardial  
 CC infarction. The polypeptides can also be used to aid wound healing and  
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
 CC maintain organs before transplantation, for supporting cell culture of  
 CC primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 48.1%; Score 551.8; DB 23; Length 821;  
 Best Local Similarity 95.1%; Pred. No. 2,7e-150;

Matches 597; Conservative 2; Mismatches 24; Indels 5; Gaps 3;

QY 520 GTTTTATACAGTAATGACATGCTAGTGATCCATTTCCCGGCTACCTGGA 579  
 DB 820 GTGTTTATCCNGTATGACATGCTAGT--CATCCATTTCCCGGCTACCTGGA 765  
 QY 580 ACATCAATGAAAGCATGATTCATTAATGCTAGATCTGATTTGTTAGTACCTTT 639  
 DB 764 ACATCAATGAAAGCATGATTC--AATGCTAGATCTGATTTGTTAGTACCTTT 706  
 QY 640 CTATATATGGGGGCTGCTACTTATACAGCAAGACACTCATGAAGATGCCAACATT 699  
 DB 705 CTATATATGGGGGCTGCTACTTATACAGCAAGACACTCATGAAGATGCCAACATT 646  
 QY 700 AAAATATCTGCAGCCCTTAAAGTTCTGCTCAAGTCTTATAGTTTTCATGTCACCTCA 759  
 DB 645 AAAATATCTGCAGCCCTTAAAGTTCTGCTCAAGTCTTATAGTTTTCATGTCACCTCA 586  
 QY 760 CTGCTTATTAACATTTGCAAGTTCTGCCGAGCCATAGACATCTACTCCCTGATCAC 819  
 DB 585 CTGCTTATTAACATTTGCAAGTTCTGCCGAGCCATAGACATCTACTCCCTGATCAC 526  
 QY 820 AGCTGCAACATGAGCAAGCATGAGATGCCATCCAACTCACAGAAAGCATGCCACTC 879  
 DB 525 AGCTGCAACATGAGCAAGCATGAGATGCCATCCAACTCACAGAAAGCATGCCACTC 466  
 QY 880 TTTCACAGCTGCTCAACCAATCTTATGTTTATGAGGAGCATCTTCAAAAATCTAC 939  
 DB 465 TTTCACAGCTGCTCAACCAATCTTATGTTTATGAGGAGCATCTTCAAAAATCTAC 406  
 QY 940 GTTATGAAAGTGCCCAAGAAATATGGTCTGTGAGAAAGACAGACAAAGTGTGAGAG 999  
 DB 405 GTTATGAAAGTGCCCAAGAAATATGGTCTGTGAGAAAGACAGACAAAGTGTGAGAG 346  
 QY 1000 TTTCCTTTTATTTCTGAGGGTCTTACAGAGCCCAAGTCTTTTATGAGTAAAGTAA 1059  
 DB 345 TTTCCTTTTATTTCTGAGGGTCTTACAGAGCCCAAGTCTTTTATGAGTAAAGTAA 286  
 QY 1060 AACTGCTGCTCTTTGCTGATATATGATGATGCTTTCCCTCAAAATTAACATC 1119  
 DB 285 AACTGCTGCTCTTTGCTGATATATGATGATGCTTTCCCTCAAAATTAACATC 226

QY 1120 TGCCTATTTCTGAAAAAATAAAAAAAM 1147  
 DB 225 TGCCTATTTCTGAAAAAATAAAAAAAM 1198

RESULT 37

ABAB08406  
 ID ABAB08406 standard; cDNA; 493 BP.

AC ABAB08406;

DT 11-JAN-2002 (first entry)

DE Human orphan GPCR homologue-encoding cDNA, SEQ ID NO:182.

KW Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;  
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW antasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
 KW antifungal; vulnery; antitumor; 88.

XX Homo sapiens.

OS WO200157188-A2.

PN 09-AUG-2001.

PD 05-FEB-2001; 2001WO-US03800.

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

PA (HSE-) HYSEQ INC.

PI Tang YF, Liu C, Drmanac RT;

DR WPI; 2001-457740/49.

DR P-PSDB; ABB11162.

PT Human proteins and DNA encoding sequences useful for preventing,  
 PT treating or ameliorating a medical condition in a mammalian subject  
 PT e.g. arthritis and cancer -

XX Claim 1; Page 402; 1963bp; English.

XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABB108225-ABB109574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical

CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a cDNA encoding a  
 CC novel human polypeptide of the invention.

XX Sequence 493 BP; 135 A; 103 C; 103 G; 152 T; 0 other;

Query Match 43.0%; Score 493; DB 22; Length 493;

Best Local Similarity 100.0%; Pred. No. 2.9e-133; Mismatches 0; Gaps 0;

Matches 493; Conservative 0; Indels 0; Gaps 0;

QY 217 AGAACCAAAAGATGCTGATACCTGAAATTTGGCTGAGAGATTACTCTTATTC 276  
 Db 1 AGAACCAAAAGATGCTGATACCTGAAATTTGGCTGAGAGATTACTCTTATTC 60  
 QY 277 ACTGCGCTTTTGGGCTGTTAATGCAATTCAGTGGGTTTAAAGGAAATATGTC 336  
 Db 61 ACTGCGCTTTTGGGCTGTTAATGCAATTCAGTGGGTTTAAAGGAAATATGTC 120  
 QY 337 AAAATACCTGAGCTTGTACACACTAACTTTGTCTGGAATGCACTTTCGCTTGT 396  
 Db 121 AAAATACCTGAGCTTGTACACACTAACTTTGTCTGGAATGCACTTTCGCTTGT 180  
 QY 397 ATCAGCAGATGAGATGATGAGAGTAAAGTCCAGCAGATGAGAGTGGGAAA 456  
 Db 181 ATCAGCAGATGAGATGATGAGAGTAAAGTCCAGCAGATGAGAGTGGGAAA 240  
 QY 457 CCATGCTGATCATCTGTTCTGTCTGTGATGAGTGGCTGCATCTTCTGAGCATA 516  
 Db 241 CCATGCTGATCATCTGTTCTGTCTGTGATGAGTGGCTGCATCTTCTGAGCATA 300  
 QY 517 CTGCTTTTATACAGTAAATGACATGCTGAGTCCATTTTCCCGCTACTTA 576  
 Db 301 CTGCTTTTATACAGTAAATGACATGCTGAGTCCATTTTCCCGCTACTTA 360  
 QY 577 GGAACATCAAGAAAGCAATGATCAATGAGATCTGATGATTTGTAGTACC 636  
 Db 361 GGAACATCAAGAAAGCAATGATCAATGAGATCTGATGATTTGTAGTACC 420  
 QY 637 TTTCTTATATGAGGAGTGTCTTATTCACAGCAGACACTCATGAGATGCCAAC 696  
 Db 421 TTTCTTATATGAGGAGTGTCTTATTCACAGCAGACACTCATGAGATGCCAAC 480  
 QY 697 ATTAAATATCTC 709  
 Db 481 ATTAAATATCTC 493

RESULT 38

AAKS2443 ID AAKS2443 standard; cDNA; 493 BP.

AAKS2443;

06-NOV-2001 (first entry)

Human polynucleotide SEQ ID NO 1972.

Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorder; arthritis; inflammation; ss.

XX Homo sapiens.

XX WO200157190-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US04098.

XX 03-FEB-2000; 2000US-0496914.

XX 27-APR-2000; 2000US-0560875.

XX 20-JUN-2000; 2000US-0598075.

XX 19-JUL-2000; 2000US-0620325.

XX 15-SEP-2000; 2000US-0654936.

XX 15-SEP-2000; 2000US-0663561.

XX 20-OCT-2000; 2000US-0693325.

XX 30-NOV-2000; 2000US-0728422.

XX (HSE-) HYSEQ INC.

XX Tang YT, Liu C, Dmanac RT, Aundt V, Zhou P, Xu C, Cao Y, Ma Y;  
 XX Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
 XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
 XX MPI: 2001-476283/51.  
 XX P-PSDB; AAM79310.

XX Nucleic acids encoding polypeptides with cytokine-like activities,  
 XX useful in diagnosis and gene therapy -  
 XX Claim 1; Page 4381; 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
 CC (AAM80020) are omitted as the relevant pages from the sequence listing  
 CC were missing at the time of publication.

XX Sequence 493 BP; 135 A; 103 C; 103 G; 152 T; 0 other;

Query Match 43.0%; Score 493; DB 22; Length 493;

Best Local Similarity 100.0%; Pred. No. 2.9e-133; Mismatches 0; Gaps 0;

Matches 493; Conservative 0; Indels 0; Gaps 0;

QY 217 AGAACCAAAAGATGCTGATACCTGAAATTTGGCTGAGAGATTACTCTTATTC 276  
 Db 1 AGAACCAAAAGATGCTGATACCTGAAATTTGGCTGAGAGATTACTCTTATTC 60  
 QY 277 ACTGCGCTTTTGGGCTGTTAATGCAATTCAGTGGGTTTAAAGGAAATATGTC 336  
 Db 61 ACTGCGCTTTTGGGCTGTTAATGCAATTCAGTGGGTTTAAAGGAAATATGTC 120  
 QY 337 AAAATACCTGAGCTTGTACACACTAACTTTGTCTGGAATGCACTTTCGCTTGT 396  
 Db 121 AAAATACCTGAGCTTGTACACACTAACTTTGTCTGGAATGCACTTTCGCTTGT 180  
 QY 397 ATCAGCAGATGAGATGATGAGAGTAAAGTCCAGCAGATGAGAGTGGGAAA 456  
 Db 181 ATCAGCAGATGAGATGATGAGAGTAAAGTCCAGCAGATGAGAGTGGGAAA 240  
 QY 457 CCATGCTGATCATCTGTTCTGTCTGTGATGAGTGGCTGCATCTTCTGAGCATA 516



XX 03-MAR-2000; 2000US-0186928.  
PR 03-MAR-2000; 2000US-0187231.  
XX  
XX (ICOS-) ICOS CORP.  
XX

PI Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;  
XX  
XX WPI; 2001-541918/60.  
XX

XX An isolated polynucleotide encoding the chemokine receptor CCR11,  
PT useful for treating rheumatoid arthritis, inflammatory bowel disease,  
PT asthma, angiogenesis, atherosclerosis, cardiac arrhythmias, Raynaud's  
PT phenomenon and migraine -  
XX

XX Example 1; Page 102-103; 110pp; English.  
XX

XX AAH77715-20 represent cDNA clones of human chemokine receptor CCR11.  
CC CCR11 is a member of the G protein coupled receptor family. A CCR11  
CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11  
CC expression or biological activity, is useful for treating many  
CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory  
CC bowel disease, and asthma. They are also useful for treating  
CC angiogenesis, atherosclerosis, vascular association diseases which may  
CC include but are not limited to hypertension, angina pectoris, cardiac  
CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's  
CC phenomenon, migraine, preterm labour, oesophageal spasm, ischemic  
CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive  
CC heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or  
CC pulmonary vascular disease.  
XX

XX Sequence 374 BP, 111 A; 92 C; 72 G; 99 T; 0 other;  
SQ

Query Match 30.4%; Score 348.6; DB 22; Length 374;  
Best Local Similarity 98.9%; Pred. No. 3e-91;  
Matches 351; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 786 CCGAGCCATACATCATCTCTCCCTGATACCAAGTCGCAACATGAGCAAGCATGA 845  
DB 1 CCGAGCCATACATCATCTCTCCCTGATACCAAGTCGCAACATGAGCAAGCATGA 60

QY 846 CATGCCATCCAGTCACAGAAAGATGACACTCTTCAAGCTGCTCAACCAATCCT 905  
DB 61 CATGCCATCCAGTCACAGAAAGATGACACTCTTCAAGCTGCTCAACCAATCCT 120

QY 906 TTATGTTTTATGGAGATCTTCAAAACTACGTTATGAAAGTGCCAAAGAAATATGG 965  
DB 121 TTATGTTTTATGGAGATCTTCAAAACTACGTTATGAAAGTGCCAAAGAAATATGG 180

QY 966 GTCTGGAGAAAGACAGACAAAGTGTGAGAGATTCTTTGATTTCTGAGGCTCTAC 1025  
DB 181 GTCTGGAGAAAGACAGACAAAGTGTGAGAGATTCTTTGATTTCTGAGGCTCTAC 240

QY 1026 AGAGCAACACAGTCTTTAGATTTAAAGGTAAGAGTCTGCTTTGCTTGATGATAC 1085  
DB 241 AGAGCAACACAGTCTTTAGATTTAAAGGTAAGAGTCTGCTTTGCTTGATGATAC 300

QY 1086 ATATGATGATGCTTTCCCTCAATAAATACATCTGCTTATTTCTGAAAAA 1140  
DB 301 ATATGATGATGCTTTCCCTCAATAAATACATCTGCTTATTTCTGAAAAA 355

Search completed: March 24, 2003, 01:36:12  
Job time : 396 secs





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83	97	8.5	560	13	BM529678	BM529678 ftd10903.y
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85	96.4	8.4	506	13	BM268628	BM268628 527036 MA
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87	95.6	8.3	309	10	BB606854	BB606854 BB606854
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92	93.2	8.1	652	10	BB620181	BB620181 BB620181
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95	91.2	8.0	488	10	AM403941	AM403941 UI-HR-EKO
96	91.2	8.0	668	9	AL660726	AL660726 AL660726
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98	91.2	8.0	672	9	AL631373	AL631373 602992407
99	91.2	8.0	804	13	B1249077	B1249077 602992407
100	90.8	7.9	628	14	BQ396595	BQ396595 NISC.n521
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102	90.4	7.9	676	9	AJ398841	AJ398841 AJ398841
103	90	7.8	487	10	BE656336	BE656336 UI-M-BHO-
104	90	7.8	534	9	AL774447	AL774447 AL774447
105	89	7.8	534	9	AL774447	AL774447 AL774447
106	89	7.8	622	9	A1648943	A1648943 UK3308.x
107	88.6	7.7	894	13	B1771103	B1771103 603059678
108	88.4	7.7	765	13	BM387369	BM387369 UI-R-CNT-
109	88	7.7	650	13	B1837704	B1837704 603086564
110	88	7.7	1119	13	BM543622	BM543622 AGENCOURT
111	88	7.7	1126	14	BM919012	BM919012 AGENCOURT
112	87.6	7.6	499	10	AM389565	AM389565 RC2-ST016
113	87.4	7.6	574	17	AO661727	AO661727 HS.5219.A
114	86.4	7.5	520	13	BM522324	BM522324 fy06e07.y
115	85.8	7.5	580	10	AV708554	AV708554 AV708554
116	85.8	7.5	598	10	AM822616	AM822616 uq13b02.y
117	85	7.4	448	10	BE245301	BE245301 TCBAPIE24
118	85	7.4	529	12	BG276842	BG276842 uv08b09.y
119	85	7.4	558	12	BE750883	BE750883 202546 MA
120	85	7.4	689	9	AJ449590	AJ449590 AJ449590
121	84.4	7.4	476	17	AQ692710	AQ692710 HS.5415.A
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123	84.2	7.3	628	10	AM227957	AM227957 up19e03.y
124	84	7.3	585	10	BE627479	BE627479 uus2b07.y
125	83.2	7.3	688	10	BE617402	BE617402 601442039
126	82.4	7.2	499	17	AZ942785	AZ942785 2M0203D07
127	82	7.1	501	12	BG407320	BG407320 dab17c07.
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130	80.4	7.0	1017	14	BM922807	BM922807 AGENCOURT
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133	79.2	6.9	588	14	BQ132127	BQ132127 fz63b02.y
134	79.2	6.9	863	13	B1661279	B1661279 60304243
135	78.4	6.8	538	10	BB654422	BB654422 BB654422

## ALIGNMENTS

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DEFINITION  
AL561603 LTI\_NFL010\_BC2 Homo sapiens CDNA clone CSDDL0111D20 5  
prime, mRNA sequence.  
853 bp mRNA linear EST 16-FEB-2001

ACCESSION  
AL561603  
VERSION  
AL561603.1  
GI:12909196

KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 853)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91060 Evry cedex - France  
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
location/Qualifiers

## FEATURES

source  
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/db\_xref="taxon:9606"  
/clone="CSDDL0111D20"  
/clone\_id="LTI\_NFL010\_BC2"  
/sex="male"  
/issue\_type="B cells from Burkitt lymphoma"  
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies. Contact : Feng Liang life technologies, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"  
BASE COUNT 212 a 197 c 170 g 255 t 19 others  
ORIGIN

Query Match 70.1%; Score 804; DB 9; Length 853;  
Best Local Similarity 95.8%; Pred.No. 5.3e-180;  
Matches 815; Conservative 17; Mismatches 18; Indels 1; Gaps 1;

1 ATGGCTTGGAAACACACACACACATTTATTTATGAGAAATGAATGATGCG 60  
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183 ATGGTATGCGCAATTTATGATGATGATGATGATGATGATGATGATGAT 242  
241 CTGATTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
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OY	601	CAATGCTGAGAGTCTGGATTGGAAATTTGTAGTAACCCCTTCATTATGAGGGGATGCTAC	660
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ACCESSION	BG205105		
VERSION	BG205105.1 GI:13726792		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 782) Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J ,E., Veloso,N., Klika,A., Hess,J., Cothen,K., Lo,K., Offenbacher ,J., Danzig,J. and Ducar,M. Creation of genome-wide protein expression libraries using random activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001)		
TITLE	Journal.		
JOURNAL	Medline		
MEDLINE	21227151		
COMMENT	Contact: Scott J. Cain Atherys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@atherys.com High quality sequence stop: 338. Location/Qualifiers 1..782		
FEATURES	source		
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Matches 521; Conservative	0; Mismatches 66; Indels 1; Gaps 1		
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Db	17	GNCTTTGGAACATGACACAGTCAACAGATTATTTATGAGAAAATGAATGATGATGCTT	76
OY	63	TTATGACTACATCAATATATGATGATCTGTATATCAAAAGAAGATGTCAAGAAATTTTGAA	122

Db 77 TTATGACTACAGTCAATATATGAACTGATCTGTATTCAAAGAAAGATGTGAGAAATTGCAAA 136

Qy 123 AGTTTCTCTCCCTGTATTTCCACAAATAGTTTTGTCATTGGACTTGCAGGCAATTTCAT 182

Db 137 AGTTTCTCTCCCTGTATTTCCACAAATAGTTTTGTCATTGGACTTGCAGGCAATTTCAT 196

Qy 183 GGTAGTGGCAATTTATGCCATTTACAAAGAAACAGAAACCAACAGATGATGTCATCCT 242

Db 197 GGTAGTGGCAATTTATGCCATTTACAAAGAAACAGAAACCAACAGATGATGTCATCCT 256

Qy 243 GAATTTGGCTGTAGCAATTTACTCTCTTATTCACCTGTGCTTTTGGCTGTAAATGC 302

Db 257 GAATTTGGCTGTAGCAATTTACTCTCTTATTCACCTGTGCTTTTGGCTGTAAATGC 316

Qy 303 AGTTTCAGTGGTGGCTTTTATGAGGAAATATATGTGCAAAATTAATCTTCAACCTTTTCAACT 362

Db 317 AGTTTCAGTGGTGGCTTTTATGAGGAAATATATGTGCAAAATTAATCTTGGGCTTTGCACACT 376

Qy 353 AAACCTTGTCTCTGGAAATGCAAGTTTCTGGCTGTATATGACATGACAGATATGTGGAGT 422

Db 377 AAACCTTGTCTCTGGAAATGCAAGTTTCTGGCTGTATATGACATGACAGATATGTGGAGT 436

Qy 423 AACTAAATGCCCAAGCCATCAGAGTGGGAAAAACAATGCTGATCATCTG-TTTCTGTG 481

Db 437 AACTAAATGCCCAAGCCATCAGAGTGGGAAAAACAATGCTGATCATCTGCCCCCTGG 496

Qy 482 TCTGATGAGCTGCCATCTTGTCTGAGCATACCCCAAGCTGGTTTTTATACATTAATGCA 541

Db 497 TGTGAACCGATGACATCTTGTCTGACAGATACCATCTGTCAACTCAATCCGCCCCGACA 556

Qy 542 ATTCGAGGTGCATTCATTTTCCGCCCTCTACAGAAATCATCATGA 589

Db 557 CCGCTTCGGCCAAACCATTTTTTCCGGATATACCTCCAGCCTGTATGA 604

	RESULT 3			
	B16I81904			
LOCUS	B16I81904	575 bp	mRNA	linear EST 17-SEP-2001
DEFINITION	461411 MARC lBOV Bos taurus cDNA 5' , mRNA sequence.			
ACCESSION	B16I81904			
VERSION	B16I81904.1	GI:15634829		
KEYWORDS	EST.			
SOURCE	Cow.			
ORGANISM	Bos taurus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
	Bovidae; Bovinae; Bos.			
REFERENCE	1 (bases 1 to 575)			
AUTHORS	Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Way,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett G.L., Heaton,M.P., Iaegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G., Partee,G., Holt,I., Karamycheva,S., Lang,F., Quackenbush,U. and Keefe,J.W.  Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013  Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel.: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt trimmed with phred v0.98f9d04.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options. PCR primers FORWARD: AGGAAGCACGTATGCACCATT BACKWARD: GTTTCCTCATGCCACGAG Plate: 135 row: L column: 20 Seq primer: ATTTAGTGTAACAATAAAG.  Location/Qualifiers			
FEATURES				

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		/clone_lib="MARC 150V"
		/issue_type="pooled"
		/lab_host="DH10B"
		/note="Vector: PCMV SPORTE; Site 1: NotI; Site 2: SalI;
		Library made from pooled tissue from lymph node, ovary,
		fet, hypothalamus, and pituitary."
BASE COUNT	162 a 109 c 129 g 175 t	
ORIGIN		
Query Match	40.6%;	Score 465.6; DB 13; Length 575;
Best Local Similarity	89.5%;	Pred. No. 7, 6e-100;
Matches 501; Conservative 0;	Mismatches 59;	Indels 0; Gaps 0
QY	1	ATGGCTTTGGACAGAACCCAGTCACAGATTATTATTATGAGAAAAATGAATGAATGCC 60
DB	15	ATGGCTGTGGAAATACCAACGAGTCACAGATTACTATTATGAGAAATGAATGAATGAC 74
QY	61	ACTTATGACTACAGTCAATATATGAACTGATTTGTATCAAAAGAAATGTCAAGAAATTTGCA 120
DB	75	ACTCAATGACTATATGATAGATGAAGATCTGTATATAAAAGAAAGGTCAAGAAATTTGCA 134
QY	121	AAAGTTTTCTCCCTGATATCCACAAATAGTTTGTGTCATTGAGCTTGAGGCAATTC 180
DB	135	AAAGTTTTCTTACTCTGCTCTTTCACAAATAGCTTTTCAATCTTGAGCTTGAGGCAATTC 194
QY	181	ATGGTATGGCAATTTATATGCTATTACAGAAACAGAGAACCAAGATGTATCATC 240
DB	195	ACTGTATGGCCGATTTATGCTATTACAAAAGCCGAGAACCAAGATGTATCATC 254
QY	241	CTGAATTTGGCTGTACAGATTACTTCCTTTATTTCACTCTGCTTTTGGCTGTTAAT 300
DB	255	TTGAATTTGGCAGATGGCGGATTTATTCCTTTATTTCACTTTGCTTTTGGCGAGTTAAT 314
QY	301	GGAGTTCATGGGGGGTTTTAGGGAAATPATATGTGCAAAATACCTCAGCTTGATACA 360
DB	315	GGAGTTCATGGGGGGTTTTAGGGAAATCATATGTGCAAAATACCTCAGCTTGATACA 374
QY	361	CTAACTTTGTCTCTGGAATGACAGTTTCTGGCTTGTATGACATAGACAGATATGTGGA 420
DB	375	GTCAATTTTGTGTCTGGAAATGACAGTTTCTGGCTTGTATGACACACAGATATGTGGA 434
QY	421	GTACTAAAGTCCCGACCAATCAGAGTGGGAAAAACAATGCTGATCATCTGTTTCTGT 480
DB	435	GTACTAAAGTCCCGACCAATCAGAGTGGGAAAAACAATGCTGATCATCTGTTTCTGT 494
QY	481	GTCTGATAGGCTGCCATCTTGTGACACATACCCAGCTGTTTTTATACAGAAATGAC 540
DB	495	GTCTGATAGGCTGCCATCTTGTGACATATCCCTCAGTGTGTTTTTATACAGAAATGAT 554
QY	541	AATGTAGTGTGATTTCCCAT 560
DB	555	AAAGCTAGTGTGTTCCCAT 574
RESULT 4		
LOCUS	BB618186	617 bp mRNA linear EST 31-AUG-2001
DEFINITION	BB618186 RIKEN full-length enriched, 6 days neonate head Mus	
ACCESSION	musculus cDNA clone 5430400N11 5', mRNA sequence.	
VERSION	BB618186	
KEYWORDS	BB618186.1 GI:15396529	
SOURCE	EST.	
ORGANISM	house mouse.	
REFERENCE	Mus musculus	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (baes 1 to 617)	
	Arakawa, K., Hori, F., Ishii, Y., Ito, M., Kawai, U., Komu, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,	

TITLE  
JOURNAL  
COMMENT

Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasakawa, D., Shiba, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M., and Hayashizaki, T., *et al.* (2001) RIKEN Mouse ESTs (Araiawa, T., *et al.* 2001) unpublished (2001)  
Contact: Yoshinide Hayashizaki

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Tel.: 81-45-503-9222

Fax: 81-45-503-9216  
Email: genome-res@sc.riken.go.jp,  
URL: <http://genome.gsc.riken.go.jp/>  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.,  
Itoh

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

Matsumura, M., Onoe, T., Takemura, T., Ozawa, N., Iizuka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.  
Riken integrated sequence analysis (RISA) system—384-Genomat sequencing pipeline with 384 multicapillary sequencer. *Genome Res.*

Komono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. *Genome Res.* 11 (2): 281-289 (2001)

Yamanaka, T., Kiyosawa, H., Kondo, S., Saito, T., Shingawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arikawa, T., Ishii, Y. and Hayashizaki, Y.

Mapping of 19032 mouse cDNAs on mouse chromosomes. I. Struct.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

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location/Qualifiers
1..617
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone="5430400N11"
/clone_1ib="RIKEN full-length enriched, 6 days neonate
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/dev_stage="6 days neonate"
/lab_host="DH10B"
/notes="Site 1: Sall; site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project Of Genome Exploration Research Group in Riken

```

Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5',

GAAGAAGAAAGATCCAGACGCTCTTTTTCCTTTTTTTTNN 3'-1, cDNA wAB  
prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0, and subtraction to Rot = 100.0. Second

stand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGACGTATTAATTAATCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified plusescript KS(+) after bulk excision from lambda F1C1. Cloning sites: 5' end: SalI; 3' end:

BamHI "	153 a	152 c	157 g	155 t

**FEATURES**  
**source**

Location/Qualifiers  
1. .617

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/organism="Mus musculus"
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/db_xref="taxon:10090"
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/sex="mixed"  
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/lab_host="PH10P"
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/note="Site 1: Sall; Site 2: BamHI, cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in

RNA. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 15',  
GAGAGAGAGAGAGATCCAGAGACTCTTTTCTTTTCTTTTCTT [3], cDNA was prepared by using trehalose thermo-activated reverse

transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGACATTCTGAGTTAATTAATTAATCCCCCCCC-3']

3'. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: LML11461 row: 1 column: 04

High quality sequence stop: 738.

## FEATURES

source

Location/Qualifiers

1..774

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/db\_xref="taxon:9606"

/clone="IMAGE:5184843"

/clone\_id="NIH MGC\_116"

/lab\_host="MDH10B"

/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site\_1: NCI; Site\_2: EcorV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcorV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."

BASE COUNT 263 a 150 c 156 g 205 t

ORIGIN

Query Match

Best Local Similarity 30.8%; Score 353.6; DB 13; Length 774;

Matches 367; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db 769 AACATTGTCAGATTCTGCGGAGCCATAGACATCTCTCCCTGATCAGCAGCTGCAAC 828

1 AACATTGTCAG-TCGCGGAGCCATAGACATCTCTCCCTGATCAGCAGCTGCAAC 59

829 ATGAGCAAGCAGATGAGATGCGCATCCAGTCAAGAAAGCATGCACTCTTTACAGC 888

60 ATGAGCAAGCAGATGAGATGCGCATCCAGTCAAGAAAGCATGCACTCTTTACAGC 119

889 TGCCTCAACCAATCTTTATGTTTATGAGAGATCTTTCAAAAACCTAGCTATGAAA 948

120 TGCCTCAACCAATCTTTATGTTTATGAGAGATCTTTCAAAAACCTAGCTATGAAA 179

949 GTGGCCAAAGATATGAGTCTCTGAGAGACAGAGACAAAGTGGAGAGTTTCTTTT 1008

180 GTGGCCAAAGATATGAGTCTCTGAGAGACAGAGACAAAGTGGAGAGTTTCTTTT 239

1009 GATTCTGAGGTCCTACAGAGCAACAGTACTTTAGCATTTAAAGGTAAACCTGCTCT 1068

240 GATTCTGAGGTCCTACAGAGCAACAGTACTTTAGCATTTAAAGGTAAACCTGCTCT 299

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300 GCCTTTGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 359

1129 CTGAAAAA 1140

360 CTGAAACTCAAA 371

## RESULT 7

LOCUS

DEFINITION

H67224 328 bp mRNA linear EST 27-OCT-1995

Y65406 r1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone

IMAGE:238667 5' similar to SP:GUSB\_BOVIN P3550 POSSIBLE GUSTATORY

RECEPTOR TYPE B ; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

AUTHORS

1 (bases 1 to 328)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,

Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W., Hawkins

, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Le, N., Mardis, E., Moore

, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,

Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,

Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

JOURNAL

MEDLINE

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1920

High quality sequence stops: 295

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 1920 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 295.

Location/Qualifiers

1..328

/organism="Homo sapiens"

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/clone="IMAGE:238667"

/clone\_id="Weizmann Olfactory Epithelium"

/sex="Female"

/tissue.type="Olfactory epithelium"

/dev\_stage="35 year old"

/note="Organ: nose; Vector: pBluescript SK-; Site\_1: EcorI

; Site\_2: XhoI; Cloned unidirectionally. Primer: Oligo

dT. Olfactory epithelium, normal. Average insert size: 0.8

kb; Uni-ZAP XR Vector. Library constructed by N. Walker,

D. Lancelot, Weizmann Institute of Science. -5' adaptor

sequence: 5' GAATTCGCGACAG 3' -3' adaptor sequence: 5'

CTCGAGTTTCTTTTCTTTTCTTTT 3' "

BASE COUNT 79 a 69 c 72 g 107 t 1 others

ORIGIN

Query Match

Best Local Similarity 28.3%; Score 324.4; DB 14; Length 328;

Matches 325; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 242 TGAATTGGCTGATGAGATTTACTCTTATTCATCTGCTTTTGGCTGTATG 301

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362 TAACTTTGCTCTGATGAGATTTTGGCTGTATGATGATGATGATGATGATGATGAT 421

121 TAACTTTGCTCTGATGAGATTTTGGCTGTATGATGATGATGATGATGATGATGAT 180

422 TAACTTAAAGTCCCGCAATCAGAGTGGGAAAAACATGCTGATCATCTGTTCTGTG 481

181 TAACTTAAAGTCCCGCAATCAGAGTGGGAAAAACATGCTGATCATCTGTTCTGTG 240

482 TCTGATGCTGCTCATCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 541

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542 ATGCTAGTGATTTCCATTTTCCCC 568

301 ATGCTAGTGATTTCCATTTTCCCC 327

RESULT 8  
BB639357  
LOCUS  
DEFINITION  
BB639357 RIKEN full-length enriched, 3 days neonate thymus Mus  
musculus cDNA clone A630091E18 5', mRNA sequence.  
ACCESSION  
BB639357  
VERSION  
BB639357.1 GI:15401392  
KEYWORDS  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 576)  
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hangaki, T., Hara, A.,  
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Komoto, H., Kouda  
, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,  
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki  
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,  
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,  
Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
Unpublished (2001)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsr.riken.go.jp,  
URL: http://genome-gsc.riken.go.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh  
, M., Komoto, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
Matsubara, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga  
, S., Kawai, T., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara  
, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa  
, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T.,  
Ishii, Y. and Hayashizaki, Y.  
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.  
Funct. Genomics 2 pre, L72-L86 (2001)  
Please visit our web site (<http://genome-gsc.riken.go.jp>) for  
further details.  
e mouse tissues.

## FEATURES

Source

Location/Qualifiers  
1..576  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="A630091E18"  
/clone\_lib="RIKEN full-length enriched, 3 days neonate  
thymus"  
/tissue\_type="thymus"  
/dev\_stage="3 days neonate"  
/lab\_host="DH10B"  
/note="Site 1: SalI; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN, Division of Experimental Animal Research in Riken

BASE COUNT 151 a 139 c 145 g 140 t 1 others  
ORIGIN

Query Match 24.9%; Score 285.4; DB 10; Length 576;  
Best Local Similarity 81.1%; Pred. No. 3.6e-57;  
Matches 331; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

1 ATGGCTTTGGAAACAGACCAAGTCAACAGATTATTTATGAGAAATGAATGAATGCG 60  
169 ATGGCTTTGGAAACAGACCAAGTCAACAGATTATTTATGAGAAATGAATGAATGCG 228  
61 ACTTATGACTAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120  
229 ACTTATGACTAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 288  
121 AAGTTTCT 180  
289 AAGTTTCT 348  
181 ATGTGATGCGCAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
349 ATGTGATGCGCAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 408  
241 CTGAATTTGGCTTGGCAATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
409 CTGAATTTGGCTTGGCAATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 468  
301 GCAATTTGGCTTGGCAATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
469 GCAATTTGGCTTGGCAATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 528  
361 CTAACTTTGGCTTGGCAATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 408  
529 GAAACTTTGGCTTGGCAATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 576

RESULT 9  
BE970160  
LOCUS  
DEFINITION  
BE970160 NIH\_MGC\_78 Homo sapiens cDNA clone IMAGE:3950182 5',  
mRNA sequence.  
ACCESSION  
BE970160  
VERSION  
BE970160.1 GI:10583005  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 711)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: CLONETECH Laboratories, Inc.  
cDNA library Preparation: CLONETECH Laboratories, Inc.  
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LMNI)  
DNA Sequencing by: InCyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMNI at:  
<http://image.llnl.gov>

contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer 5'-CTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT  
GAGAGAGAGAGAGAGATCCAGAGAGATCCAGAGAGATCCAGAGAGATCCAGAGAGATCCAG  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Rot = 20.0 and subtraction to Rot = 459.0. Second  
strand cDNA was prepared with the primer adapter of  
sequence 5' GAGAGAGAGATCCAGAGAGATCCAGAGAGATCCAGAGAGATCCAGAGAGATCC  
3'. cDNA was cleaved with XhoI and BamHI. Vector: a  
modified pBluescript KS(+) after bulk excision from Lambda  
PLC I."

Plate: L10C816 row: d column: 23  
High quality sequence stop: 611.  
Location/Qualifiers

## FEATURES

source

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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3950182"  
/clone\_1ib="NIH MGC 78"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: pancreas; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggccatcggcc); Site\_2: SfiI (ggccatcggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCCAGCGCCAGCATG-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.2 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 252 a 125 c 146 g 188 t

Query Match 23.1%; Score 264.6; DB 12; Length 711;  
Best Local Similarity 98.0%; Pred. No. 3.1e-52;  
Matches 289; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 846 CATGCCATCCAGTCACAGAAAGATGCACTCTTTCACAGCTGCTCAACCCATCCT 905  
DB 1 CATGCCATCCAGTCACAGAAAGATGCACTCTTTCACAGCTGCTCAACCCATCCT 60  
QY 906 TTATGTTTATGGAGCATCTTTCAAAACCTAGTTATGAAGTGGCCAGAAATATGG 965  
DB 61 TTATGTTTATGGAGCATCTTTCAAAACCTAGTTATGAAGTGGCCAGAAATATGG 120  
QY 966 GTCTCGAAGAGACAGACAAAGTGTGAGAGATTTCTTTGATTTCTGAGGGTCTTAC 1025  
DB 121 GTCTCGAAGAGACAGACAAAGTGTGAGAGATTTCTTTGATTTCTGAGGGTCTTAC 179  
QY 1026 AGAGCCAAACAGTACTTTAGATTTAAAGTAAAGTCTGCTGCTTTGCTTGGATATC 1095  
DB 180 AGAGCCAAACAGTACTTTAGATTTAAAGTAAAGTCTGCTGCTTCTTGGATATC 238  
QY 1086 ATATGATGATGCTTTCCCTCAATAAATACATCTGCTTATTTGAAAAAATA 1140  
DB 239 ATATGATGATGCTTTCCCTCAATAAATACATCTGCTTATTTGAAAAAATA 293

RESULT 10 296 bp mRNA linear EST 21-DEC-1999  
A176946/c wj14d04.x1 NCI CGAP Kid12 Homo sapiens CDNA clone IMAGE:2402791 3'  
LOCUS similar to SW:GUSB\_BOVIN P35350 POSSIBLE GUSTATORY RECEPTOR TYPE B  
DEFINITION  
; mRNA sequence.

ACCESSION A176946  
VERSION A176946.1 GI:5235975  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 296)  
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-1@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/JMUL at:  
www.bio.jiml.gov/bbrp/image/image.html  
Insert Length: 372 Strd Error: 0.00  
Seq primer: -40UP from Gibco.

## FEATURES

source

1..296  
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/clone="IMAGE:2402791"  
/clone\_1ib="NCI CGAP Kid12"  
/cissue\_type="2 pooled tumors (clear cell type)"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP K1d5 was purified, and ss circles were made in vitro. Following HAP hybridization reaction. The driver was PCR-amplified CDNA from a pool of 5,000 clones made from the same library (clones 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 85 a 51 c 49 g 110 t 1 others

Query Match 22.9%; Score 262.4; DB 9; Length 296;  
Best Local Similarity 95.1%; Pred. No. 1e-51;  
Matches 269; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 865 GAAAGATGCACTCTTTCACAGCTGCTCAACCCATCTTATGTTTATGGAGCA 924  
DB 296 GAAAGATGCACTCTTTCACAGCTGCTCAACCCATCTTATGTTTATGGAGCA 237  
QY 925 TCTTCAAAATACGATATGAAGTGGCCAGAAATATGGTCTCGAAGAGAGA 984  
DB 236 TCTTCAAAATACGATATGAAGTGGCCAGAAATATGGTCTCGAAGAGAGA 177  
QY 985 CAAAGTGTGAGAGATTTCTTTGATTTCTGAGGCTCTTACAGAGCCAACTACTTT 1044  
DB 176 CAAAGTGTGAGAGATTTCTTTGATTTCTGAGGCTCTTACAGAGCCAACTACTTT 117  
QY 1045 AGCATTTAAAGTAAAGTCTGCTGCTTTGCTTGGATATGATGATGCTTCCC 1104  
DB 116 AGCATTTAAAGTAAAGTCTGCTGCTTTGCTTGGATATGATGATGCTTCCC 57  
QY 1105 CTCAATTAATACATCTGCTTATTTCTGAAAAAATAAAM 1147  
DB 56 CTCAATTAATACATCTGCTTATTTTGAATAAATAAATAA 14

RESULT 11 369 bp mRNA linear EST 09-SEP-1996  
AA050273 mjl4a03.x1 Soares mouse embryo NMME3.5 14.5 Mus musculus CDNA  
LOCUS clone IMAGE:476044 5' similar to SW:GUSB\_BOVIN P35350 POSSIBLE  
DEFINITION GUSTATORY RECEPTOR TYPE B ; mRNA sequence.

ACCESSION AA050273  
VERSION AA050273.1 GI:1529944  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.  
1 (bases 1 to 369)  
TITLE Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.

JOURNAL The WashU-HMI Mouse EST Project  
COMMENT Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project



Db	241	TCCTTTGATCTCGAGGCTTCACAGAGCAACCACTGTTCTTTACACTTAAATATAA	300
Qy	1062	CTGCTCT 1068 	
Db	301	CTGCTCT 307	
RESULT 13			
AL322657			
LOCUS			
DEFINITION	Al322657	839 bp	mRNA
ACCESSION	mjl4a03.y1 Soares mouse embryo	NDME13.5 14.5	Mus musculus cDNA
VERSION	clone IMAGE:476044 5'	similar to SW:USB BOVIN P33550	POSSIBLE
KEYWORDS	GUSTATORY RECEPTOR TYPE B ;		mRNA sequence.
REFERENCE	Al322657		
AUTHORS	Al322657.1	GI:4057086	
ORGANISM	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
LOCUS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 839)		
ORGANISM	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,		
REFERENCE	Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,		
AUTHORS	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,		
ORGANISM	Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and		
REFERENCE	Waterston,R.		
ORGANISM	The WashU-HHMI Mouse EST Project		
COMMENT	Unpublished (1996)		
LOCUS	Contact: Marra M/Mouse EST Project		
REFERENCE	WashU-HHMI Mouse EST Project		
AUTHORS	Washington University School of Medicine		
ORGANISM	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
REFERENCE	Tel: 314 286 1800		
AUTHORS	Fax: 314 286 1810		
ORGANISM	Email: mouseest@watson.wustl.edu		
REFERENCE	This clone is available royalty-free through INLH ; contact the		
AUTHORS	IMAGE Consortium (info@image.lnhl.gov) for further information.		
ORGANISM	MG1:267788		
REFERENCE	This read is a RESEQUENCE of a previously sequenced mouse clone		
AUTHORS	This read has been verified (found to hit its original self in the		
ORGANISM	correct orientation)		
REFERENCE	Putative full length read		
AUTHORS	vector to vector length is 840		
ORGANISM	Seq primer: -40RP from Gibco		
REFERENCE	High quality sequence scop: 461.		
AUTHORS	Location/Qualifiers		
ORGANISM	1. 839		
REFERENCE	/organism="Mus musculus"		
AUTHORS	/strain="C57BL/6J"		
ORGANISM	/db_xref="taxon:10090"		
REFERENCE	/clone="IMAGE:476044"		
AUTHORS	/clone_idb="Soares mouse embryo NDME13.5 14.5"		
ORGANISM	/sex="unknown"		
REFERENCE	/tissue.type="embryo"		
AUTHORS	/dev_stage="13.5-14.5dpc total fetus"		
ORGANISM	/lab_host="DH10B"		
REFERENCE	/note="vector: p773D-Pac (Pharmacia) with a modified		
AUTHORS	polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA		
ORGANISM	was primed with a Not I - oligo(dT) primer [5',		
REFERENCE	TGTTACCAATCATCTGAAGTGGAGCGCGCGGAATTTTTTTTTTTTTTTTTTTT		
AUTHORS	T 3'] , on equal amounts of mRNA from 2 13.5dpc and 2		
ORGANISM	14.5dpc embryos [total RNA provided by Minoru Ko, Wayne		
REFERENCE	State Univ., from 2 ] ; double-stranded cDNA was ligated to		
AUTHORS	Eco RI adaptors (Pharmacia), digested with Not I and		
ORGANISM	cloned into the Not I and Eco RI sites of the modified		
REFERENCE	p773D vector. Library went through one round of		
AUTHORS	normalization, and was constructed by Bento Soares and		
ORGANISM	M.Fatima Bonaldo.		
REFERENCE	"		
AUTHORS	266 a 188 c 181 g 200 t 4 others		
ORGANISM			
BASE COUNT			
ORIGIN			
Query Match	21.3%	Score 244.6;	DB 9; Length 839;
Best Local Similarity	87.3%;	Pred. NO. 1.7e-47;	

Matches	268;	Conservative	0;	Mismatches	39;	Indels	0;	Gaps	
QY	762	GCCTTAATACATTGTCAGTCTTCCGAGCCATPAGACATCTACTCTCCGTATCACCG	821						
Db	1	GGCCATAATACGTTTGTAAGTTCTGCCAAGCCATAGATGCATCTACTCTATCAACCG	60						
QY	822	CTGCACATGAGCAACCAACGATGAGCATGCGCATCCCAAGTCACAGAAAGCATGCACTCTT	881						
Db	61	CTGCAGATATAGACAAACGATGATGATGTCGCCATCCAACTCACAGAGAGCATGCGCTCTT	120						
QY	882	TCACAGCTGCTCCAAACCCAAATCCTTTATGTTTATATGAGAGCATCTTTCAAAAATACGT	941						
Db	121	CCACAGCTGCTCCAAACCCCACTCTGTATGTCCTTCAATGGGGGCTCTCTTCAAAAATCATAT	180						
QY	942	TATGAAATGCGCCAAAGAAATATGGTCTCTGGAGAAACAGAGACAAAGTGTGAGAGATT	1001						
Db	181	CATGAAAGTGGCCAAAGAAATATGATTCCTGGAGAAACAGAGACAGAAACGTGAGAGAAAT	240						
QY	1002	TCCTTTTATGTTCTGAGGGGCTTACAGAGCCACCGTACTTTTACATTTAAAGTAATAA	1061						
Db	241	TCCTTTTATGTTCTGAGGGGCTTACAGAGCCACCGTACTTTTACCATTTAAATATATAA	300						
QY	1062	CTGCTCT 1068							
Db	301	CTGCTCT 307							
RESULT 14									
Bi067951									
LOCUS		624 bp	mRNA	linear	EST 15-JUN-2001				
DEFINITION		pgfin.pk002.p22 normalized chicken fat cDNA library Gallus gallus							
		cDNA clone pgfin.pk002.p22 5' similar to sp P35350 GUSB_BOVIN							
		POSSIBLE GUSTATORY RECEPTOR TYPE B (PRL PROTEIN) pit JN0621 G							
		protein-coupled receptor type B - bovine, mRNA sequence.							
ACCESSION		Bi067951							
VERSION		Bi067951.1			GI:14475473				
KEYWORDS		EST.							
SOURCE		chicken.							
ORGANISM		Gallus gallus							
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
		Archosauria; Aves; Neognathae; Galliformes; Phasianidae;							
		Phasianinae; Gallus.							
		1 (bases 1 to 624)							
REFERENCE		Cogburn,L.A., Morgan,R.W. and Burnside,J.							
AUTHORS		Chicken ESTs from fat							
TITLE		Unpublished (2001)							
JOURNAL		Contact: Larry A. Cogburn							
COMMENT		University of Delaware							
		Townsend Hall, Newark, DE 19717, USA							
		Tel: 302-831-1335							
		Fax: 302-831-2822							
		Email: cogburn@udel.edu, www.chickest.udel.edu.							
FEATURES		Location/Qualifiers							
source		1. .624							
		/organism="Gallus gallus"							
		/db_xref="taxon:9031"							
		/clone="pgfin.pk002.p22"							
		/cclone_id="normalized chicken fat cDNA library"							
		/sex="Male and Female"							
		/tissue type="fat"							
		/lab_host="E.coli EMDH10B"							
		/note="Vector: pSPORT1"							
BASE COUNT		167 a 158 c 115 g 176 t							8 others
ORIGIN									
Query Match		21.0%; Score 240.4; DB 13; Length 624;							
Best Local Similarity		62.7%; Pred. No. 1.7e-46;							
Matches 389; Conservative		0; Mismatches 222; Indels 9; Gaps 1;							
QY	313	TGGGTTTATGAGAAATATGTCACAAATATCTTACGCTTGATACACACTTAACTTTGTC	372						
Db	2	TGGGAATGGGAAACTCATGTGCAAGCTCACTTCTTACATTTACACATGAATTTACG	61						



QY 373 TCTGGAATGCAAGTTCTGGCTTGATGACATAGACATATGAGCAATGATAAAGTC 432  
 DB 62 TCTGGAATGCAAGTTCTGGCTTGATGACATAGACATATGAGCAATGATAAAGTC 121  
 QY 433 CCCAGCCATCAGGAGGAGGAAAACCATGCTGATCATCTGTTCTGTTCTGATGGCT 492  
 DB 122 CAAGCTACAGAGAGAGCTGAGAAAACACTGAGTTTACTGCAATCTGCTGGCTGCT 181  
 QY 493 GCCATCTTCTGACATACCCAGCTGGTTTTTA-----TACAGTAATGACAA 543  
 DB 182 GCCCTACTGCTCAGCATCCCTGAACTATATTAACCAAGTATACACAACAATAGG 241  
 QY 544 GCTAGTGCATCTCCATTTTCCCGGCTACCTAGCAATCAATGAAGATGATTCAA 603  
 DB 242 AATGAATGCTCTCTATATTTTCCAGAACATGAAAACATTTAAAGACACATTCAG 301  
 QY 604 ATGCTAGATCTGATGATGATTTGATGATCCCTTTTATATGAGGAGTGTGCTATT 663  
 DB 302 ATCTGAGAGTTATCTGGAGATTTCTGCTTCTTCTAGTAATGATGACCTGATTTCA 361  
 QY 664 ATCAAGCAGAGACATCATGATGAATGCCAAACATTAATATCGACCCCTAAAGTT 723  
 DB 362 GTTACTGCTCGGGAATCTTTAGATCTGCAAAATGCTAAATCTAGACCTTTCATGTT 421  
 QY 724 CTGCTCAGATGTTATGATTTGATTTGATGCTGACCTGCTTATTAATGATGATGCT 783  
 DB 422 CTGCTCAGATGTTATGATTTGATTTGATGCTGACCTGCTTATTAATGATGATGCT 481  
 QY 784 TGCCGAGCATAGACATCATCTACTCCCTGATCAACAGCTGCAACATGAGCAAGCATG 843  
 DB 482 TGCGAGAGCATAGATGATGATCTACTATGATTAACGAGCTGNNNGAGTAACATATA 541  
 QY 844 GACATGCGCATATCAGTACAGAAAAGCATGCACTCTTTTCAACCTGCTCAACCCATC 903  
 DB 542 GACGTTGGCTCCAGGTACCAAGAGAGAGCTGTTTCAACCTGCTCAACCCATTT 601  
 QY 904 CTTTATGTTTATGAGAGC 923  
 DB 602 CTGTAAGCTCTCTNNATG 621

RESULT 15 577 bp mRNA linear EST 07-FEB-2002  
 BM490381  
 LOCUS ppp2n.pk003.e10 Normalized Chicken Pituitary/Hypothalamus/Pineal  
 DEFINITION Library (ppp2n) Gallus gallus cDNA clone ppp2n.pk003.e10 5' similar  
 to ref|NP\_057641.1 (NM\_016557) orphan seven-transmembrane receptor,  
 chemokine related (Homo sapiens) ref|XP\_016022.1 (XM\_016022)  
 orphan seven-transmembrane receptor, chemokine related (Homo  
 sapiens) sp|Q9NPB9|CKRB\_HUMAN C-C CHEMOKINE RECEPTOR TYPE, mRNA  
 sequence.  
 BM490381  
 VERSION BM490381.1 GI:18611312  
 KEYWORDS EST.  
 SOURCE chicken.  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 577)  
 AUTHORS Porter,T.E. and Cogburn,L.A.  
 TITLE ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA  
 library, USDA/IRFAS Animal Genome Project  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Larry A. Cogburn  
 University of Delaware  
 Townsend Hall, Newark, DE 19717, USA  
 Tel: 302-831-1335  
 Fax: 302-831-2822  
 Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES  
 source 1..577  
 /organism="Gallus gallus"

/strain="Commercial broiler chickens"  
 /db\_xref="taxon:9031"  
 /clone="ppp2n.pk003.e10"  
 /clone\_lib="Normalized Chicken  
 Pituitary/Hypothalamus/Pineal Library (ppp2n)"  
 /sex="Male and Female"  
 /tissue\_type="Pituitary Gland/Hypothalamus/Pineal Gland"  
 /dev\_stage="Embryonic (d12,d14,d19); post-hatch (1,3,5,7,9  
 weeks)"  
 /lab\_host="E. coli BMDH10B"  
 /note="Vector: pCMVSPORT6; Library made from equivalent  
 pools of total RNA isolated from each tissue at different  
 ages. Single pass sequencing from 5'-end"  
 BASE COUNT 151 a 132 c 123 g 167 t 4 others  
 ORIGIN

Query Match 20.8%; Score 239; DB 13; Length 577;  
 Best Local Similarity 67.0%; Pred. No. 3.6e-46;  
 Matches 357; Conservative 0; Mismatches 170; Indels 6; Gaps 1;

QY 1 ATGGCTTTGAAACAGAACAGCAGTCAACAGATTATTTATGAGAAAATGAATGAGC 60  
 DB 44 ATGGCTTTGAAACAGAACAGCAGTCAACAGATTATTTATGAGAAAATGAATGAGC 103  
 QY 61 ACTTAT-----GACTACAGTCAATATGACTGATCTGATCAAGAAAGTCCAGAGA 114  
 DB 104 AACTGATGATGATTAACAACAATACAGAGTTCTCTGGAAGAAAGATGTGAGAAAA 163  
 QY 115 TTGCAAAAGTTTTCCTCCCTGATTTCCCAATAGTTTTCGTCATGGACTTGACAGC 174  
 DB 164 TTGCAAAAGTTTTCCTCCCTGATTTCCCAATAGTTTTCGTCATGGACTTGACAGC 223  
 QY 175 AATTCCATGGTAGTGCAATTTATGCTATTACAGAAAACAGAAACCAAAACAGATGTG 234  
 DB 224 AATTCCATGGTAGTGCAATTTATGCTATTACAGAAAACCAAAACAGATGTG 283  
 QY 235 TACATCCTGAATTTGGCTGATGAGATTTTACCTCTTATTCAGTCTGCTTTGGGCT 294  
 DB 284 TACATCCTGAATTTGGCTGATGAGATTTTACCTCTTATTCAGTCTGCTTTGGGCT 343  
 QY 295 GTTAATGCAAGTTGATGAGGAGGTTTATGAGAAAATGATGCAAAATATTCAGCTTG 354  
 DB 344 GCAAAATGCAAGTTGATGAGGAGGTTTATGAGAAAATGATGCAAAATATTCAGCTTG 403  
 QY 355 TACACATAAATCTTCTCTGGAATGAGATTTCTGCTTTGATGCAATPACATAT 414  
 DB 404 TACACATAAATCTTCTCTGGAATGAGATTTCTGCTTTGATGCAATPACATAT 463  
 QY 415 GTGGCAGTAACTAAAGTCCCAAGCCATCAGAGGTGGGAAACCATGCGATCATCTGT 474  
 DB 464 AGGGCTAAGCTTGAATCCCAAGCCATCAGAGGTGGGAAACCATGCGATCATCTGT 523  
 QY 475 TTCTGTTCTGATGAGTGGCTGATGAGATTTCTGCTTTGATGCAATPACATAT 527  
 DB 524 ATCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 576

RESULT 16 501 bp mRNA linear EST 31-AUG-2001  
 BB242286  
 LOCUS BB242286  
 DEFINITION musculus full-length enriched, 3 days neonate thymus Mus  
 accession BB242286  
 version BB242286.2 GI:15410521  
 keywords EST.  
 source house mouse.  
 organism Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 501)  
 AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.  
 Hiramoto,K., Horii,Y., Ito,M., Kawai,J., Konno,H., Kouda,  
 M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,



No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

BASE COUNT 128 a 77 c 72 g 124 t 1 others

Query Match 18.3%; Score 209.4; DB 13; Length 402;  
Best Local Similarity 99.5%; Pred. No. 3,7e-39;  
Matches 210; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGGCTTTGGAACAGACAGTCAAGATTTATTTATGAGAAATGAATGATGCG 60  
Db 192 ATGGCTTTGGAACAGACAGTCAAGATTTATTTATGAGAAATGAATGATGCG 251  
Qy 61 ACTTATGACTACAGTCAATATGAACTGATCTGATCAAGAAAGATGTCAGAAATTTGCA 120  
Db 252 ACTTATGACTACAGTCAATATGAACTGATCTGATCAAGAAAGATGTCAGAAATTTGCA 311  
Qy 121 AAAGTTTTCCTCCCTGATTTCTCAGATAGTTTTCGTCATGAGCTTGAGGCAATTCC 180  
Db 312 AAAGTTTTCCTCCCTGATTTCTCAGATAGTTTTCGTCATGAGCTTGAGGCAATTCC 371  
Qy 181 ATGGATGAGCAATTTATGCTTATTAACAAGA 211  
Db 372 ATGGATGAGCAATTTATGCTTATTAACAAGA 402

RESULT 18  
BI067954 560 bp mRNA linear EST 15-JUN-2001  
LOCUS BI067954  
DEFINITION pgf1n.pk005.o8 normalized chicken fat cDNA library Gallus gallus  
CDNA clone pgf1n.pk005.o8 5' similar to sp|P35350|GUSB BOVIN  
POSSIBLE GUSTATORY RECEPTOR TYPE B (PPRI, PROTEIN) p1r|U0621 G  
protein-coupled receptor type B - bovine, mRNA sequence.

ACCESSION BI067954  
VERSION BI067954.1 GI:14475476  
KEYWORDS EST.  
SOURCE chicken.  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 560)  
AUTHORS Cogburn, L.A., Morgan, R.W. and Burnside, J.  
TITLE Chicken ESTs from fat  
JOURNAL Unpublished (2001)  
COMMENT Contact: Larry A. Cogburn  
University of Delaware  
Townsend Hall, Newark, DE 19717, USA  
Tel: 302-831-1335  
Fax: 302-831-2822  
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES  
source location/Qualifiers

1..560  
/organism="Gallus gallus"  
/db\_xref="taxon:9031"  
/clone="pgf1n.pk005.o8"  
/clone\_lib="normalized chicken fat cDNA library"  
/sex="Male and Female"  
/tissue\_type="fat"  
/lab\_host="E.coli EMD10B"  
/note="Vector: pSPORT1"

BASE COUNT 143 a 139 c 124 g 153 t 1 others

Query Match 18.2%; Score 208.4; DB 13; Length 560;  
Best Local Similarity 63.9%; Pred. No. 6.3e-39;  
Matches 336; Conservative 0; Mismatches 181; Indels 9; Gaps 1;

Qy 227 CAGATGTGATACCTCGAATTTGGCTGAGCATTTTACTCTTACTCTTGCCTT 286  
Db 93 CAGATGTGATACCTCGAATTTGGCTGAGCATTTTACTCTTACTCTTGCCTT 152

Qy 287 TTTGGGCTGTTATGACATTTATGAGGCTTTTGGGAAAATATGAGCAAAATACCT 346  
Db 153 TTTGGGCTGTTATGACATTTATGAGGCTTTTGGGAAAATATGAGCAAAATACCT 212

Qy 347 CAGCCTTGACACCTAACTTTGCTCGAATGAGTTCGCTGTTATGAGCAATAG 406  
Db 213 CTTACTTTACACATGAAATTTTCACTGATGCTGTTCTGACCTGATACATCTGG 272

Qy 407 ACAGATATGAGGAGTAACTTAAAGTCCCAAGCAATCAGAGTGGGAAAACATGCTGGA 466  
Db 273 ATGATACAGAGGCTACCTGTAATCCCAAGTACAGAAAGACCTGAAAACATGCTGGA 332

Qy 467 TCATCTGTTCTGCTGCTGAGTGGCTGCACTTCTGTCAGTACCCGCTGTTTCTT 526  
Db 333 TTACTGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 392

Qy 527 ATACAGTA-----AATGCAATGCTAGGTGATTCCTCAATTTTCCCGCTACTAG 577  
Db 393 ACCAATGATACACACACACATGAGATGATGCTTCTTATTTTCAAGCAATGAG 452

Qy 578 GAACATCATGAAAGCATTTGATCAAAATGCTGAGATCTTGCAATTTGATTTACCT 637  
Db 453 AAACATTTTAAAGCAACCATTCAGATCTTAAAGTTTATCCCTGAGTTTCTGCTTCTT 512

Qy 638 TTCTTATTTATGGGGTGTGCTACTTTATCAAGCAAGCACTCAT 683  
Db 513 TTCTTATTTATGGGGTGTGCTACTTTATCAAGCAAGCACTCAT 558

RESULT 19  
AU058992 243 bp mRNA linear EST 29-APR-1999  
LOCUS AU058992  
DEFINITION g-protein coupled receptor type B, mRNA sequence.  
ACCESSION AU058992  
VERSION AU058992.1 GI:4717441  
KEYWORDS EST.  
SOURCE pig.  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 243)  
AUTHORS Hamasima, N. and Suzuki, H.  
TITLE Characterization of a porcine fat tissue cDNA library II  
JOURNAL Unpublished (1999)  
COMMENT Contact: Noriyuki Hamasima  
Animal Genome Research Program Team  
SRAFP-Institute  
446-1 Ippaiyuka, Kamiyokoba, Tsukuba, Ibaraki 305-0854, Japan  
Tel: 81-298-38-2190  
Fax: 81-298-38-2337  
Email: hamasima@gene.staff.or.jp.

FEATURES  
source location/Qualifiers

1..243  
/organism="Sus scrofa"  
/db\_xref="taxon:9823"  
/clone="PI1G5"  
/clone\_lib="pig back fat"  
/tissue\_type="back fat"  
/note="Vector: pUC18; primary culture, from mRNA  
Differential Display"

BASE COUNT 68 a 66 c 42 g 67 t

Query Match 17.8%; Score 204.6; DB 9; Length 243;  
Best Local Similarity 90.1%; Pred. No. 5e-38;  
Matches 219; Conservative 0; Mismatches 24; Indels 0; Gaps 0;





Db 181 TACGAGCTAGGAGACATCATGAAAGCACTGATCAATGCTGAAATCTGATGGTTT 240  
Qy 628 GTA 630  
Db 241 ATA 243

RESULT 23  
AA215577 217 bp mRNA linear EST 13-AUG-1997  
LOCUS 2795D10.1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:683419 5'  
DEFINITION similar to SW:GUSB\_BOVIN P35350 POSSIBLE GUSTATORY RECEPTOR TYPE B  
/; mRNA sequence.  
AA215577  
VERSION AA215577.1 GI:1815340  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 217)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 1277 Std Error: 0.00  
Seq primer: -28ml3 rev2 RT from Amer sham  
High quality sequence stop: 97.  
Location/Qualifiers  
1. .217  
/organism="Homo sapiens"  
/db\_xref="GDB:5586739"  
/db\_xref="taxon:9606"  
/clone="IMAGE:683419"  
/clone\_id="NCI\_CGAP\_GCB1"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, Igd-),  
provided by Dr. Louis M. Staudt (NCI). Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
primed with a Not I - oligo(dT) primer  
[5'-TGTTACCACTGAGAGTGGAGCGCGCTCATTTTCTTTTCTTTT-3'  
1. Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p773 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 68 a 57 c 34 g 52 t 6 others  
ORIGIN

Query Match 15.9%; Score 182.4; DB 9; Length 217;  
Best Local Similarity 95.8%; Pred. No. 9.1e-33;  
Matches 205; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

Qy 657 CTACTTTATCAAGCAAGCACTCATGAGATGCCAAATTAATATCTGACCCCT 716  
Db 1 CTACTTTATCAAGCAAGCAAGCACTCATGAGATGCCAAATTAATATCTGACCCCT 60  
Qy 717 AAAAGTTCTGCTCAAGTC-GTTATAGTTTCACTGCTCACTGCTTATTAACATTG 775  
Db 61 AAAAGTTCTGCTCAAGTCAGTTAGTTTCACTGCTCACTGCTTANAAACATTG 120  
Qy 776 TCAAGTTCTGCGAGGATGACATCATCTACCTCCCGATCAGCAGCTGGAATAGAGA 835  
Db 121 TCAAGTTCTGCGAGGATGAAATCATCTACCTCCCGATCAGCAGCTGGAATAGAGA 180

Qy 836 AACGATGAGATC-GCCATCCAACTCAGAGAA 868  
Db 181 AACGATGAGATCGGCATTCAGATGAAAGTAAACAGAAA 214

RESULT 24  
AM985634 528 bp mRNA linear EST 02-JUN-2000  
LOCUS uf3g11.v1 Soares mammary gland NMLMG Mus musculus cDNA clone  
DEFINITION IMAGE:1528772 5' similar to SW:GUSB\_BOVIN P35350 POSSIBLE GUSTATORY  
RECEPTOR TYPE B /; mRNA sequence.  
AM985634  
VERSION AM985634.1 GI:8180069  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 528)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MG1:944872  
Seq primer: -40RP from Glibco  
High quality sequence stop: 470.  
Location/Qualifiers  
1. .528  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1528772"  
/clone\_id="Soares\_mammary\_gland\_NMLMG"  
/sex="Female (lactating)"  
/tissue\_type="mammary gland"  
/lab\_host="DH10B"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from mammary  
gland tissue from a lactating female, and was then primed  
with a Not I - oligo(dT) primer. Double-stranded cDNA was  
ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the  
modified p773 vector. Library is normalized. Library  
was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 174 a 118 c 118 g 118 t  
ORIGIN

Query Match 15.7%; Score 180.6; DB 10; Length 528;  
Best Local Similarity 89.0%; Pred. No. 2.4e-32;  
Matches 195; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 850 GCCATCAAGTACAGAAAGATGCACTCTTTACAGCTGCTCAACCCATCTTTAT 909  
Db 1 GCCATCAAGTACAGAGAGATGCGCTCTTCCACAGCTGCTCAACCCATCTTTAT 60  
Qy 910 GTTTTATGAGGAGCATCTTTCAAAAACCTAGCTTATGAAAGTGGCAAGAAATATGGTCC 969  
Db 61 GTTTTATGAGGAGCTCTTTCAAAAACCTATATCATGAAAGTGGCAAGAAATATGATCC 120  
Qy 970 TGGAGAAAGAGAGCAAGAGTGGAGAGTTCCTTTTATTTGAGGGTCTTACAGAG 1029  
Db 121 TGGAGAAAGAGAGCAAGAGTGGAGAAATTCCTTTTATTTGAGGGTCTTACAGAG 180  
Qy 1030 CCAACAGTACTTTTAAAGTAAAGTAAAGTCTCT 1068  
Db 181 CCAACAGTCTTTTACATTTAATATAAAGTCTCT 219

RESULT 25

AM355490 471 bp mRNA linear EST 07-MAY-2001  
LOCUS  
DEFINITION pftic.pk001.d5 chicken fat cDNA library pSPORT1 Gallus gallus cDNA  
clone pftic.pk001.d5 5' similar to POSSIBLE GUSTATORY RECEPTOR TYPE  
B (PERI PROTEIN), mRNA sequence.  
ACCESSION AM355490 GI:6857503  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Gallus gallus  
chicken.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 471)  
Burnside, J., Cogburn, L.A. and Cogburn, L.A.  
Chicken fat ESTs  
Unpublished (2000)  
JOURNAL  
CONTACT: Joan Burnside  
Molecular Endocrinology  
University of Delaware  
40 Townsend Hall, Newark, DE 19717, USA  
Tel: 302 831-1345  
Fax: 302-831-3411  
Email: joan@udel.edu, www.chickest.udel.edu.  
Location/Qualifiers  
1..471  
/organism="Gallus gallus"  
/db\_xref="taxon:9031"  
/clone="pftic.pk001.d5"  
/clone\_id="chicken fat cDNA library pSPORT1"  
/sex="Male and Female"  
/tissue\_type="fat"  
/lab\_host="B. coli DH10B"  
/note="Vector: pSPORT1"  
BASE COUNT 127 a 106 c 101 g 133 t 4 others  
ORIGIN  
Query Match 13.9%; Score 159.6; DB 10; Length 471;  
Best Local Similarity 66.2%; Pred. No. 2.3e-27;  
Matches 261; Conservative 0; Mismatches 126; Indels 7; Gaps 2;  
QY 1 ATGGCTTTGGAACAGAACAGATTAATTATTAAGGAAATGAATATATGCG 60  
DB 53 ATGGCTGGTTGTGACAACTCACTGATTGAGTGAAGAGATGATATCTC 112  
QY 61 ACTTAT-----GACTACAGTCAATATGACTGATCTATCAAGAAAGATGAGAA 114  
DB 113 AACTCTGATGATGATTATTAACATACATGATTTCTCTGTGAAAAAGAGATGAGAAA 172  
QY 115 TTGCAAAAGTTTCTCCCTGATATCTTCAATATGTTTCTGATTTGACTTGACAGGC 174  
DB 173 TTGATGAAGATTTCTCCCTGATTTCTATGATGATGATTTCACTGTTGAGTTGCTGGA 232  
QY 175 AATTCATGATGATGGAATTTATGCTATTAACAAGAAACAGAAACCAAAACAGATGTG 234  
DB 233 AATTCATGATGATGGAATTTATGCTATTAACAAGAAACCAAG-ACCAAGACAGATGTG 291  
QY 235 TACATCTGATTTGAGTGTGATGATTTATCTCTTATTTACCTCTGCTTTTGGCT 294  
DB 232 TACATCAATGACCTTACATGCTATGCTATTTGCTCTTACGCTCCCTTTTGGCT 351  
QY 239 GTTATGACATTCATGAGGTTGTTTAAAGGAAATATATGCAAAATTAATCTTACGCTTG 354  
DB 352 GCAATGACATTCATGAGGTTGTTTAAAGGAAATATATGCAAAATTAATCTTACGCTTG 411  
QY 355 TACACACTAACTTGTCTCTGAAATGCAAGTTG 388  
DB 412 TACACATGATTTTCAATCTCCAGCATNGCTGTTG 445  
RESULT 26  
BG264784/c BG264784 539 bp mRNA linear EST 20-FEB-2001

daa32f04.x1 NICHD XGC Lul1 Xenopus laevis cDNA clone IMAGE:4057879  
3', similar to SW:GUSB\_BOVIN P35350 POSSIBLE GUSTATORY RECEPTOR TYPE  
B, mRNA sequence.  
ACCESSION BG264784  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM African clawed frog.  
Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
Xenopodinae; Xenopus.  
1 (bases 1 to 539)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Other ESTs: daa32f04.y1  
Contact: Robert Strusberg, Ph.D.  
Email: cgaab@r-mail.nih.gov  
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Washington University Genome Sequencing Center  
through the I.M.A.G.E. Consortium/LNLN at: [info@image.lnl.gov](mailto:info@image.lnl.gov)  
Seq primer: -40UP from Gibco  
High quality sequence stop: 417.  
Location/Qualifiers  
1..539  
/organism="Xenopus laevis"  
/db\_xref="taxon:8155"  
/clone="IMAGE:4057879"  
/clone\_id="NICHD XGC Lul1"  
/dev\_stage="adult"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: lung; Vector: pCMV-SPORE6; Site 1: NCI;  
Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2.6 kb. Constructed by Life  
Technologies. Note: This is a Xenopus Gene Collection (XGC  
Library.)"  
BASE COUNT 179 a 95 c 94 g 171 t  
ORIGIN  
Query Match 12.9%; Score 147.8; DB 12; Length 539;  
Best Local Similarity 64.6%; Pred. No. 1.4e-24;  
Matches 237; Conservative 0; Mismatches 127; Indels 3; Gaps 1;  
QY 691 CCAACATTAATATCTGACCCCTAAAGTTCTGCTACAGTCTTATAGTTTCATT 750  
DB 539 CCCAATATTAAGATCAAGATCTCTTAAGTGTGAGTGTGCGCTTCTTCCA 480  
QY 751 GTCACTCACTGCTTATTAATGATGATGATGATGATGATGATGATGATGATGATG 810  
DB 479 GTACTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATG 420  
QY 811 CTGATCAAGCTGCAACATGACCAACGATGACATGCGATCCATGCAAGTCAAGAAC 870  
DB 419 TTATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
QY 871 ATGCACTCTTTACAGCTGCTTCAACCAATCTTATGTTTATGGAAGATCTTTC 930  
DB 359 TTAGCTTTGTTACCTGTTGCTTCAATCAATCAATCAATCAATCAATCAATCAAT 300  
QY 931 AAAAATGATTAAGGAGGCAAGAAATATGAGTCTGGAAGAAAGAGAG---ACAA 987  
DB 299 AAATGTTACATTTCAAGATGCAAAAAGATGAGTCTTTACGAAAGCAAGAAATACC 240  
QY 988 AGTGTGAGAGATTTCTTTTGAATTTGAGGCTCTTACAGAGCAACGATCTTTAGC 1047  
DB 239 AGCCCTGAAGATTTCTTATGATTCAGAAACCAATGTTGAAGAAACGAGCTTTTCT 180  
QY 1048 ATTAAA 1054  
|||||







transcriptase and subsequently enriched for full-length by cap-triaper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGATTAATTAATTCCTCCCTCCCTCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from lambdaBda PLC I."

BASE COUNT 178 a 152 c 165 g 155 t

ORIGIN

Query Match 12.7%; Score 145.4; DB 10; Length 650;  
Best Local Similarity 77.6%; Pred. No. 5.2e-24;  
Matches 201; Conservative 0; Mismatches 56; Indels 2; Gaps 2;

QY 1 ATGGCTTTGAAACAGACCACTCAACAGATTATTTATGAGAAATGAATGATGCC 60  
DB 279 ATGGCTTGAAGCTGAACCACTCAACAGATTATTTATGAGAAATGAATGATGCC 338  
QY 61 ACTTATGACTACAGTCATATGAACTGATCTGTATCAAGAAGATGAGAAATTTGCA 120  
DB 339 ACTCAGACTACAGTCATATGAACTGATCTGTATCAAGAAGATGAGAAATTTGCA 398  
QY 121 AAAGTTTCTCCCTGTATCTCTCAATAGTTTTCGTATGACTTGC-AGGCAATTC 179  
DB 399 AAAGTTTCTCCCTGTATCTCTCAATAGTTTTCGTATGACTTGC-AGGCAATTC 458  
QY 180 CATGTAGTGGCAATTTATGCTTATTAACAAGAAACCAAAACAGATGTGTACAT 239  
DB 459 CGTATTTGGGCGATTAGCGCTTTTCAAGAAGAGAGACCAAAACCGATGTGTACAT 518  
QY 240 -CCGTAATTTGGCTGTAGC 257  
DB 519 CCTGAACCTGGCTGTAGC 537

## RESULT 29

AM190975/c 328 bp mRNA linear EST 22-NOV-1999  
LOCUS x143f02.x1 NCI\_CGAP\_Pan1 Homo sapiens cDNA clone IMAGE:2677467 3'  
DEFINITION similar to SW:GUSB\_BOVIN P5350 POSSIBLE GUSTATORY RECEPTOR TYPE B  
; mRNA sequence.

ACCESSION AM190975 GI:6465455  
VERSION EST.  
KEYWORDS human.  
SOURCE

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 328)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

## JOURNAL

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov

## COMMENT

Life Technologies catalog #: 11548-013  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

## FEATURES

Location/Qualifiers  
1..328  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="IMAGE:2677467"  
/clone\_lib="NCI CGAP\_Pan1"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.72 kb. Life Technologies catalog #:  
11548-013"

BASE COUNT 86 a 57 c 78 g 106 t 1 others

ORIGIN

Query Match 12.3%; Score 141.4; DB 10; Length 328;  
Best Local Similarity 82.1%; Pred. No. 4.7e-23;  
Matches 271; Conservative 0; Mismatches 47; Indels 12; Gaps 9;

QY 673 AGGACACTGATGAAGATGCGCAAACTTAATATCTGACCCCTTAAAGTTGCTGCA 732  
DB 319 AGGACACTGATGAAGATGCGCAAACTTAATATCTGACCCCTTAAAGTTGCTGCA 263  
QY 733 GTCGTATAGTTTCACTTGTCTCACTCACTGCTTAAATCATGTGACGTCGCCAGCC 792  
DB 262 GTGGTATATAGTTTCACTTGTCTCACTCACTGCTTAAATCATGTGACGTCGCCAGCC 205  
QY 793 ATGACATCATCTACTCCCTGATCAACAGCTGCAACATGAGCAACGATGACATGCC 852  
DB 204 AGCATCATCTACTCCCTGATCAACAGCTGCAACATGAGCAACGATGACATGCC 152  
QY 853 ATCAAGTCAAGAAAGATGCGACTCTTTCAACGCTGCTTCAACCTTATATTT 912  
DB 151 ATCAAGTCAAGAAAGATGCGACTCTTTCAACGCTGCTTCAACCTTATATTT 92  
QY 913 TTTATGGAGCATCTTTCAAAATCTAGTAAGAGGCGCAAAATATGGGTCCTGG 972  
DB 91 TTTATGGAGCATCTTTCAAAATCTAGTAAGAGGCGCAAAATATGGGTCCTGG 32  
QY 973 AGAAGACAGAGCAAAAGTGTGAGAGATT 1002  
DB 31 AGAAGACAGAGCAAAAGTGTGAGAGATT 2

## RESULT 30

B1653693 871 bp mRNA linear EST 12-SEP-2001  
LOCUS 603300354P1 NCI\_CGAP\_Mam3 Mus musculus cDNA clone IMAGE:5340828 5',  
DEFINITION mRNA sequence.

ACCESSION B1653693 GI:15567929  
VERSION EST.  
KEYWORDS house mouse.  
SOURCE

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 871)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov

## COMMENT

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
plate: LLM11865 row: 1 column: 13

High quality sequence stop: 835.

## FEATURES

Location/Qualifiers  
1..871  
/organism="Mus musculus"  
/strain="129,C57BL/6J,FVB/N"  
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/clone\_image="IMAGE:5340828"  
/clone\_lib="NCI CGAP\_Mam3"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="10 months"  
/lab\_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI. Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies. Investigators  
providing samples: Lohar Heminghaus/Chu-Xia Deng, NIH  
Reference for transgenic model: Xu et al., Nature Genetics  
22, 37-43 (1999)."

BASE COUNT 164 a 274 c 221 g 212 t

Query Match 10.8%; Score 123.8; DB 13; Length 871;  
Best Local Similarity 49.9%; Pred. No. 6.8e-19;  
Matches 379; Conservative 0; Mismatches 362; Indels 18; Gaps 2;

226 ACAGATGTCATCCCGAATTTGGCTGTACAGATTACCTTCTTATTCATCTCCCT 285  
Db 1 ACGATACCTTCTGCTACCTGCGCTGGCAACATCTTTCTTCTGATTTCTCC 60  
286 TTTGGGCTGTTAATGCAATTCATGGGTGTTTAAAGGAAATATGTGCAAAATACT 345  
Db 61 TTTGGGCTGTTAATGCAATTCATGGGTGTTTAAAGGAAATATGTGCAAAATACT 120  
346 TCAGCTTGTACACTTAACTTTGTCTGTGATGCAATTTCTGCTGTGATACAGATA 405  
Db 121 TTTGGCATCTTAAGTTAAGCTTTCTTACCGGAGTGTGCTGCTCTATGATCAGATT 180  
406 GACGATATGT-----GGCATTAATAAGTCCCGCAATCAGAGTGGGA 453  
Db 181 GACGCTACGATGCAATGTCACGCGCTGTCGCTATCCGACCGCGCGCTGCTT 240  
454 AAACCATGCTGATCATCTGTTCTGTGTCTGATGCTGCTGCTGCTGCTGCTGCTGCT 513  
Db 241 CTCATCAGCAAGCTGCTGCTGTGGGATCGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
514 CAGCTGTTTATTAACATTAATGCAATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 573  
Db 301 GAGCTGCTCTACAGCGCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
574 CTAGGATCATCAATGAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 627  
Db 361 GTCATGCTCCCAAGTGAAGGCTTGTATCACTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
628 GTAGTACCTTTCTTATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 687  
Db 421 CTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
688 ATGCCAATTAATATCTGACCCCTTAAAGTTCGCTCAGAGTGTATGATGATGATGATGATGAT 747  
Db 481 GCAGCGCACTTGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
748 ATTGTCATCAATGCTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807  
Db 541 ATAGTCTTCAAGTCTGCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
808 TCCCTGATCAGCAGTGTCAATGAGCAAAAGCAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 867  
Db 601 ATCACCATAAGAGAGCTGCGAAGCAAGCAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
868 AGCATGCACTTTTCAAGCTGCTCAACCCATCTTATGTTTATGAGGAGCATCT 927  
Db 661 ACCCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
928 TTCAAAAATCACTTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 966  
Db 721 TTCCGAGGAGCTCTTCAAGCTCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 759

RESULT 31  
BMS45259 1051 bp mRNA linear EST 20-FEB-2002  
LOCUS BMS45259  
DEFINITION AGENCOURT 6497171 NIH\_MGC\_124 Homo sapiens cDNA IMAGE:5726963  
5', mRNA sequence.  
ACCESSION BMS45259  
VERSION BMS45259.1 GI:18777197

KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Invitrogen  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNL12720 row: e column: 12  
High quality sequence start: 20  
High quality sequence stop: 753.  
Location/Qualifiers

## FEATURES

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/organism="Homo sapiens"  
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/clone="IMAGE:5726963"  
/clone\_1b="NIH MGC 124"  
/tissue\_type="hippocampus"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV  
(destroyed); Site 2: NotI; RNA source male hippocampus,  
age 27. Library is oligo-dT primed and directionally  
cloned (EcoRV site is destroyed upon cloning). Average  
insert size 1.4 kb, insert size range 0.9-4 kb. Library is  
normalized and enriched for full-length clones and was  
constructed by C. Gruber (Invitrogen). Research Genetics  
tracking code 012."

BASE COUNT 240 a 302 c 238 g 271 t

Query Match 10.6%; Score 121.2; DB 13; Length 1051;  
Best Local Similarity 49.6%; Pred. No. 2.8e-18;  
Matches 343; Conservative 0; Mismatches 343; Indels 6; Gaps 1;

90 CTGTATCAAGAAAGATGATGAGAAATTTGCAAAAGTTTCTCTGTATTCCTACAAAT 149  
Db 148 CTGTATCCGGAAGAAAGATGATGAGAAATTTGCAAAAGTTTCTCTGTATTCCTACAAAT 207  
150 AGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 209  
Db 208 CATCTTCTTAAGTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 267  
210 GAAACGAGAAACCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 269  
Db 268 GAAACGAGAAACCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327  
270 TCTATTCATCTGCTTTTGGCTGTTAATGCAATGATGATGATGATGATGATGATGATGATGATGAT 329  
Db 328 TGTATCAGCTTCCCTTGTGGCAGTGAATGCGGCAAACTGATGATGATGATGATGATGATGATGAT 387  
330 AATGTGCAAAATTAATCTTCAAGCTTGTACACAACTTAATCTTGTCTGGAATGAGATTTCT 389  
Db 388 CTAATGCAAGAGAGTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 447  
390 GGCCTGAT 449  
Db 448 GGCCTGAT 507  
450 GGGAAAACCATGCTG-----GATCATCTGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 503  
Db 508 AAGGAAGCTGTGGCTGCAAAAGGAGTGTATGTTGGCGTGTGATCCCTGCTGCTGCT 567  
504 GAGCATACCCAGCTGTTTATTAACAGTAATGACAAATGATGATGATGATGATGATGATGATGATGAT 563



/tissue type="sympathetic trunk"  
 /dev stage="adult, 16 yr"  
 /lab host="DH10B"  
 /note="vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
 NotI; Site\_2: SalI; cDNA made by oligo-dT priming.  
 Directionally cloned using the following adaptors:  
 5'-TCGACCCGACGCTCCG-3' and  
 5'-GACTAGTCTAGATCGGACGCGCCCTT(15)-3'. Size selected >  
 1 kb for average insert length 1.9 kb. This is a primary  
 library, non-amplified library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine); available through Life  
 Technologies."

BASE COUNT 223 a 270 c 217 g 238 t 2 others  
 ORIGIN

Query Match 10.1%; Score 116.2; DB 14; Length 950;  
 Best Local Similarity 51.2%; Pred. No. 4.3e-17;  
 Matches 299; Conservative 0; Mismatches 279; Indels 6; Gaps 1;

90 CTGTATCAAAAGATGTCAGAAATTTGCAAAAGTTTCTCCCTGATTCCTCACAAT 149  
 Db CTGTTCCGTAAGAAATGCTAATTTCAATPAATCTTCTCCACCATCTCTCAT 213  
 150 AGTTTCCTCATTTGAGCATTCGAGCAATTCATGTCAGCAATTTATGCTATTCAA 209  
 Db CATCTTTCTTAATGCGCATTTGGGCAATGATGTCATCTGTCATGGGTTACAGAA 273  
 210 GAAACAGAAACCAAAACAGATGTGTACATCTGATTTGGCTGTAGAGATTTACTCT 269  
 Db GAACTGAGAAAGATGACGACCAAGTACAGGCTGACCTGTAGTGGCCGACCTCTCT 333  
 270 TCTATTCACCTGCTCTTTGGGCTGTTAATGAGTTCATGGTGGGTTTAGGAAAT 329  
 Db TGTCACTACGCTCTCTTCTGGGCACTTGATGCTGCGCAACTGTGTTGGAACT 393  
 334 TGTCACTACGCTCTCTTCTGGGCACTTGATGCTGCGCAACTGTGTTGGAACT 393  
 330 AATGCAAAATTAATCTGAGCTTGTACACACTAACTTGTCTCTGGAATGACGTTCT 389  
 Db CCTATGCAAGGAGATCCATGTCATCTACAGTCAACCTCTACAGAGTGTCTCATCT 453  
 390 GCGTTGATCAGCATGACATATGTGGCAGTAACTAAATCCCGACCAATCAGAGT 449  
 Db GGCCTTCAATGCTGACGCGCTACCTGCGCATGCTCCACCAACAGTCAAGGCC 513  
 450 GGGAAAC-----CATGCTGATCATGCTGTTCTGTGCTGATGAGTGGCTCATCTGCT 503  
 Db AAGGAAGCTGTGGCTGAAAGAGTGTCTATGTGGCTGTGATGCTGCTGCTCTCT 573  
 514 GAGCATACCCAGCTGTTTATTATACAGTAATGACAAATGCTAGTSCATTTCCATTT 563  
 Db GACTATTCGCACTTCTATCTTGTCCAGTCACTGAGGAGTACAGATATATCTGGA 633  
 574 GAGCATACCCAGCTGTTTATTATACAGTAATGACAAATGCTAGTSCATTTCCATTT 563  
 Db CCCCCGCTACCTAGAAACATCAATGAAAGCATTTCAATGCTAGAGATCTGATGG 623  
 634 CCGCTTCTACCCCAATGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 693  
 624 ATTGTGATACCTTTCTATTATGAGGGGTGTGCTACTTATCA 667  
 Db CTTATCTGCTGCTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 737

RESULT 34 910 bp mRNA linear EST 25-SEP-2001  
 B1762229

LOCUS 60304913991 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5189552 5',

DEFINITION mRNA sequence.

ACCESSION B1762229 GI:15753807

KEYWORDS EST.

SOURCE human.  
 ORGANISM Homo sapiens  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 910)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILMIL at:  
<http://image.llnl.gov>  
 Plate: LLM11473 row: m column: 09  
 High quality sequence stop: 827.

FEATURES  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:5189552"  
 /clone\_11b="NIH\_MGC\_116"  
 /lab\_host="DH10B"  
 /note="Organ: pooled colon, kidney, stomach; Vector:  
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 3 colonies, age 26 yo male, 49 yo  
 female, 71 yo male colon; 46 yo male kidney, and pool of 2  
 stomachs, 62 yo male and 70 yo female. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.4 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 023. Note: this is a NIH-MGC Library."

BASE COUNT 210 a 260 c 208 g 232 t  
 ORIGIN

Query Match 10.1%; Score 115.6; DB 13; Length 910;  
 Best Local Similarity 51.2%; Pred. No. 6e-17;  
 Matches 299; Conservative 0; Mismatches 279; Indels 6; Gaps 1;

90 CTGTATCAAAAGATGTCAGAAATTTGCAAAAGTTTCTCCCTGATTCCTCACAAT 149  
 Db CTGTTCCGTAAGAAATGCTAATTTCAATPAATCTTCTCCACCATCTCTCAT 213  
 150 AGTTTCCTCATTTGAGCATTCGAGCAATTCATGTCAGCAATTTATGCTATTCAA 209  
 Db CATCTTTCTTAATGCGCATTTGGGCAATGATGTCATCTGTCATGGGTTACAGAA 273  
 210 GAAACAGAAACCAAAACAGATGTGTACATCTGATTTGGCTGTAGAGATTTACTCT 269  
 Db GAACTGAGAAAGATGACGACCAAGTACAGGCTGACCTGTAGTGGCCGACCTCTCT 333  
 274 GAACTGAGAAAGATGACGACCAAGTACAGGCTGACCTGTAGTGGCCGACCTCTCT 333  
 270 TCTATTCACCTGCTCTTTGGGCTGTTAATGAGTTCATGGTGGGTTTAGGAAAT 329  
 Db TGTCACTACGCTCTCTTCTGGGCACTTGATGCTGCGCAACTGTGTTGGAACT 393  
 334 TGTCACTACGCTCTCTTCTGGGCACTTGATGCTGCGCAACTGTGTTGGAACT 393  
 330 AATGCAAAATTAATCTGAGCTTGTACACACTAACTTGTCTCTGGAATGACGTTCT 389  
 Db CCTATGCAAGGAGTCCATGTCATCTACAGTCAACCTCTACAGAGTGTCTCATCT 453  
 394 GAGCATACCCAGCTGTTTATTATACAGTAATGACAAATGCTAGTSCATTTCCATTT 563  
 Db GACTATTCGCACTTCTATCTTGTCCAGTCACTGAGGAGTACAGATATATCTGGA 633  
 514 AAGGAAGCTGTGGCTGAAAGAGTGTCTATGTGGGTGTGATCCTGCTGCTGCT 573  
 450 GGGAAAC-----CATGCTGATCATGCTGTTCTGTGCTGATGAGTGGCTCATCTTGTCT 503  
 Db CTTATCTGCTGCTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 737  
 624 ATTGTGATACCTTTCTATTATGAGGGGTGTGCTACTTATCA 667  
 Db CTTATCTGCTGCTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 737  
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/db xref="taxon:3606"
/clone="IMAGE:4772288"
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/clone_type="embryonal carcinoma"
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/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site:1: SfiI (ggcgccgcgcgcgc); Site:2: SfiI (ggccatctggcc); SfiI (ggcgccgcgcgcgc); Site:2: SfiI (ggccatctggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTAGGCGC-3' and 3' adaptor sequence: 5'-ATTCTCAGGCGCCGAGCGCGCCGACATC-dT(30)-BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC library"

```

Query Match	Similarity	9.9%	Score 113.6	DB 12	Length 750
Best Local	Similarity	51.2%	Pred. No. 1.8e-16		
Matches	294	Conservative	0	Mismatches 274	Indels 6
					Gaps 1
QY	100	GAAGATGTCAGAGAAATTGGCAAAAGTTTTCTCCCTGTATTCTCCACATATGTTTGGTC	159		
Db	1	GAAGAAATATGCTAATTTCATATTAATCTTCCGCGCCACCATCTACATCATCTTCTTA	60		
QY	160	ATTGACCTTTCAGGCAATTCCTAGTACGGCAATTATAGCTATTAAAGAAACAGGA	219		
Db	61	ACTGGCATTGTGGGAAATGGATTGGTATCTCTGGTCATAGGTTACAGAAAGAAATGGA	120		
QY	220	ACCAAAACAGATGTATACATCTGAAATTTGGCTGTAGAGAAATTACTCTCTATTCACT	279		
Db	121	AGCATGACGGAACAATGACAGGCTGCACCTGTACAGTGGCGACCTCTCTTGTATCAG	180		
QY	280	CTGCCTTTTGGGCTGTATATGACAGTTCATGGGTGGTATTAGGAAATTAATGTGCAA	339		
Db	181	CTTCCCTTCTGGGCAAGTATGTCGCTGGCAAACTGGTACTTGGGAACCTTCTATGCAAG	240		
QY	340	ATACTTACGCTTGTACACACTAACTTTGTCTCTGAAATGCACTTTCTGGCTGTATC	399		
Db	241	GCAGTCATATGTATACACAGTCAACCTCTACAGACAGTCTTCACTCTGACCTTCAAC	300		
QY	400	AGCATAGACAGATATGTGACAGTAACTAAATGCCACGCAATCAGAGTGGGAAAC--	457		
Db	301	AGTCTGAGACCGCTACTCTGGCCATCTGCCACGACACCAACATGACAGGCGAAGAGCTG	360		
QY	458	---CATGCTGATCATCTGTTCTGTGTCTGTATGGCTGCACATCTTGTCTGACATACC	513		
Db	361	TTGGCTGAAGAAAGTGGTCTATGTGTGGCGTCTGGATCCCTGCGCTCTGTACTATTC	420		
QY	514	CAGCTGTTTTTTATACAGTAATGACAAATGCTAGTGATTCCTATTTTCCCGGCTAC	573		
Db	421	GACTTCATTTTCCCAACCTCAGTGGGACAGATGACAGATATATCTGTACCGCTTTCAC	480		
QY	574	CTAGAAACATCATGAAGAAACATTTGATTTCAAAAGCTAGAGATTCGATTTGATTTAGTA	633		
Db	481	CCCAATGACTTTGGGGTGTGTGTGTTCCAGTTTCACACATATGATTTGGCTTATCTCG	540		
QY	634	CCCTTCTTATTAATGGGGGTGTGCTACTTATCA	667		
Db	541	CTGTATTGTCTATCTGTCTGCTGCTATTCATTTA	574		
RESULT 37					
LOCUS	AL558854	841 bp	mRNA	linear	EST 16-FEB-2001
DEFINITION	AL558854 ltr1 NFl008 TC2 Homo sapiens cDNA clone GS00D15YE18 5		prime, mRNA	sequence.	
ACCESSION	AL558854				
VERSION	AL558854.1	GI:12903783			
KEYWORDS	EST.				

SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 841)  
Li, W.-B., Gruber, C., Tsesee, Y. and Polyes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
Location/Qualifiers  
1. 841

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cclone_id="CSODJ015YE18"
/cclone_idb="LRI_NFL008_TC2"
/sex="male"
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/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-0150 (dT) primer. Five prime and enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

```

Query Match	Similarity	9.8%	Score	112.2	DB 9	Length	841
Best Local	Similarity	49.0%	Pred.	10.38-16			
Matches	368	Conservative	1	Mismatches	364	Indels	18
							Gaps
QY	38	ATGAGAAAATGAAATGATGACCTTATGACTACAGTCATCATATGAACTGATCTGTATCA	97				
Db	73	ACGATTACATCGSAGACAACACACAGTGGACTATACCTTGTTCGAGTCTTGTGTCTCA	132				
QY	98	AAGAAAGTCTCAGAAATTTGCAAAAGTTTCTCTCCCTGTATTCCTCACATAGTTTCG	157				
Db	133	AGAAAGACGTGGCGAACTTTAAAGCTGGTCTCCCTATCATGTACTCATCATTTGTT	192				
QY	158	TCATTGCACTTCGACGACCTTCATGATAGTGGCAATTATTCCTATTCAGAAACAGA	217				
Db	193	TCTGGGCTTACTGCGCAATGGGCTGTGTCTTCTATCTATATTCATATTCAGAGCTCA	252				
QY	218	GAACCAAAACAGATGTGATCTCTGAATTTGGCTGTAGACAGATTACTCTTATTTCA	277				
Db	253	AGACCATGACCATACCTACCTGCTCAACCTGGCGGTGGCAACATCTCTTCTCTCTGA	312				
QY	278	CTCTGCTTTTGGGCTGTTAATGCAGTTTCATGGGTGGGTTTATAGGAAAAATATGTGCA	337				
Db	313	CCCTTCCCTTCTGGGCTTACAGCGCGGCAATCCGGGTCTTCGGTGTCCACTTTTGA	372				
QY	338	AAATACCTCAGCCTTGTACACACTAACTTTGTCTCTGAAATGCAAGTTCTGGCTTTGA	397				
Db	373	AGCTCATCTTTGTGCATCTACAGATGAGCTTCTTCACTGTGCACTGCTCCACTTCTTTGCA	432				
QY	398	TCAGCATGACAGATATGTGGCAGTAACTAAAG-----TCCCAACCAATCA	444				
Db	433	TCAGCATTAACCGCTACGTGGCCATGTCTCAAGGCTGTCTCAGCTCACCCCAACAGTGC	492				
QY	445	GGAGTGGGAAAAACATGCTGATCATCTGTCTGTGTCTGGATGGCTGCCATCTTGGTG	504				
Db	493	CGGCTCTTCTCATCGCAAGCTGTCTGTGTGGGGCATGTGGAATCACTACACAGTGTCT	552				
QY	505	AGCATACCCAGCTGATTTTATACAGTAAATGACAATGCTAGAGTCATCCCATTTTC	564				
Db	553	TCCATCCAGAGCTCTCTTACAGTACCTCCAGAGGACGACGACGTATGACAGAGATGGCA	612				

QY 565 CCCCCCTACCTAGGACATCAATGAAAGCATTTGATTCATATGCTAGAGATCTGCAT---- 620  
 Db 613 TGGCTCTCATACAGAGCATGTGGAGGCTTTATACCATTCAGGTGGCCACAGATG9TG 672  
 QY 621 -TGGATTGTAGTACCTCTTTCTATATGAGGGGTGTGCTACTTTATACAGAGACGAC 679  
 Db 673 ATCGGCTTCTGTGCTCCCTGCTGGCCATGAGCTTCTGTACCTTGTATCATATCCGACACC 732  
 QY 680 TCATGAAAGATGCAACATTAATAATCTCGACCCCTTAAAGTTCTGCTCAGCTGCTTA 739  
 Db 733 TGGCTCAGGACGACGACCTTTGAGCCGACACAGGCTCATAGGTATCATCTGCTGCTG 792  
 QY 740 TAGTTTCATTTGCTACCTCACTGCTTATTA 770  
 Db 793 TGGTCTTCAMAGTCTTCAGCTGCCCTACAA 823  
 RESULT 38  
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 LOCUS AUI78161 UV irradiated OLNI cell line cDNA library (OLC) Oryzias  
 DEFINITION  
 AUI78161 UV irradiated OLNI cell line cDNA library (OLC) Oryzias  
 coupled receptor type B - bovine, mRNA sequence.  
 ACCESSION AUI78161 GI:13426997  
 VERSION AUI78161.1  
 KEYWORDS EST.  
 SOURCE Japanese medaka.  
 ORGANISM Oryzias latipes  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Acanthopterygii; Acanthopterygii; Percomorpha; Atherinomorpha;  
 Belontiiformes; Adrianiichthyidae; Oryziinae; Oryzias.  
 REFERENCE 1 (bases 1 to 253)  
 Narnese, K., Mitan, H. and Tanaka, M.  
 Medaka EST project in University of Tokyo (2001)  
 COMMENT Unpublished (2001)  
 CONTACT: Kiyoshi Narnese  
 Department of Biological Sciences  
 Graduate School of Science, University of Tokyo  
 Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan  
 Tel: 81-3-5841-4443  
 Fax: 81-3-5841-4410  
 Email: narnese@biol.s.u-tokyo.ac.jp  
 This clone was isolated from UV irradiated OLNI cell line cDNA  
 library (OLC) 5' end sequences.  
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 source 1..253  
 /organism="Oryzias latipes"  
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 location/Qualifiers  
 BASE COUNT 41 a 81 c 70 g 60 t 1 others  
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 Best Local Similarity 65.6%; Pred. No. 5,4e-16;  
 Matches 162; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Db 184 TCACCCGCTCCTTACGCTTCATGAGGCTCTTCTTTAGAGTACGCTNCGACGCCG 243  
 QY 953 CCAAGA 959  
 Db 244 CCAAGA 250  
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 DEFINITION  
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 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 914)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Inyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Plate: L14M1450 row: n column: 23  
 High quality sequence stop: 851.  
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 /note="Organ: pooled brain, lung, testis; Vector:  
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 6 male brains, age range 23-27; 1  
 male lung, age 27; and 1 male testis, age 69. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.8 kb.  
 Insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 021. Note: this is a NIH MGC Library."  
 BASE COUNT 180 a 268 c 229 g 237 t  
 ORIGIN  
 Query Match 9.7%; Score 111.6; DB 13; Length 914;  
 Best Local Similarity 55.8%; Pred. No. 5.3e-16;  
 Matches 213; Conservative 0; Mismatches 169; Indels 0; Gaps 0;



Db 310 AGACCATGACCGAATCTACCTGCTCAACCTGGCGGTGGACAGATCTCTCTCTGA 369  
 QY 278 CTCTGCTTTTGGGCTGTATATGACATCTTCACTGGTGGTTTGGGAAATATATGCA 337  
 Db 370 CCTTCCCTTTGTGGGCTTACAGCGGCGCAAGTCTGGGTTTGGGTGTCTCATTTTGA 429  
 QY 338 AAATTAATCTTACGCTTTGACACTTAACTTTGCTCTGAAATGCACTTCTGGCTTGA 397  
 Db 430 AGCTATCTTTGGCATCTACAGATGAGCTTCTTCACTGGGATGCTCTTACTTCTTGA 489  
 QY 398 TCAGCATGACAGATATGTGGC 419  
 Db 490 TCAGCATGACCGCTACGTGGC 511

RESULT 40  
 LOCUS B0710222 921 bp mRNA linear EST 16-JUL-2002  
 DEFINITION AGENCOURT\_7977107 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6215717  
 5', mRNA sequence.

ACCESSION B0710222  
 VERSION B0710222.1 GI:21849121  
 KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 921)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: Dr. Mark Watson  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: LICM2385 row: b column: 06  
 High quality sequence stop: 598.  
 Location/Qualifiers

# FEATURES

source

1. .921  
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 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:  
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 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGCACGAG(G). Library constructed by Ling Hong in the  
 laboratory of Gerald W. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH MGC Library."

BASE COUNT 176 a 277 c 229 g 239 t

Query Match 9.7%; Score 111.6; DB 14; Length 921;  
 Best Local Similarity 55.8%; Pred. No. 5.3e-16;  
 Matches 213; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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 Db 124 ACGATTACATCGGAGACACACAGTGAATGACCTTTGTCAGTCTTTGGCTCA 183  
 QY 98 AAGAGATGTGAGAGAAATTTGCAAAAGTTTCTCCCTGATTCCTCACAATAGTTTGG 157  
 Db 184 AGAAGAGCGTGGGAATTTAAAGCTGGTTCCTCCCTATCATGATCTCCATTTGTT 243  
 QY 158 TCATTGACTTGACGGAATTCATGTGATGCGAATTTATGCTATTACAGAAACAGA 217

Db 244 TCGTGGCCCTACTGAGGCAATGAGCTGTGTCGTGATACCTATATCTATTTCAAGAGCTCA 303  
 QY 218 GAACCAAAACAGATGTGTACATCTGAAATTTGGCTGTAGCAGATTACTCTCTATTC 277  
 Db 304 AGACATGACGATACCTACTGCTCAACCTGGGTGGCAGACATCTCTCTCTCTGA 363  
 QY 278 CTCTGCTTTTGGGCTGTAAATGCAATGATGAGGTGTTTAAAGGAAATATATGCA 337  
 Db 364 CCTTCCCTTCTGGGCTTACAGCGGCGCAAGTCTGGGTCTTGGTGTCCACTTTTGA 423  
 QY 338 AAATTAATCTTACGCTTTGACACTTAACTTTGCTCTGAAATGCACTTCTGGCTTGA 397  
 Db 424 AGCTATCTTTGCCATCTACAGATGAGCTTCTTCACTGCTCTTCTTGA 483  
 QY 398 TCAGCATGACAGATATGTGGC 419  
 Db 484 TCAGCATGACCGCTACGTGGC 505

Search completed: March 24, 2003, 09:39:22  
 Job time : 2202 secs



GenCore version 5.1.4 p5 4578  
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## OM nucleic - nucleic search, using sw model

Run on: March 24, 2003, 01:14:05 ; Search time 70 Seconds

(without alignments)  
5025.118 Million cell updates/sec

Title: US-09-721-495B-1

Perfect score: 1147  
Sequence: 1 atgagcttcggaacagacacca.....tctgaaaaaaaaaaaaaaaam 1147Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 135 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/PTUS.COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133.6	98.8	1660	2	US-08-966-316-17 Sequence 17, Appl
2	166.2	14.5	1900	1	US-08-153-848-18 Sequence 18, Appl
3	166.2	14.5	1900	3	US-09-299-843A-18 Sequence 18, Appl
4	166.2	14.5	1900	4	US-09-088-337B-18 Sequence 18, Appl
5	166.2	14.5	1900	5	PCT-US93-11153-18 Sequence 18, Appl
6	166.2	14.5	2058	1	US-08-153-848-6 Sequence 6, Appl
7	166.2	14.5	2058	3	US-09-299-843A-6 Sequence 6, Appl
8	166.2	14.5	2058	4	US-09-088-337B-6 Sequence 6, Appl
9	166.2	14.5	2058	5	PCT-US93-11153-6 Sequence 6, Appl
10	166.2	14.5	2160	1	US-08-153-848-14 Sequence 14, Appl
11	166.2	14.5	2160	3	US-09-299-843A-14 Sequence 14, Appl
12	166.2	14.5	2160	4	US-09-088-337B-14 Sequence 14, Appl
13	166.2	14.5	2160	5	PCT-US93-11153-14 Sequence 14, Appl
14	164.8	14.4	2577	4	US-09-266-464-1 Sequence 1, Appl
15	164.8	14.4	2085	4	US-09-299-843A-65 Sequence 65, Appl
16	164.6	14.4	2085	4	US-09-088-337B-65 Sequence 65, Appl
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20	159.8	13.9	2154	5	PCT-US93-09636-1 Sequence 1, Appl
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26	153.6	13.4	1679	4	US-09-517-605-14 Sequence 14, Appl
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28	153.6	13.4	1737	1	US-08-076-093A-3 Sequence 3, Appl
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33	153.6	13.4	1737	2	US-08-801-238-3 Sequence 3, Appl
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44	143	12.5	2254	4	US-09-088-337B-27 Sequence 27, Appl
45	143	12.5	2254	4	US-09-088-337B-27 Sequence 27, Appl
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97	92.4	8.1	1383	4	US-08-861-105-13 Sequence 13, Appl
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101 90 7.8 1155 4 US-09-534-185-3 Sequence 3, Appl1  
102 90 7.8 1181 4 US-09-045-583-1 Sequence 1, Appl1  
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104 90 7.8 2440 4 US-08-724-984A-1 Sequence 1, Appl1  
105 87.6 7.6 1414 3 US-08-466-343D-1 Sequence 1, Appl1  
106 86.4 7.5 1026 4 US-09-116-458-1 Sequence 6, Appl1  
107 86.4 7.5 1137 4 US-09-045-583-6 Sequence 6, Appl1  
108 86.4 7.5 1137 4 US-09-534-185-6 Sequence 4, Appl1  
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111 80.2 7.0 792 4 US-08-833-752-1 Sequence 1, Appl1  
112 74.6 6.5 1086 4 US-09-146-980-1 Sequence 1, Appl1  
113 74.4 6.5 2111 2 US-08-966-316-6 Sequence 6, Appl1  
114 70.4 6.1 1572 1 US-08-041-219A-5 Sequence 5, Appl1  
115 70.4 6.1 1572 1 US-08-417-122-5 Sequence 5, Appl1  
116 70.4 6.1 2268 4 US-09-050-159-133 Sequence 133, App  
117 68.8 6.0 2517 3 US-08-982-493-5 Sequence 5, Appl1  
118 67.8 5.9 1670 3 US-08-709-838-1 Sequence 1, Appl1  
119 67.8 5.9 1670 4 US-08-829-839-1 Sequence 1, Appl1  
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125 65.6 5.7 1679 2 US-08-805-627A-5 Sequence 5, Appl1  
126 65.6 5.7 1679 2 US-08-801-238-5 Sequence 5, Appl1  
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128 65.6 5.7 1679 3 US-09-104-296-5 Sequence 3, Appl1  
129 65.6 5.7 1679 3 PCT-US94-06380-3 Sequence 7, Appl1  
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131 65.6 5.7 2818 4 US-08-628-655-1 Sequence 1, Appl1  
132 64.6 5.6 14176 1 US-08-307-499-1 Sequence 14, Appl1  
133 64.6 5.6 14176 4 US-08-299-268-1 Sequence 1, Appl1  
134 64.6 5.6 14176 4 US-09-299-268-1 Sequence 14, Appl1  
135 64.6 5.6 14176 4 US-09-299-268-1 Sequence 14, Appl1

## ALIGNMENTS

RESULT 1  
US-08-966-316-17  
Sequence 17, Application US/08966316  
Patent No. 5932445  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
APPLICANT: Au-Young, Janice  
APPLICANT: Reddy, Roopa  
APPLICANT: Murty, Lynn E.  
APPLICANT: Mathur, Preete  
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/966,316  
FILING DATE: Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER:  
APPLICATION DATA:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36, 749  
REFERENCE/DOCKET NUMBER: PF-0424 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1660 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: UTRNOT11  
CLONE: 2547002  
US-08-966-316-17  
Query Match 98.8%; Score 1133.6; DB 2; Length 1660;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1136; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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84 ACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 143  
121 AAAGTTTCT 180  
144 AAAGTTTCT 203  
181 ATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
204 ATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 263  
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421 GTAACTTTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
444 GTAACTTTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 503  
481 GTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
504 GTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563  
541 AATGCTAGTGTGATTCCTATTTCCCGGCTAGTGAAGATCAATGAAGATGAT 600  
564 AATGCTAGTGTGATTCCTATTTCCCGGCTAGTGAAGATCAATGAAGATGAT 623  
601 CAATGCTAGTGTGATTCCTATTTCCCGGCTAGTGAAGATCAATGAAGATGAT 660  
624 CAATGCTAGTGTGATTCCTATTTCCCGGCTAGTGAAGATCAATGAAGATGAT 683  
661 TTATATCAGCAGACAGACATCATGATGATGATGATGATGATGATGATGATGAT 720  
684 TTATATCAGCAGACAGACATCATGATGATGATGATGATGATGATGATGATGAT 743  
721 GTTCTGCTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
744 GTTCTGCTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 803





```

APPLICANT: Godiske, Ronald
            Gray, Patrick W.
            Schwellhart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray &
            Borum
            STREET: 6300 Sears Tower, 233 South Wacker Drive
            CITY: Chicago
            STATE: Illinois
            COUNTRY: USA
            ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: intron
LOCATION: 1..168
FEATURE:
NAME/KEY: exon
LOCATION: 169..1245
FEATURE:
NAME/KEY: CDS
LOCATION: 169..1242
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1246..1900
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-088-337B-18

Query Match          14.5%; Score 166.2; DB 4; Length 1900;
Best Local Similarity 50.2%; Pred. No. 1.6e-38;
Matches 479; Conservative 0; Mismatches 458; Indels 18; Gaps 2

38 ATGAGGAAATGAATGATGAGCACTTATGACTACGTCGTCATGTAATGAACTGATCTGATCA 97
197 ACGATTATTCGGAAGACAACACCAACGAGTGACTACCTTGTTCCAGTCTTTGTGTGCTCA 256
98 AAGAGATGTCAGAGATTGCAAAAGTTTCTCCCTGGTATTCCTCACAATAGTTTTCG 157
257 AGAAGACGCGGGAAGCACTTAAAGCTGGTTCCTCCCTATCATGTAATCATCATATTGTT 316
158 TCATTGCAATTGAGGCATTCATGATGTGTGTGCAATTTATGCGCTATTCACAAGAACAGA 217
317 TCGTGAGCCATCGGCAATAGGAGCTGGTGTGCTGTGTAACATATCATATTTTCAGAGGCTCA 376

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01 218 GAACCAAAACAGATGTGTAATCCGGAATTTGGCTGAGAGATTTACTCTCTTATATCA 277
02 377 AGACCAATGACCGATACCTACCTGCTCAACTGGGGGAGGAGACATCTCTTCTCCTGA 436
03 278 CTCGACCTTTTGGGTGTGTTAATGCAATTCAGTTCAGGAGTGGGTTTAAAGGAAAAATATGTGA 337
04 437 CCGTCCCTTTCTGGGCTTACAGCGGGCCAAAGTCCCTGGGCTTTCGGTGTGCACTTTTGA 496
05 338 AAATACTTACGCTTGTATCAACACTTAACTTGTCTCGGAATGCACTTCTGGCTTGA 397
06 497 AGCTCACTTTGGCACTTCAAGAAATGAGCTTCTTGAAGTGATCTCTTACTCTTGTGCA 556
07 398 TCAGCATAGACATATATGT-----GGCAGTAATAAGTCCCAAGCCATAG 445
08 557 TCAGCATAGACCGCTACGTGGCCATGTGTCAGGCTGTCTCAGCTCACCGCACCGTGGCC 616
09 446 GAGTGGGAAAAACATGCTGTGATCATCTGTTTCTGTGTGTCGAATGGCTGCATCTGTGTA 505
10 617 GCGTCTCTTCATCACAAGCAAGCTGTCTGTGTGGGATCTGGATATCAAGCCAGAGTCTT 676
11 506 GCATACCCCAAGCTGTTTTTTTATACAGTAATGACATGCTAAGTGCAATTTCCATTTTC 565
12 677 CCATCCCAAGCTCTGTACAGTACGCTTCCAGAGGACGAGGAGCAACGATGAT 736
13 566 CCGGCTACTAGGAATCATATGAAAGCAATTGATTTCAATGTAG-----AGATCTGCA 619
14 737 GCTCTCATACACAGACATGTGAGAGCCTTTATACCATTCAGATGGGCCCAATGGTA 796
15 620 TTGATTTTGTAGTACCTCTTTCTTATTAATGGGGGTGCTACTTTATCACAAGACAC 679
16 797 TCGGCTTCTGTGTCCTCTGCTGAGGCAATAGCTTCTGTACCTTGTATCATTCGCAACC 856
17 680 TCATGAAATGCGCAACATTAAATATCTGCAAGCCCTTAAAGTTCTGCTCAAGTCTTA 739
18 857 TGCTCCAGGACCGCACTTGAACGCAACAAGGCATCAAGTGTATCATCTGTGTGTCG 916
19 740 TAGTTTCAATGTACACTCACTGCTTATTAATGATGTCAGTTCTGCCAGCACAATAGCA 799
20 917 TGGTCTTCAATGCTTTCACAGTCCCTTCAATGGGGTGTCTGGCCAGAGGGTGGCA 976
21 800 TCATCTACTCCCTGATCACCAGCTGCAACATGACAGCAACGATGACATCGCATCCAG 859
22 977 ACTTCAATACACAGATAGACCTGTGAGCTCAGTAAGCACTCAACATCGCTTACGACG 1036
23 860 TCACGAAAGCATGCACTCTTTTACAGCTGCTCCTCAACCCATTCCTTATGTTTTATG 919
24 1037 TCACCTTACAGCTGCGCTGTGCTCGCTGCTCAACCTTTCTTGTAGCCTTCAATCG 1096
25 920 GAGCATCTTTCAAAACATCAGTTATGAAATGGCCAAAGATATAGGATCTGGAG 974
26 1097 GCGTCAAGTTCGCAAGCATCTTCAAGCTTTCAGAGCTTTCAGAGACCTGGGCTCCTCAG 1151

RESULT 5
PCT-US93-1153-18
; Sequence 18, Application PC/TUS931153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11153  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Noland, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1900 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: intron  
LOCATION: 1..168  
FEATURE:  
NAME/KEY: exon  
LOCATION: 169..1245  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 169..1242  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 1246..1900  
PCT-US93-11153-18

Query Match 14.5%; Score 166.2; DB 5; Length 1900;  
Best Local Similarity 50.2%; Pred. No. 1.6e-38;

Matches 479; Conservative 0; Mismatches 458; Indels 18; Gaps 2;

QY 38 ATGAGGAAATGAATGAGCACTTATGACTACATCAATGAATGATCTGATCA 97  
DB 197 ACGATTACATGAGCAACACAGCAGTGAATGCTTTGCTGCTGCTCA 256  
QY 98 AAGAGATGTCAGAGATTTTGCAAAAGTTTCTCTCTGATTCCTCAATGTTTGC 157  
DB 257 AGAAGGACGTCGGAACCTTAAAGCTGTGTTCTCTCATCATGTACTCATATTGTT 316  
QY 158 TCATTGACTTGGAGCAATTCATGAGTGTAGTGAATTTATGCTTATCAAGAAACAG 217  
DB 317 TCGTGGGCTTACTGGGCAATGAGGCTGTCTGTGACCTTATCTATTCAAGAGCTCA 376  
QY 218 GAACCAAAAGATGTGTATCTCTGAATTTGCTGTAGAGATTTACTCTTTTATGCA 277  
DB 377 AGACATGACCGATACCTGCTCAACCTGGGCGAGACATCTCTCTCTGA 436  
QY 278 CTCGCTTTTGGGCTGTAATGACGTTTATGAGGCTTTTAAAGGAAATATGCA 337  
DB 437 CCTTCTCTTGGGCTTAAGCGCGGCCCAAGTCTGGGCTTCTGGTGCACCTTTGCA 496  
QY 338 AATTAATCTGAGCTTGTACACACTTAACTTTGTCTGTGAATGCAATTTGCTTGA 397  
DB 497 AGCTCATCTTGGCATCTAAGATAGAGTCTTTCAGTGGCAGTCTCTCACTTTTGA 556  
QY 398 TCGCATGACATATGT-----GGAGTAACTAAAGTCCCAAGCAATCAG 445  
DB 557 TCGCATTTGACCCCTAGTGGCCATGTCAGAGCTGTCTCAGTCAACCCGACCGGCC 616  
QY 446 GAGTGGGAAAACATGCTGATCATCTGTTTCTGTGTGATGAGTGTGCACTTGTCTGA 505  
DB 617 GCGTCTTCTCATCAGCAAGCTGTCTGTGTGGCATTTGATTAAGCAAGTGTCTCT 676

QY 506 GCATACCCAGCTGGTTTTTTATACAGTAATGACAAATGCTAGTGCATTCCTATTTCC 565  
DB 677 CCATCCAGAGCTCTGTACAGTGAACCTCCAGAGAGACGACGTAGCAAGAGCGCAT 736  
QY 566 CCGCTACCTAGGAACATCAATGAAGAATGATTTCAATGCTAG-----AGATCTGA 619  
DB 737 GCTCTCATCAGAGCATGTGGAGGCTTTATACCATTCAGTGGCCCGCATGTGTA 796  
QY 620 TTGATTTGATGATACCTTTCTTATATGAGGGTGTCTACTTTATCAAGCAAGACAC 679  
DB 797 TGGCTTTCTGTGCTCCCGCTGCGCATGAGGCTTCTGTACTCTTCAATCCGCAACC 856  
QY 680 TCATGAAGTGGCAACATTAATAATCTCAGACCCCTTAAAGTTTGTCTCAGCTGTTA 739  
DB 857 TGCTCCAGGCAAGCACTTTGAGCGCAACAGGCCATCAGATGATCATTCCTGTGTG 916  
QY 740 TAGTTTCAATGTCACTGACCTTATTAACATTTGCAAGTTCTGCCGACCATAGACA 799  
DB 917 TGTCTTCAATGATCTTCCAGCTGCTTCAATGGGCTGTCTGCGCCAGAGCTGCA 976  
QY 800 TCATTAATCTCCTGATCAACAGCTGCAACATGAGCAACGATGACATGCGCATTCAG 859  
DB 977 ACTTCAACATCACAGTAGCACTGTGAGCTCAGTAAGCACTCAACATTCGCTACGAC 1036  
QY 860 TCACAGAAAGCATGGCAGCTTTTCAAGCTGCTTCAACCAATCTTATGTTTATG 919  
DB 1037 TCACCTACAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1096  
QY 920 GAGCATCTTTCAAAACATACGTTATGAAGTGCCAGAAATATGAGTCTGAG 974  
DB 1097 GCGTCAAGTTCGCAACGATCTCTTCAAGCTCTTCAAGGACCTGGGCTGCTGAG 1151

RESULT 6  
US-08-153-848-6

/ Sequence 6, Application US/08153848  
/ Patent No. 5759804

/ GENERAL INFORMATION:

/ APPLICANT: Godiska, Ronald

/ APPLICANT: Gray, Patrick W.

/ APPLICANT: Schweikart, Vicki L.

/ TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors

/ NUMBER OF SEQUENCES: 64

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

/ STREET: 6300 Sears Tower, 233 South Wacker Drive

/ CITY: Chicago

/ STATE: Illinois

/ COUNTRY: USA

/ ZIP: 60606

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/153,848

/ FILING DATE: 17-NOV-1992

/ CLASSIFICATION: 514

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 07/977,452

/ FILING DATE: 17-NOV-1992

/ ATTORNEY/AGENT INFORMATION:

/ NAME: No. 5759804e1, Greta E.

/ REGISTRATION NUMBER: 35,302

/ REFERENCE/DOCKET NUMBER: 31794

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (312) 474-6300

/ TELEFAX: (312) 474-0448

/ TELEX: 25-3856

/ INFORMATION FOR SEQ ID NO: 6:





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Db 410 AGAAGACGTGCGAAGCTTAAAGCTGCTCTCCATCATGTAATCATATTGTT 469
Qy 158 TCATTGACCTTGACGGAATTCATGAGTGGCAATTTATGCTATTACAAAGAAAGA 217
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Qy 218 GAACCAAAACAGATGTGATACCTGTAATTTGGCTGTAGAGATTTTACTCTTCTATTCA 277
Db 530 AGACCATACCGATACCTACTGCTCAACCTGGGGTGGGAGACATCTCTCTCTCTGA 589
Qy 278 CTGTCCTTTTGGGCTGTATATGCAAGTTCATGGGTGGGTTTATGAGAAATAATGTGA 337
Db 590 CCGTCCCTTCTGGGCTTACAGCGCGGCAAGCTCTGGGTCTTCTGCTCCACTTTTGA 649
Qy 338 AAATACTTACGCTTGACACATAAATTTGCTCTGAAATGCAATTTCTGGCTGTA 397
Db 650 AGCTATCTTTTCCATACAAAGATGAGCTTCTTCAAGGGAGTCTCTTCTTTGCA 709
Qy 398 TCAGCATAGACAGATATGT-----GGCAGTAACTAAAGTCCCAAGCAATCAG 445
Db 710 TCAGCATAGACCGTACGTAGCGCATGCGCAGGCTGTCTAGCTCACCGCACCGTCC 769
Qy 446 GAGTGGGAAAACATGCTGATCATCTGTTTCTGTGTCTGATGGCTGCCATCTTGCTGA 505
Db 770 GCGTCTTCTCATGACAGAGCTGTCTGTGTGGGCACTGTGATCTAGCACAAGTGTCT 829
Qy 506 GCATACCCGCTGTTTATATACATTAATGACATGCTAGTGTGATTCATTTTC 565
Db 830 CCAATCCAGAGCTCTCTGACAGTACCTCCAGAGAGACAGAGACAAAGCAATGGAT 889
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Db 890 GCTCTCATACAGAGAGATGGAGGCTTTATCACCATCCAGGTGGCCAGATGGTGA 949
Qy 620 TTGATTTTGAATACCTTTTCTTATTTATGGGGTGTGCTACTTTATACAGCAAGAAC 679
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Qy 680 TCATGAAGATGCCAAATTAATATCTCGACCCCTTAAAGTTCTGCTCAGAGTGTGA 729
Db 1010 TGCTCCAGGACGCAACTTTGAGGCAACAGGCAATCAAGGATATGCTGTGTGTG 1069
Qy 740 TAGTTTCAATGCTCACTCAATGCTTTATTAATTTGCAAGTTCTGCGGACATAGACA 799
Db 1070 TGGTCTTCAATAGTCTTCCAGTGTGCTTACATAGGGGTGTGCTGCGCCAAAGGTTG 1129
Qy 800 TCATCTACTCCCTATACACAGCTGCAACATGAGCAAAAGCAATGAGATGCCATCCAG 859
Db 1130 ACTTCAACATCACCAAGTAGACCTGTAGCTCAGTAACTCAATCATGCTTACAGAG 1189
Qy 860 TCACAGAAAGATGCACTTTTACAGAGTGCCTCAACCAATCCCTTATGTTTATGG 919
Db 1190 TCACCTTCAAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1249
Qy 920 GAGCATCTTCAAAACATGATTAAGAGTGGGCAAGAAATATGGGCTCTGAG 974
Db 1250 GCGTCAGATTCCGGAAGATCTTTCAAGCTTTTCAAGAGACCTGGGTGCTGAG 1304

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RESULT 8  
 US-09-088-337B-6  
 ; Sequence 6, Application US/09088337B  
 ; Patent No. 6348574

GENERAL INFORMATION:  
 APPLICANT: Godiska, Ronald  
 Gray, Patrick W.

TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 66  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

```

; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2058 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 166..1395
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-088-337B-6

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Query Match 14.5%; Score 166.2; DB 4; Length 2058;  
 Best local Similarity 50.2%; Pred. No. 1.6e-38;  
 Matches 479; Conservative 0; Mismatches 458; Indels 18; Gaps 2;

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Qy 38 ATGAGAAATGAATGATGATGCACTTATGACTACAGTCAATATGAATGATCTGTATCA 97
Db 350 AGGATTAATGAGAGACACACACAGTGAATCACTTTGTTGAGTCTTGTGCTCA 409
Qy 98 AAGAAGATGACAGAAATTTGCAAAAGTTTCTCCCTGTAATTCCTCAATAGTTTGG 157
Db 410 AGAAGACGTGCGGAACCTTAAAGCTGTGCTCCCTATCATATGTAATCTTATGTT 469
Qy 158 TCATTGACTTGACGCAATTCATGTGAGGCAATTTATGCTATTACAAAGAAAGAGA 217
Db 470 TCGTGGGCTTACTGGGCAATGGGCTGTGCTGTGACCTATATCTATTTTCAAGAGCTCA 529
Qy 218 GAACCAAAACAGATGTGATACCTGTAATTTGGCTGTAGAGATTTTACTCTTATTTCA 277
Db 530 AGACCATACCGATACCTACTGCTCAACCTGCGGTGGGAGACATCTCTCTCTGTA 589
Qy 278 CTGTCCTTTTGGGCTGTATATGCAAGTTCATGGGTGGGTTTATGAGAAATAATGTGA 337
Db 590 CCGTCCCTTCTGGGCTTACAGCGCGGCAAGTCTCTGGGTCTTGGTGTGCACTTTTGA 649
Qy 338 AAATACTTACGCTTGTACACTTAACTTTGCTCTGAAATGCAATTTCTGCTGTGA 397
Db 650 AGCTATCTTTTCCATACAAAGATGAGTCTTCTCAATGAGTGTCTCTCTTTTGA 709
Qy 398 TCAGCATAGACAGATATGT-----GGCAGTAACTAAAGTCCCAAGCAATCAG 445
Db 710 TCAGCATAGACCGTACGTAGCGCATGCTCCAGGCTGTCTCAAGCTCACCGCACCGTCC 769
Qy 446 GAGTGGGAAAACATGCTGATCATCTGTTTCTGTGTCTGATGGCTGCCATCTTGCTGA 505

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Db	890	GCTCTCATACAGAGCAGATGTGAGGCTTTATACACATCCAGGTGGCCAGATGTGGA	949
Qy	620	TTGATTTGTAATACCTTTCTTATATATGGGGGTGTCTACTTTTATCACAGCAAGAAAC	679
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Qy	680	TCATGAGATGSCAAACATTAAATATCTGACCCCTTAAAGTTGCTGCAAGTCGTTA	739
Db	1010	TGCTCCAGGACAGCACTTTGAGCGCAAAAGGCATCAAGTGAATCATCGTGTGTGCG	1069
Qy	740	TAGTTTCATATGTCACTCAACGTGCTTATTAACAATGTCAAGTTCTGCGGAGCATAGACA	799
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Qy	800	TCATCTACTCCCTGATCAGCAGCTGCACCATGAGCAAGCATGCACTCGCATCCACAG	859
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Qy	860	TCACAGAAAGCATGCACTCTTTCACAGCTGCTCAACCAATCCTTATATGTTTTATAG	919
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?      SEQUENCE CHARACTERISTICS
?      LENGTH: 2058 base pairs
?      type: nucleic acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?      MOLECULE type: DNA (genomic)
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 166..1395
?
PCT-US93-11153-6

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QY 218 GAACCAAAAGATGTGTACATCTGTAATTTGGCTGAGAGATTTACTCTTTATTTCA 277
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QY 338 AAATTAATCTGACCTTTTACACACTAACTTTGCTCTGAAATGAGTTTCTGGCTGTA 397
DB 452 AGCTCATCTTGGCTTACAGATGAGTCTTCAATGAGATGCTCTTACTCTTGTGA 511
QY 398 TCAGCATAGACAGATATGT-----GGCAGTAATTAAGTCCCGCAATTCAG 445
DB 512 TCAGCATAGACGCTTACGCTGCGCATTCGTCAGCTCTCAGCTACCGGCACTGGGCC 571
QY 446 GAGTGGAAAAACATGTGTATCATCTGTTCTGTGTCTGTGATGCTGCTCATCTTGTGA 505
DB 572 GCGTCTTCTCATCAGCAAGCTGCTGTGTGGGCTATCTGATATCTAGCCACAGTGTCT 631
QY 506 GCATACCCGAGCTGTTTATATACATTAATGACATGCTAGTGTGATTCCTCATTTTC 565
DB 632 CCATCCAGAGCTCTGTACAGTACCTCCAGAGAGACAGACAGTGAACAGATGCGAT 691
QY 566 CCCGCTACTAGAAACATCAATGAAGCATTTCAATGCTAG-----AGATCTGCA 619
DB 692 GCTCTCTATACAGACATGTGAGGCTTTATCACATTCAGGTGGCCAGATGCTGA 751
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DB 812 TGCTCCAGGACGCAACTTTGAGGCAACAGGCCATCAAGTATATGCTGTGTG 871
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DB 932 ACTTCAATCATCAGTGAAGCTGTGAGCTCAGTAAGCAATCAATGCTGCTGACAG 991
QY 860 TCACAGAAAGATGCACTCTTTTCAAGGCTGCTCAACCCATCTTATGTTTATG 919
DB 992 TCACCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1051
QY 920 GAGCATCTTTCAAAAACATGCTTATGAAGTGCCCAAGAAATATGGTCTGAG 974
DB 1052 GCGTCAAGTTCGCAAGATCTCTTCAAGCTTCTCAAGAGACCTGGGCTGCTGAG 1106

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## RESULT 14

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US-09-266-464-1
Sequence 1. Application US/09266464
GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
FILE REFERENCE: LK98-16
CURRENT APPLICATION NUMBER: US/09/266,464
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2577
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

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LOCATION: (58) ... (1131)  
US-09-266-464-1

Query Match 14.4%; Score 164.8; DB 4; Length 2577;  
Best Local Similarity 51.0%; Pred. No. 4,7e-38;  
Matches 481; Conservative 0; Mismatches 442; Indels 21; Gaps 3;

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QY 52 ATGAATGGCACTTATAGTACATGATATATGAACTGATCTGTATCAAAAGATGTCGA 111
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QY 112 GAATTTGCAAAAGTTTCTCTCTGATTTCTCTCAAAATGTTTGTGATGGAATTGCA 171
DB 154 CAGTTGGAGCAATTTCTCTCCACCTTTGATGCTGCTGCTGCTGCTGCTGCTGCT 213
QY 172 GGCATTCATGATGTGAGCAATTTATGCTTATACAAAGAAACAGAAACCAACAGAT 231
DB 214 GGCATTCATGATGTGAGCAATTTATGCTTATACAAAGAAACAGAAACCAACAGAT 273
QY 232 GTTACATCTGAAATTTGAGCTGTAGCAATTTACTCTTATTTCACTCTGCTTTTGG 291
DB 274 ATGTTCTTTGAAATTTGCAATTTGCACTCTCTCTTTCTTCTCACTCTTCTCTG 333
QY 292 GCTTTATGCACTTATGAGGCTTTTATGAGAAATATATGCAAAATATGCACTTCA 351
DB 334 GGCATTCATGATGTGAGCAATTTATGCTTATACAAAGAAACAGAAACCAACAGAT 393
QY 352 TTGACACACTTAACTTTGCTCTGAAATGCACTTCTGCTTGTATGAGATAGACAGA 411
DB 394 ATGTACATGATTAATTTCTTACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 453
QY 412 TATGTGAGCAATTAAGTCCGAG-----CCAATCAGAGTGGAAAAACAT----- 460
DB 454 TACATTCATGCTCCAGGCTATGAGAGACATCTTGTGAGGAGAAAAAGCTTTTGTAC 513
QY 461 -GCTGATCATCTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 519
DB 514 AGCAAAATGTTTGTCTTACATCTGAGGATTTGAGAGCTGCTCTGTGATCCCAAAATC 573
QY 520 GTTTTATATAGTAATGA-----CAATGCTAGTGTGATTTCCATTTTCCCGGC 570
DB 574 TTTATACGCAATTAAGAGAGATCCGCAATGCTATCTGTGACATGATGTTTACCTGAC 633
QY 571 TACCTAGAAATCAATGAAGCAATGATTAATATGATGATGATGATGATGATGATG 630
DB 634 GATGAGGACCAAACTGAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 693
QY 631 GTTACCTTTCTTATATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 690
DB 694 CTTCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 753
QY 691 CCAAACTTAAATATCTGACCCCTTAAAGTTCTGCTACAGCTGTTATGATTTTCAAT 750
DB 754 AAGATGCTTCCAGACCAAAAGCTTAAAGTACATCATCTGCTGACCGCTTTTGTG 813
QY 751 GTTACCTTCACTGCTTATTAATGATGATGATGATGATGATGATGATGATGATGAT 810
DB 814 TTGTCTCAGTTTCCCTTACAACTGCAATTTTGTGTGAGACATGAGACCTTATGCA 873
QY 811 CTGATACAGCTGCAACATGAGCAAAAGCAATGAGCAATGAGCAATGAGCAATGAG 870
DB 874 TTATCTCAACAGTGTGCTTTCACAAACATGATGATGATGATGATGATGATGATG 933
QY 871 ATGCACTCTTTCACAGCTGCTTCAACCAATCTTATGTTTATGAGCAATCTTTC 930
DB 934 ATGCTCTTCTTCAAGTGTGCTGAGACCTGTTCTATGTTTGTGTGAGATGATTC 993
QY 931 AAAAATCAGTATGAAGTGTGCAAAAGAAATATGGTCTGAG 974
DB 994 CGCGGATCTGTGAAAAACCTGAAAGAACTTGGTGTGATCAG 1037

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RESULT 15

US-09-299-843A-65  
; Sequence 65, Application US/09299843A  
; Patent No. 6107475  
; GENERAL INFORMATION:  
; APPLICANT: Godiska, Ronald  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Schweikart, Vicki L.  
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/299,843A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/088,337  
; FILING DATE: 01-JUN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/153,848  
; FILING DATE: 17-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/977,452  
; FILING DATE: 17-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jill E. Unl  
; REGISTRATION NUMBER: 43,213  
; REFERENCE/DOCKET NUMBER: 27866/32059B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2085 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 177..1310  
; US-09-299-843A-65  
Query Match 14.4%; Score 164.6; DB 3; Length 2085;  
Best Local Similarity 50.1%; Pred. No. 4.8e-38;  
Matches 478; Conservative 0; Mismatches 459; Indels 18; Gaps 2;  
QY 38 ATGAGGAAATGAATGATGCACTTATGACGTCAATATGAATGATCTGTATCA 97  
DB 265 ATGACGTACATCGGAGAAATACCAAGGTGACACCTGTACGAGTGGTGTCTCA 324  
QY 98 AAGAAGATGTCAGAGATTTTGCAAAAGTTTCTCCCTGATTCCTCACAAATGTTTG 157  
DB 325 AAGAAGATGTCAGAGATTTTGCAAAAGTTTCTCCCTGATTCCTCACAAATGTTTG 384  
QY 158 TCATTGACTTGGAGCAATTCATGAGTATGAGCAATTTATGCTTATTAAGAAACAGA 217  
DB 385 TCGTGGCCCTGCTGCGAAGGGGTGTGATGACGTACATCATTTTCAAGAGCTCA 444  
QY 218 GAACCAAAAGATGTGTACATCTGGAATTTGCTGTAGAGATTTACTCTTTTATTC 277

DB 445 AGACCATGAGGATACATCACTGCTCAACTGCGCGTGAGACATCTTTTCTCTTA 504  
QY 278 CTCTGCTTTTGGGCTGTGTAATGCACTTCAATGGGTGGGTTTATGAGAAATTAATGCA 337  
DB 505 TTCTTCCCTTCTGGGCTTACAGCCGAAAGCTCTGTGATCTTTGGGCTTACTGTGTA 564  
QY 338 AAATACTTACGCTTTGTACACACTAACTTTGTCTGTGAATGCAATTTGCTGTGTA 397  
DB 565 AGGCGATCTTTGGCATATTAAGTTAAGCTTTTACAGCGGAGTCTGTGCTCTTATGCA 624  
QY 398 TCAGCATGACGATATGT-----GGCATGATCTAAAGTCCCGCAATTCAG 445  
DB 625 TCAGCATGACGCTGACGATGACCATGCTCCAGGCGGTGTCCGTCATGACCGCGCC 684  
QY 446 GAGTGGGAAATCAATGCTGATCATCTGTTCTGTGTGTGATGAGTCCCATTTGTGTA 505  
DB 685 GGTGCTTCTATACAGCAAGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 744  
QY 506 GCATACCCGAGCTGTTTATATACAGTAAATGACATGCTAGGTGATTTCCATTTTCC 565  
DB 745 CCATCCCGAGCTGCTTACAGCGGCTCCAGAAAGACAGCGGAGAGACAGCTGAGAT 804  
QY 566 CCCGCTACCTAGGAACATCAATGAAAGATTTGATTTCAATGCTAG-----AGATCTGCA 619  
DB 805 GCTCACTGTGATGCTCCAGGCTGTGATCACCATCAAGTGGCCAGATGTTT 864  
QY 620 TTGATTTGATGATCACTTTCTTATATGAGGGGTGTGCTTATATACAGCAAGACAC 679  
DB 865 TTGGGTTCTTATGCTGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 924  
QY 680 TCATGAAGATGCAAAATTAATATCTGACCCCTTAAAGTTCTGCTCAAGTCTTGA 739  
DB 925 TGCTCAGGACGCAACTTATGAGCGGAAACAGGCAATCAAGTATCATGCTGTGTG 984  
QY 740 TAGTTTATGCTGCTCAATCTGCTTATATCATTTGCAAGTTCTGCGAGCCATAGCA 799  
DB 985 TAGTCTTATGCTTCTTCAAGTCTTCAATGAGGTGTGTGTGTGTGTGTGTGTGT 1044  
QY 800 TCATCTACTCTGCTGATCAAGCTGCAACATGAGCAAAAGCATGAGATGCGATCCCAAG 859  
DB 1045 ACTTAAATCAACCAATGAGCTGTGCGAAGCCAGCAAGCTCAATCTGTATAGC 1104  
QY 920 GAGCATCTTTCAAAATCACTGATGAAAGTGGCCAGAAATATGGTCTGTGAG 974  
DB 1165 GCGTCAGTCCGAGCGACCTTTCATGAGCTTTCAAGGACTTGGGCTGTGCTCAG 1219  
RESULT 16  
US-09-088-337B-65  
; Sequence 65, Application US/09088337B  
; Patent No. 6348574  
; GENERAL INFORMATION:  
; APPLICANT: Godiska, Ronald  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Schweikart, Vicki L.  
; TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS



SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/088,337B  
FILING DATE: 01-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/153,848  
FILING DATE: 17-Nov-1993  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6348574and, Grete E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 177..1310  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-088-337B-65  
Query Match 14.4%; Score 164.6; DB 4; Length 2085;  
Best Local Similarity 50.1%; Pred. No. 4,8e-38;  
Matches 478; Conservative 0; Mismatches 459; Indels 18; Gaps 2;  
38 ATGAGAAATGAATGCACTTATGACATGACATGCAATGAACTGATCTGTATCA 97  
265 ATGACTACATGGGGAAGATACACGGTGACATACCCCTGTAGAGTGGTGCTTCA 324  
98 AAGAAGATGTCAGAAATTTGCAAAAGTTTCCCTCCCTGATTCCTCAAAATGTTTCG 157  
325 AGAAGGATGTGGGAACCTTAAGGCTGGTTCCTGCTCATGATTAATCTGTCACTGCT 384  
158 TCATTGACTTGACAGCAATTCATGATGAGCAATTTATGCTATTACAAAGAAAGAGA 217  
385 TCGTGGCTCTGCTGGCAACGGCTGGTGAATGACATCATATTTCAAGAGGCTCA 444  
218 GAACCAAAACAGATGTGATCATCTGAAATTTGGCTGTAGCAGATTTACTCTTATTTCA 277  
445 AGACCATGACGATACCTACCTGCTCAACCTGGCGGTGGCAGACATCTTTTCTCTCTAA 504  
278 CTCGCTCTTTTGGCTGTATGCAATTCATGGGTGGCTTTTGGGGAATAATATGCA 337  
505 TTCTTCCCTTGGGGCTTACAGCGCAAGCCAAAGTCTGATCTTTGGCGCTTCACTGTGTA 564  
338 AAATTAATCTGACCTTGTACACATACTTGTCTCTGAAATGCAAGTTTCTGGCTGTGA 397  
565 AGGAGATCTTTGGCATCTTAAGTAACTTCTTCAAGGGAGTGTGTCTCTTAAGCA 624  
398 TCAGATGACAGATATGT-----GGCAGTAATCTAAAGTCCCAAGCAATCAG 445  
625 TCAGATGACAGCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 684  
446 GAGTGGGAAAACATGCTGATCATCTGTTCTGTGCTGATGAGGCGCATCTTGGCTGA 505  
665 GGTGCTCTTCTATCAAGCAAGCTGTCTGTGTGGGATCTGAGTGTGAGGCTCTTCTCTCT 744  
506 GCATACCCAGCTGCTTTTATACAGTAATGACATGATGATGATGATGATGATGATGATGAT 565  
745 CCATCCCGAGAGTGTCTTAAGCGCGCTCCAGAAAGAGAGAGAGAGAGAGAGAGAT 804  
566 CCGGCTACCTAGGAACATCATGAAAGCATTTGATTTCAATATGTAG-----AGATCTGCA 619

Db 805 GCTCAGTGTGATGAGCCCAAGTGAAGGCTTGTATCATCATCATCAAGTGGCCCAAGATGTT 864  
Qy 620 TTGATTTGATGATACCTTTCTTATTTATGGGGTGTGCTACTTTATGACAGAGAGAC 679  
Db 865 TTGGTCTTCTAGTGTCTTATGCTGTGCTATGATGATTTCTGTACTCATTTATCATTCGTA 924  
Qy 680 TCATGAGATGCGAAACATTAATATATTCGACCCCTTAAAGTTCTGTCTACAGTCTGA 739  
Db 925 TGTCTCAGGACGCAACTTTTGGAGCGAAAGGCGCATCAAGGTATGATTTCCCGGTGG 984  
Qy 740 TGTGTTTATGATGCTACATGCTGCTTAAATGATGCAATGTCAGGCGGAGCATAGACA 799  
Db 985 TGTCTTATGATGCTTCAAGCTGCTTCAATGAGGTGCTGCTGATGACGAGTGGCTCA 1044  
Qy 800 TCATCTACTCCCTGATGACAGCTGCAACATGAGCAAGCATGAGCATGCGCATTCAG 859  
Db 1045 ACTTCAACATGACCAATGACGCTGCAAGCAAGCATGAGCATGAGCATGAGCATGAG 1104  
Qy 860 TCACAGAAAGATGCGACTCTTTTACAGCTGCTTCAACCCATCTTTATTTTATAG 919  
Db 1105 TCACCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1164  
Qy 920 GAGCATCTTTTCAAAACTACGTTATGAAAGTGGCCCAAGAAATATGAGTCTGAG 974  
Db 1165 GCGTCAAGTTCGCGACGACCTTCTTCAAGCTTTCAAGACTTGAAGACTTGGGCTGCTCAG 1219  
RESULT 17  
US-08-383-750-1  
Sequence 1, Application US/08383750  
Patent No. 574301  
GENERAL INFORMATION:  
APPLICANT: Birkenbach, Mark  
APPLICANT: Kieff, Elliot  
TITLE OF INVENTION: Epstein Barr Virus Induced Genes  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, N.W.,  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/383,750  
FILING DATE: Herewith  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Fox, Samuel, L.  
REGISTRATION NUMBER: 30,353  
REFERENCE/DOCKET NUMBER: 0627.3300001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2154 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 64..1197  
US-08-383-750-1  
Query Match 13.9%; Score 159.8; DB 1; Length 2154;  
Best Local Similarity 49.7%; Pred. No. 1.2e-36;

Matches	475;	Conservative	0;	Mismatches	462;	Indels	18;	Gaps	2
QY	38	ATGAGGAAAATGAATGAATGGCACTTATGACTACAGTCAATATGACTGATCTGTATGA	97						
Db	152	ACGATTTCATCGGAGACCAACACAGTGGAGTACACTTTGTTCGAGCTTGTGTGTCCA	211						
QY	98	AAGAAGATGTCAAGAAATTTGCAAAAAGTTTCTCCCTGATTTCCCACAATAGTTTGC	157						
Db	212	AGAGAGCGTGGGAACTTTAAAGCTGGTTCTCTCTATCATATACTCATCATTTTGT	271						
QY	158	TCATTGGACTTGCAAGGCAATTCACATGGTAGTGGCAATTTATGCTATTAACAAGAAACAGA	217						
Db	272	TCGTGGGCTTACTGGGCAATGGGCTGTGTGTGTGACATATATCTATTTCAAGAGGCTCA	331						
QY	218	GAACCAAAACAATGTGTATCATCTGGAATTTGGCTGTAGCAATTTACTCTTATATCA	277						
Db	332	AGACCAATGACCAATACCTACCTGTCTAACCTGTGGGTGGCAACATCTCTTCTCTCGTA	391						
QY	278	CTCTGCTTTTGGGCTGTATTAATGACAGTTTCATGGGAGGTTTAAAGGAAATAATATGTA	337						
Db	392	CCCTTCCTCTTCTGGGCTTACAGCGGGCCAAATCTCGGATCTTCGGTGTCCACTTTTGA	451						
QY	338	AAATACTTCAGCCTTTGACACACTAACTTTGTCTCTGAAATGCAATTTCTGGCTTGA	397						
Db	452	AGCTCATCTTTCACATCTACAGATGAGCTTCTTCAGTGGACATGCTCTACTTCTTTGA	511						
QY	398	TCAGCATAGACAGATATGT-----GGCAGTATCTTAAATGCCCAACCAATCAG	445						
Db	512	TCAGCATATGACCGCTACCGTGGCATGTCCACAGGCTGTCTCACTCAACCGCACCGTGCC	571						
QY	446	GAGTGGGAAAAACATGCTGGATCATCTGTGTTCTGTGTCTGATGTGGCTGCATCTTGCTGA	505						
Db	572	GGGTCTTCTCATCAGCAAGCTGTCTGTGTGGGACGCCCATCTACGCAACAGTGTCT	631						
QY	506	GCATACCCAGCTGTTTATTAACAGTAATGACATGTAGTGTGATTTCCATTTTCC	565						
Db	632	CCATCCCAAGCTCTGTACAGTGAATTCACAGGAGCAGCAGTAGAGCAAGCAATGCAT	691						
QY	566	CCCGCTACTAGGAACATCAATGAAGATTTGATTCMAATGTAG-----AGATCTGA	619						
Db	692	GCTCTCTATCAACAGACATGTGAGGCTTTATATCAACATCAAGGTGGCCGAGATGTGA	751						
QY	620	TTGATTTGTATGATCCCTTTCTTATTTATGGGGGTGTGACTTTATCAACAGCAAGACAC	679						
Db	752	TGGCTTTCTGTGTCCCTCGCTGGCATGAGCTTGTTACTGTATCATCATCCGACCC	811						
QY	680	TCATGAAGATGCCAAACATTAATAATATCTGACCCCTTAAAGTTTGCTCATAGTCGTTA	739						
Db	812	TGCTCCAGGACGCAACTTTGAGCGCAACMAAGCCATCAAGGTGATCATCGCTGTGGTGC	871						
QY	740	TAGTTTCAATGTCACTCAACATGCGCTTATTAATTTGTCAAGTTTCGCGAGCATATGCA	799						
Db	872	TGGTCTTCAATGATCTTTCACAGTGGCTCTTACATGAGGAGTGTCTGTGCCAAGATGTGGCCA	931						
QY	800	TCATCTACTCCCTGATCAACCAAGCTCAACATGAGCAAAAGCATGACATCTGCATCTCAAG	859						
Db	932	ACTTCACATCAACCAATGACCATGTGAGCTCAGTAAGCACTCAACATCTGCCTACGAG	991						
QY	860	TCACAGAAAGCATGGAATCTTTTACAGCTGTGCTCAACCCAAATCCTTATGTTTATATG	919						
Db	992	TCACTTACAGCTGTGCTGTGCGTGTGCTGTGATCAACCTTTCTTTGTAACGCTTCAATCG	1051						
QY	920	GAGCATCTTTCAAAAACTAACGTTATGAAGTGGGCAAGAAATATGGGTCGTGGAG	974						
Db	1052	GGGTCAAGTTTCGACAGATATCTTCAAGCTTTCAAGGACCTGGAGTGTCTCAG	1106						

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RESULT 18
US-08-383-751A-1
; Sequence 1, Application US/08383751A
; Patent No. 5753516
; GENERAL INFORMATION:
; APPLICANT: Heagy, Wyrta E.

```

```

APPLICANT: Finberg, Robert W.
TITLE OF INVENTION: Identification and Uses of Opioid
RECEPTORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,751A
FILING DATE: 03-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: DPCI:001/WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
FEATURE:
NAME/KEY: CDS
LOCATION: 64..1197
US-08-383-751A-1
Query Match 13.9%; Score 159.8; DB 1; Length 2154;
Best local Similarity 49.7%; Pred. No. 1,2e-36;
Matches 475; Conservative 0; Mismatches 462; Indels 18; Gaps 2
QY 38 ATAGAGAAATGAATGAAATGGACTTATGACCTACAGTCATCATATGAATGAACTGATCA 97
DB 152 AGATTACATCGAGACAACACACAGTGACCTACACTTTGTTCAGAGCTTGTGCTCCA 211
QY 98 AAGAAGATGCAGAGAAATTTGCAAAAGTTCCCTCCGTAATCCCAAGATGTTTGG 157
DB 212 AGAAGACGCGGGAACCTTAAAGCTGGTCTCCCTCATCATGATCATCATATTGTT 271
QY 158 TCATTGGACTTGAGGCAATTCATGATGATGAGCAATTTATGCTATTACAGAAAACA 217
DB 272 TCGTGCGCTACTCGGCCAATGGGCTGGCTGCTGATGACCTATATCTATTTCAAAGGCTCA 331
QY 218 GAACAAAAAGATGTGATCATCTCGAATTTGGCTGTAGACAGATTACTCTCTTATCA 277
DB 332 AGACATGACGATACCTACCTGCTCACTCGGCGGTGACAGACATCTCTCTCTGA 391
QY 278 CTCTGCTTTTTGGCTGTATATGACATTCATGAGGTGGTTTAGGAAAAATATGCA 337
DB 392 CCCCTCCCTTGGGGCTAACAGCGCGGCAAGTCTGGGATCTTCGGGTCACTTTTGA 451
QY 338 AAATAACTCAGCGTTGTACACATAAACCCTTGCTCGGAATGCAAGTTCTGGCTTGA 397
DB 452 AGCTCATCTTTGCAATCTACAAAGATGAGCTTCTTCAAGTGGAGCTCTCATCTTTTGA 511
QY 398 TCAGCATAGACAGATATGT-----GGCAGTAACTAAAGTCCCAGCCAAATGAG 445
DB 512 TCAGCATAGACGCTACGTCGTCATGTCACATGTCACAGGCTGTCTCAGCTCACCGCACCGTGCC 571
QY 446 GAGTGGAAAAACCATGCTGATCATCTGTTTCTGTGTCTGATGCTGCTCCATCTTGCTGA 505

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Db 572 GCGCTCTTCATCAGCAAGTGTCTGTGTGGGAGCGGCATATCAGCAGTGTCT 631
Qy 506 GCATATCCCAAGCTGGTTTATTAACATTAATGCAATGCTAGTGCATTTCC 565
Db 632 CCATCCCAAGCTCTCTACAGTACCTCCAGAGAGACAGTACAGCATGCAT 691
Qy 566 CCCGCTACCTAGGAACATCAATGAAGCATTTGATTAATAGTGA-----AGATCTGCA 619
Db 692 GCTCTCTATCAGAGCATGTGAGGCTTTATCACCATCCAGTGGCCCAATGTGA 751
Qy 620 TTGATTTGATAGTACCTTTCTTATTAATGAGGCTGTGCTACTTTATCAGCAAGAAC 679
Db 752 TCGGCTTTGTGTCTCCCTGTGCGCATGAGCTTGTGTACTTTGATCATCCGACCC 811
Qy 680 TCATGAAGATCCCAATTAATATCTGAGACCCCTTAAGTTTGTCTCAGTGTGA 739
Db 812 TGCTCCAGGACGCACTTTGAGGCAACAGGCAATCAAGGTATCATGCTGTGTG 871
Qy 740 TAGTTTCAATGTGACATCACTGCTTATTAATGATTCAGTTCTGCGGACATAGACA 799
Db 872 TGGCTTCAATAGTCTTCAAGTCTGCTTCAATGAGGCTGTGCTGCGGACATAGACA 931
Qy 800 TCATCTACTCCCTGATGACAGCTGCAACATGAGCAAAAGCATGAGCATGCCATCAG 859
Db 932 ACTTCAATCAGCAAGTACAGCTGTGAGCTCAGTAAAGCAATCAATCATGCGCTAGAG 991
Qy 860 TCACAGAAAGCATGCACTTTTACAGCTGCTCAACCCCAATCTTTATGTTTATG 919
Db 992 TCACCTACAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1051
Qy 920 GAGCATCTTCAAAACATGAGTATGAAGTGGCAAGAAATATGAGTCTGAG 974
Db 1052 GCGTCAAGCTTCCGCAAGATATCTTCAAGCTTCAAGGACCTGGGCTGCTGAG 1106

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## RESULT 19

US-08-352-678-1  
Sequence 1, Application US/08352678

Patent No. 6043351  
GENERAL INFORMATION:

APPLICANT: Birkendach, Mark  
APPLICANT: Kieff, Elliott

TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES  
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue  
CITY: Boston

STATE: MA  
COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/352,678

FILING DATE: 30-NOV-1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/980,518

ATTORNEY/AGENT INFORMATION:  
FILING DATE: 25-NOV-1992

NAME: Gates, Edward R.  
REGISTRATION NUMBER: 31,616

REFERENCE/DOCKET NUMBER: B0801/7044  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

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/ LENGTH: 2154 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 64..1197
/ US-08-352-678-1

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## Query Match

13.9%; Score 159.8; DB 3; Length 2154;

Best Local Similarity 49.7%; Pred. No. 1.2e-36; Indels 18; Gaps 2;

Matches 475; Conservative 0; Mismatches 462;

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Qy 38 ATGAGAAATGAATGATGAGCACTTATGACTACAGTCAATGAACTGATCTGATCA 97
Db 152 ACGATTTACATGGAGAACACACACAGAGACCTACCTTTGTGAGCTTTGAGTCTCA 211
Qy 98 AAGAAATGTCAGAAATTTGCAAAAGTTTCTCCTGTAATCTCTCAATATGTTTGG 157
Db 212 AGAAGAGCGTGGGAACTTTAAAGCTGTTCTCTCATATGATCTCAATCTATGTT 271
Qy 158 TCATTTGACTGAGGCAATTCATGATGAGGCAATTTATGCTTATTAAGAAAGACA 217
Db 272 TGTGGGCTTACTGGGCAATGGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 331
Qy 218 GAACCAAAACAGATGTGATCATCTGAATTTGGCTGTAGCAGATTTACTCTTATTTCA 277
Db 332 AGACATGACGATACCTACCTGCTCAACCTGCGTGGAGACATCTCTTCTCTGCA 391
Qy 278 CTCTGCTTTTGGGCTGTATGAGTTCATGAGGCTTTTAAAGAAATATGTTGCA 337
Db 392 CCTTCCCTTGGGCTGTATGAGTTCATGAGGCTTTTAAAGAAATATGTTGCA 451
Qy 338 AATTAATCTTACGCTTTGATCACTAACTTTGCTGGAATGAGTTCGCTGTTGTA 397
Db 452 AGCTCATCTTGTCCATCTACAGATGAGCTTCTTGAAGGCTCTCTTCTCTTCTGCA 511
Qy 398 TCAGATAGACAGATATGT-----GGCAGTAACTAAAGTCCCAAGCAATGAG 445
Db 512 TCAGATAGACAGATATGT-----GGCAGTAACTAAAGTCCCAAGCAATGAG 571
Qy 446 GAGTGGAAACCATGCTGATCATCTGTTTGTGTCTGATGAGTCTGCTCTTCTGCA 505
Db 572 GCGTCTTCTCATCAGCAAGCTGTCTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAG 631
Qy 506 GCATATCCCAAGCTGTTTATTAAGTAAATGAGAGGAGGAGGAGGAGGAGGAGGAG 565
Db 632 CCATCCCAAGCTGTTTATTAAGTAAATGAGAGGAGGAGGAGGAGGAGGAGGAG 691
Qy 566 CCCGCTACCTAGGAACATCAATGAAGATTTGATTAATGAGTGA-----AGATCTGCA 619
Db 692 GCTCTCTATCAGAGCATGTGAGGCTTTATCACCATCCAGTGGCCAGATGTGA 751
Qy 620 TTGATTTGATAGCTTTTATTAATGAGGCTGTGCTACTTTATCAGAGAGAGAC 679
Db 752 TCGGCTTTGTGTCTCCCTGTGCGCATGAGCTTGTATCCTTGTATCATCCGACCC 811
Qy 680 TCATGAAGATGCAAAATTAATATCTGACCCCTAAAGTTCTGCTCAAGTGTGA 739
Db 812 TGCTCCAGGACGCACTTTGAGGCAACAGGCAATCAAGGTATCATCTGTGTGTG 871
Qy 740 TAGTTTCAATGTGACTCACTGCTTATTAATGATTTGAGGAGCATAGACA 799
Db 872 TGGTCTTCAATAGTCTTCAAGCTGCTTCAATGAGGAGTGTGCTGCGGAGAGTGA 931
Qy 800 TCATCTACTCTCTGATCAGCTGCAACATGAGCAAGCATGAGCATGCGCATCAG 859
Db 932 ACTTCAACATCACAGTACAGCTGTGAGCTCAGTAAAGCACTCAACATGCTTACGAG 991
Qy 860 TCACAGAAAGCATGCACTTTTCAAGCTGCTCAACCCCAATCTTTATGTTTATG 919
Db 992 TCACCTACAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1051

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QY 920 GAGCATCTTCAAAAAGTACGTTATGAAAGTGGCCAGAAATATGGGCTGAG 974  
Db 1052 GCGTCAGATTCCGCAACGATATCTTCAAGCTCTTCAAGGACCTGGGCTGCTCAG 1106

## RESULT 20

PCT-US93-09636-1  
; Sequence 1, Application PC/TUS9309636  
; GENERAL INFORMATION:  
; APPLICANT: Birkendach, Mark  
; APPLICANT: Kieff, Elliot  
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/09636  
; FILING DATE: herewith  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2154 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 64..1197  
; PCT-US93-09636-1

Query March 13.9%; Score 159.8; DB 5; Length 2154;

Best Local Similarity 49.7%; Pred. NO. 1.2e-36;  
Matches 475; Conservative 0; Mismatches 462; Indels 18; Gaps 2;

QY 38 ATGAGAAAATGAATGAAATGCACTTATGACTACAGTCAATATGAACGATCTGTATCA 97  
Db 152 ACGATTATCATGGAGACAAACAGAGGACTACACTTGTGAGATCTTTGTGCTCCA 211  
QY 98 AAGAAGATGTGAGAAATTTGCAAAAAGTTTCTCCTGTAATTCCTCAATAGTTTTCG 157  
Db 212 AGAAGAGAGTCGGAACCTTAAAGCTGGTTCCTCCATCATGATCATCATCTTTGTT 271  
QY 158 TCATTGACCTTGAGGCAATTCATGATGATGGAATTTATGCTATTAAGAAAAGAGA 217  
Db 272 TCGTGGGCTTACGCGCATGGGCTGGTGGTGGTGAAGCTATATCTATTTTCAAGGGCTCA 331  
QY 218 GAACCAAAAAGATGTGTATCTCTGAATTTGGCTGAGAGATTTACTCTCTATTTCA 277  
Db 332 AGACCATGACCGATACCTACTGCTCAACCTGGGGGAGAGACATCTCTTCTCTGA 391  
QY 278 CTGCGCTTTTGGGCTGTTATGACAGTTCAATGGGGGTTTAAAGAAAATTAATGTCGA 337  
Db 392 CCGTCCCTTCGCGCTACAGCGCGGCAAGTCTCGGCTTCTTGCGTCCACTTTTGGCA 451  
QY 338 AATAATCTTACGCTTGTAGACACTAAACTTGTCTCTGGAATGCAATTTCTGGCTGTA 397  
Db 452 AGCTCATCTTTGCTCATCAAGATGAGCTTCTTCAAGGAGATGCTCTCTCTTGGCA 511  
QY 398 TCACATAGACAGATATGT-----GGCAGTAATAAGTCCCGAGCAATCAG 445

Db 512 TAGCATTTACCGCTACGAGGCGCATGCTCAAGGCTGTCTCAGCTCAACCGCACCGTGGCC 571  
QY 446 GAGTGGAAAACCATGTGTGATCATCTGTTTCTGTGTGTGATAGGCTGCCATTTTGCTGA 505  
Db 572 GCGTCTTCTCATCAGCAAGCTGTCTGTGTGGGAGCGCCATCTACATCAACAGTGTCTCT 631  
QY 506 GATACCCGAGCTGGTTTTTTTATACAGTAAATGACATGTAGTGTGATCCATTTTCC 565  
Db 632 CCATCCCAAGCTCTGTATGATGACCTCCAGAGGAGAGAGAGATGAGACATGCGAT 691  
QY 566 CCGGCTACTTGAAGACATCAATGAAAGCAATGATTAATCAATGCTAG-----AGATTCGA 619  
Db 692 GCTCTCATCAACAGAGATGGAGGCTTATCACCATCAGGTGGCCGAGATGTGA 751  
QY 620 TTGATTTGTATACCTTTTCTTATATAGGGGGTGTGTACTTTATATCAACAGAGACAC 679  
Db 752 TCGGCTTCTGTGCTCCCTGCTGGCAGTGAAGCTTGTGTACTTGTCTATCAATCCGACCC 811  
QY 680 TCATGAAGATGCAAAACATTAATATCTCGAACCCCTAAAGTTCTGCTCACAGTCTTA 739  
Db 812 TGCTCAGGACAGCACTTTGAGGCCAACAAGCCATCAAGTATATATCGTGTGTG 871  
QY 740 TAGTTTCAATGTCTCACTCACTGCTTAAACATTTGCAAGTTCTGCCAGCATAGCA 799  
Db 872 TGCTCTTCAATGCTTCCAGCTGCTCAATAGGGGTGTCTGCCAGACGCTGCGCA 931  
QY 800 TCATCTACTCCCTGATCAACCGAGTCAACATGAGCAAGCAAGCATGAGCATTCGAC 859  
Db 932 ACTTCAACATCAACGATGACACTGTGAGCTGATGACAACTCAACATCGCTAGACG 991  
QY 860 TCACAGAAAGCATGCGCACTCTTTCACAGCTGCTCAACCCATCTTATGTTTATG 919  
Db 992 TCACCTAGAGCTGTGCGCTGCGCTGCTGTGTGCAACCTTTCTGTAGCGCTTCAATG 1051  
QY 920 GAGCATCTTCAAAAATCTAGCTTATGAAAGTGGCCAAATAATGAGTCTGAG 974  
Db 1052 GCGTCAGATTCCGCAACGATATCTTCAAGCTCTTCAAGGACCTGGGCTGCTCAG 1106

## RESULT 21

US-08-153-848-45  
; Sequence 45, Application US/08153848  
; Patent No. 5759804  
; GENERAL INFORMATION:  
; APPLICANT: Godiska, Ronald  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Schweikart, Vicki L.  
; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/153,848  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/977,452  
; FILING DATE: 17-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5759804and, Greta E.  
; REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448  
 TELE: 25-3856  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1317 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 201..1211  
 US-08-153-848-45

Query Match 13.4%; Score 153.6; DB 1; Length 1317;  
 Best Local Similarity 49.6%; Pred. No. 5.9e-35;  
 Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;

90 CTGTATCAAGAGATGTCAGAGATTGGCAAAAGTTTCTCCCTGATTCCTCACAAT 149  
 236 CTGTTCCGTGAAGAAAATGCTAATTCAATAATCTTCGCCACACATCACTGCAT 295  
 150 AGTTTGTGATGGAAGTTCGAGCAATTCATGATGAGCAATTTATGCTATTACAA 209  
 296 CATCTTCTTAATGCGATTTGGGCAATGATGTCATCTGTCATGGGTTACAGAA 355  
 210 GAAACAGAAACAAAACAGATGTGACATCTGAAATTTGGCTGAGCAATTTACTCT 269  
 356 GAACTGAGAGATGACGAGCAAGTACAGGCTGACCTGTCACTGAGCCGACCTCTT 415  
 270 TCTATCTACTGCTGCTTTTGGGCTGTAATGACGTTCAAGGGGTTTAAAGAAAT 329  
 416 TGTATCAACGCTTCCCTTGGGAGATGATGCGTGGCAAACTGTGACTTTGGAACTT 475  
 330 AATGCAAAATACTCAGCCTTGATACACACTAACTTTGCTCTGGAATGCAATTTCT 389  
 476 CCTATGCAAGGACATGATGATCTACACAGTCAACCTCAGCAGATGTCATCTCT 535  
 390 GAGCTGTATCAGATGACAGATATGTGCACTAATAAGTCCCAAGCAATCAGAGT 449  
 536 GGCCTTATCAGTCTGACGCGCTACCTGCGCATGCTCAGCCCAAGTCAAGAGCC 595  
 450 GGGAAAC-----CATGCTGATCATCTGTTCTGTGTCTGATGCGTGCATCTTCT 503  
 596 AAGGAAGCTGTGGCTGAAAAGTGTCTATGTGGCGTGTGATCCCTGCTGCT 655  
 504 GAGCATACCCAGGCTGTTTTTATAGTAATGACAAATGCTAGGTCATCTCCATTTT 563  
 656 GACTATTCCTGATCTTCTTTCGCAAGTCAAGTGAAGGACAGATACAGATATCTGTA 715  
 564 CCCCCGCTACCTAGGACATCAATGAAGATGATTAATGTAAGATCTGATTTG 623  
 716 CCGCTTACCCCAATGACTTGTGGGTGTGTGTCAAGTTTCAAGACATCATGTTGG 775  
 624 ATTGTAGTACCTTTCTTATTAATGAGGGTGTGCTACTTTATCAGACAGAGAACCT 683  
 776 CCTATCTGCTGTGATGTGATCTCTGCTATTTGCAATTCATCTCCAGGCTGTC 835  
 684 GAAGATGCAAAATTAATATATCTGACCCCTAAAGTTTGTGCTCAGTCTTATAGT 743  
 836 ACATCTCAAGGGCCACGAAAGCGAGAGCCCTCAAGACCAAGTCACTCCATCTGCG 895  
 744 TTTCATGTCACTCAAGTCTTATTAACATTTGCAAGTTGTCGCGAGCCATGACATCAT 803  
 896 TTCTTCCGCTGTGGCTGCTTACTTACATTTGGGATCAGATCACTCTTCACTCTCT 955  
 804 CTACTCCCTGATCAGCACTGCAATGAGCAAGCAAGCAATGCAATCCCAAGTCAAC 863  
 956 GGAATATCAACGAAAGGTGTGAGTTGAGAACCTGTGACCAAGTGAATTTCAATCAC 1015

QY 864 AGAAGATCGCACTCTTTCACAGCTGCTCAACCAATCTTATGTTTANGGAGC 923  
 DB 1016 CGAGGCCCTAGCTTCTTCACTGTTGTGTGAACCCCATCTCTATGCTTCCGAGC 1075  
 QY 924 ATCTTCAAAACT 937  
 DB 1076 CAAATTTAAACT 1089

RESULT 22

US-09-299-843A-45  
 Sequence 45, Application US/09299843A  
 Patent No. 6107475

GENERAL INFORMATION:  
 APPLICANT: Godieka, Ronald  
 APPLICANT: Gray, Patrick W.  
 APPLICANT: Schweikert, Vicki L.  
 TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors  
 NUMBER OF SEQUENCES: 66  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 ADDRESS: Borun  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/299,843A  
 FILING DATE:

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/088,337  
 FILING DATE: 01-JUN-1998

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/153,848  
 FILING DATE: 17-NOV-1993

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/977,452  
 FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:  
 NAME: J111 E. Uhl  
 REGISTRATION NUMBER: 43,213  
 REFERENCE/DOCKET NUMBER: 27866/32059B

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448

TELEX:  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 1317 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 201..1211  
 US-09-299-843A-45

Query Match 13.4%; Score 153.6; DB 3; Length 1317;  
 Best Local Similarity 49.6%; Pred. No. 5.9e-35;  
 Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;

QY 90 CTGTATCAAGAGATGTCAGAGATTGGCAAAAGTTTCTCCCTGATTCCTCACAAT 149  
 DB 236 CTGTTCCGTGAAGAAAATGCTAATTCAATAAATCTTCCGCCACACATCACTCAT 295

Qy	150	AGTTTGGCTATTGGACCTTGAGGGCAATTCAGTAGTGGCAATTATGCGCATTAACA	209
Db	236	CATCTTCTTAACGTGCATGTGGGCAATGATTTGGTATCTGGTCAATGGTTTACAGAA	355
Qy	210	GAACAAGAGAAACAAAACAGATGTATCATCTGAATTGGCTGTAGACAGATTTACTCT	269
Db	356	GAAACTGGAGAGCATGACGGCAAGTACAGGCTGCACCTGTCAAGTGGCCGACCTCCTCT	415
Qy	270	TCATATCATCTGGCTTTTGGGCTGTATATGCAAGTTCAAGGGTGGGTTTAGGGAATAAT	329
Db	416	TGTATATACGGTCTCTCTTCTGGGGAGTTGATGCGGTGGCAAACTGGTACTTTGGGAAC	475
Qy	330	AATGTGCAAAATAACTTCAGCCTTGTATACACACTAAACTTTGTCTGTGAATCAGACTTCT	389
Db	476	CCTATGCAAGGCACTCCATGTATCATCTACACAGTCAACCTCTACAGAGATGCTCATCT	535
Qy	390	GACTTGTATCAGCATATGACAGATATGTGGCAGTACTAAATGCTCCCAACCAATCAGAGT	449
Db	536	GACCTTATCATAGTCTGACACGGCTACCTGGCCATCTGTCCACGCCACCAACAGTACAGAGCC	595
Qy	450	GGGAAAC-----CATGCTGGATCATCTGTCTGTGCTGTGATGGCTGCATCTGTCT	503
Db	596	AAGGAGCTGTGGCTGAAAAAGTGGTCAATGTTGGGTGTGGATCTCGCCCTCTGTCT	655
Qy	504	GAGCATACCCAGCTGGTGTTTTTATACAGTAAATGACAAATGCTAGGTGATCCCATTTT	563
Db	656	GACTATTTCCGACTTCATCTTTGCCAAGCTCAGTGAGGCAAGATGACAGATATATCTGTGA	715
Qy	564	CCCCGCTACCTAGGAACATCAATGAAAGCATTTGATTTCAATGCTTAGAGATCTGCATTGG	623
Db	716	CCGCTTCAACCCCAATGACATGTGGGGTGTGTGTGTTCACAGTTTCACACATATAGTTGG	775
Qy	624	ATTGTGATACCTTTCTTATATAGGGGGTGTGCTACTTATACAGCAAGACACTAAT	683
Db	776	CCTTATCTGCTGGTATTTGTATCTCTGTCTCTGTATTTGATTTATATCTCCAACTGTCT	835
Qy	684	GAAAGTGCMAAACATTAAAAATATCTGCAGCCCTTAAAGTTCTGTCTCAGAGTGTATAGT	743
Db	836	ACACTCCMAAGGGCCACACGAAGGCAAGGCGCTCAAGACCAACAGTCACTCCTCATCTGGC	895
Qy	744	TTTTCATTTGTACTCAACTGCTTTATATACATTTGTCAAGTTTCTGCCAGGCCATAGACATCAT	803
Db	896	TTTTCTTGCCCTGTGGGTGCTGCTTATACATATGGGATTCAGATCTGACTCTTATCTCTCT	955
Qy	804	CTACTCCCTGATTCACAGCTGCAACATGAGCAAAAGCATGAGCATGCGCATCCAGTCAAC	863
Db	956	GGAATATATCAGAGAGGGTGTGAGTTTGAAACAATGTGCACAAATGGAATTTCCATATC	1015
Qy	864	AGAAAGCATGCACTCTTTTCAACAGTGGCTCAACCCCAATCTTTATGTTTTTATGGAGAC	923
Db	1016	CGAGGCGCTACTTTCTTTCACAGTGTGTGAACCCCAATCTCTATATGCTTTTCTTGAGAC	1075
Qy	924	ATCTTTCAAAAATCT 937	
Db	1076	CAAAATTTAAAACTT 1089	

RESULT 23  
US-09-088-337B-45  
Sequence 45, Application US/09088337B  
Patent No. 6348574  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
Gray, Patrick W.  
Schweikart, Vicki L.  
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Born  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois

```

1      COUNTRY: USA
2      ZIP: 60606
3
4      COMPUTER READABLE FORM:
5      MEDIUM TYPE: Floppy disk
6      COMPUTER: IBM PC compatible
7      OPERATING SYSTEM: PC-DOS/MS-DOS
8      SOFTWARE: PatentIn Release #1.0, Version #1.25
9
10     CURRENT APPLICATION DATA:
11     APPLICATION NUMBER: US/09/088,337B
12     FILING DATE: 01-Jun-1998
13     CLASSIFICATION: <Unknown>
14
15     PRIOR APPLICATION DATA:
16     APPLICATION NUMBER: US 08/153,848
17     FILING DATE: 17-NOV-1993
18     APPLICATION NUMBER: US 07/977,452
19     FILING DATE: 17-NOV-1992
20
21     ATTORNEY/AGENT INFORMATION:
22     NAME: No. 634857and, Greta E.
23     REGISTRATION NUMBER: 35,302
24     REFERENCE/DOCKET NUMBER: 31794
25
26     TELECOMMUNICATION INFORMATION:
27     TELEPHONE: (312) 474-6300
28     TELEFAX: (312) 474-0448
29
30     TELERX: 25-3856
31
32     INFORMATION FOR SEQ ID NO: 45:
33     SEQUENCE CHARACTERISTICS:
34     LENGTH: 1317 base pairs
35     TYPE: nucleic acid
36     STRANDEDNESS: single
37     TOPOLOGY: linear
38     MOLECULE TYPE: cDNA
39     FEATURE:
40     NAME/KEY: CDS
41     LOCATION: 201..1211
42
43     SEQUENCE DESCRIPTION: SEQ ID NO: 45:
44     US-09-088-337B-45
45
46     Query Match      13.4%   Score 153.6;   DB 4;   Length 1317;
47     Best Local Similarity 49.6%;   Pred. No. 5,9e-35;
48     Matches 424;   Conservative 0;   Mismatches 424;   Indels 6;   Gaps 1.

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Qy	90	CTGTATCAAAAGAAAGTGCAGAAATTTGCAAAAGTTTTCTCCCTGATTTCTCAAT	145
Db	236	CTGTATTCGTGAAGAAAAATGCTAAATTTCAATAAAATCTTCTCCACCATCTACAT	295
Qy	150	AGTTTTCGTATTGACCTTGACGGCAATTCATGATGAGCAATTTATGCTATTCA	205
Db	296	CATCTTTTAATCGGCATTGTGGCCAAATGATTTGTCATCTCGTCATAGGTTACAGAA	355
Qy	210	GAACAAGAACCAAAACAATGTGTATCTCTGAATTTTGCTGTACAGATTTATCTCT	265
Db	356	GAACATGAACAACATGACGACAAAGTACAGCTGCACCTGTACATGAGCCGACCTCTT	415
Qy	270	TCTATTCACCTCTGCTTTTGGCTGTAAATGCAATTCATGGGTGGGTTTTAGGAAAT	325
Db	416	TGTCAATCAGGCTTCCCTCTGTGGCAGTTGATGCGCGTGGCAACTGTACTTTGGAACTT	475
Qy	330	AATGTCAAAAATTAATCAAGCTTGTACACTTAACTTTGTCTCTGAAATGCACTTTCT	385
Db	476	CTATATCAAGGACATGCATGTATCATCTACACATCAACTCTACAGCAGTGTCTCATCTCT	535
Qy	390	GGTTTATTCACATATGACATATATGAGCAGTAACTAAAGTCCCAAGCATCAGAGT	445
Db	536	GGCTTTCATCACTGTGACACCCCTTACCTGGCCATCTGCACGCCACCAACATCAGAGGCC	595
Qy	450	GGGAAAAAC-----CATGCTGAATCATCTGTTTCTGTGTGATGAGCTGCATCTTGCT	505
Db	596	AAGGAAGCTGTTGGCTGAAGAGTGATCTATATGTGCGCTGTGATCTCCGCTCTCTGCT	655
Qy	504	GACCAATACCCCAAGCTGTTTTTATAAGTAATATGACATGCTAGTGATTTCCCATTTT	565
Db	656	GACTATTTCCCACTCATCTTGTGCCAACATGACAGTGGGACAGATGACAGATATATGTGA	715



Patent No. 6429308  
GENERAL INFORMATION:  
APPLICANT: IJIMA, Osamu  
APPLICANT: GOTO, Takeshi  
APPLICANT: SHIMADA, Takashi  
TITLE OF INVENTION: HIV Infection Inhibitors  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/582,224A  
CURRENT FILING DATE: 2000-07-21  
PRIORITY FILING DATE: 1999/11/24  
PRIORITY FILING DATE: 1999/11/24  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Microsoft Word  
SEQ ID NO 5  
LENGTH: 1664  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: CDNA of CXCR4  
US-09-582-224A-5

Query Match 13.4%; Score 153.6; DB 4; Length 1664;  
Best Local Similarity 49.6%; Pred. No. 6,7e-35;  
Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;

QY 90 CTGATCAAGAGATGTCAGAGAAATTTGCAAAAGTTTCTCCCTGATTTCCCAAT 149  
DB 157 CTGTTCCGTAAGAAATGCTAATTTCAATTAATCTTCTGCCCCCACTTACTCAT 216  
QY 150 AGTTTGGTCAATGACCTTGGCAAAATTCATGATGAGCAATTTATGCTATTACA 209  
DB 217 CATCTTCTTAATGAGATGAGGCAATGATGATGATGATGATGATGATGATGATG 276  
QY 210 GAACAGAGAAACCAAAACAGATGTCATCTTCAATTTGGCTGTAGCAATTTACTCT 269  
DB 277 GAAAGTGAAGAGATGAGCAAGTACAGCTGACCTGCACTGAGCTGAGCTGAGCT 336  
QY 270 TCTATCACTGCTGCTTTTGGGCTTAATGACATTCATGAGGAGGTTTAAAGGAAAT 329  
DB 337 TGTATCACTGCTTCTTCTGAGGAGTGTGATGCTGAGCAATGCTGAGCTGAGCT 396  
QY 330 AATGCAAAATTAATCTTCACTGATGACATTAATTTGCTCTGAAATGAGTTCT 389  
DB 397 CCAATGCAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 456  
QY 390 GCGTTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 449  
DB 457 GCGCTTCACTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 516  
QY 450 GGAAGAAC-----CATGCTGATGATGATGATGATGATGATGATGATGATGAT 503  
DB 517 AAGGAGAGCTGAGTGAAGAGTGTGATGATGATGATGATGATGATGATGATGAT 576  
QY 504 GAGCATACCCAGCTGTTTAAATGATGATGATGATGATGATGATGATGATGATGAT 563  
DB 577 GACTATTCAGCATCTTCTTGGCAAGTCAAGAGGAGGAGGAGGAGGAGGAGGAG 636  
QY 564 CCCCCGCTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 623  
DB 637 CCGCTTACCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 696  
QY 624 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 683  
DB 697 CTTATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 756  
QY 684 GAAGAGCCAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 743  
DB 757 AACTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 816  
QY 744 TTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 803  
DB 817 TTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 876

QY 804 CTACTCCCTGATCAGAGTGAACATGAGCAAAAGCATGAGCAATGCGATCAAGTCAC 863  
DB 877 GGAATCATCAAGCAAGGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 936  
QY 864 AGAAGCATGAGCTCTTTTCAAGCTGCTCAACCAATCTTTATGTTTATGAGGAGC 923  
DB 937 CGAGGCTTACCTTCTTCACTGATGATGATGATGATGATGATGATGATGATGATG 966  
QY 924 ATCTTCAAAACT 937  
DB 997 CAATTTAAACCT 1010

RESULT 26  
US-09-517-605-14

Sequence 14, Application US/09517605  
Patent No. 6391567  
GENERAL INFORMATION:  
APPLICANT: Litman, Dan R.  
APPLICANT: Kwon, Douglas S.  
APPLICANT: van Kooyk, Yvette  
APPLICANT: Geijtenbeck, Theo  
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO  
FILE REFERENCE: 1049-1-017  
CURRENT APPLICATION NUMBER: US/09/517,605  
CURRENT FILING DATE: 2000-03-02  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 14  
LENGTH: 1679  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-517-605-14

Query Match 13.4%; Score 153.6; DB 4; Length 1679;  
Best Local Similarity 49.6%; Pred. No. 6,7e-35;  
Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;

QY 90 CTGATCAAGAGATGTCAGAGAAATTTGCAAAAGTTTCTCCCTGATTTCCCAAT 149  
DB 169 CTGTTCCGTAAGAAATGCTAATTTCAATTAATCTTCTGCCCCCACTTACTCAT 228  
QY 150 AGTTTGGTCAATGACCTTGGCAAAATTCATGATGAGCAATTTATGCTATTACA 209  
DB 228 CATCTTCTTAATGAGATGAGGCAATGATGATGATGATGATGATGATGATGATGAT 288  
QY 210 GAACAGAGAAACCAAAACAGATGTCATCTTCAATTTGGCTGTAGCAATTTACTCT 269  
DB 289 GAAAGTGAAGAGATGAGCAAGTACAGGCTGACCTGCACTGAGCTGAGCTGAGCT 348  
QY 270 TCTATCACTGCTTCTTCTGAGGAGTGTGATGATGATGATGATGATGATGATGAT 329  
DB 349 TGTATCACTGCTTCTTCTGAGGAGTGTGATGATGATGATGATGATGATGATGAT 408  
QY 330 AATGCAAAATTAATCTTCACTGATGACATTAATTTGCTCTGAAATGAGTTCT 389  
DB 409 CCTATGCAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 468  
QY 390 GCGTTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 449  
DB 469 GCGCTTCACTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 528  
QY 450 GGAAGAAC-----CATGCTGATGATGATGATGATGATGATGATGATGATGAT 503  
DB 529 AAGGAGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 588  
QY 504 GAGCATACCCAGCTGTTTAAATGATGATGATGATGATGATGATGATGATGATGAT 563  
DB 589 GACTATTCAGCATCTTCTTGGCAAGTCAAGAGGAGGAGGAGGAGGAGGAGGAG 648  
QY 564 CCCCCGCTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 623



Db	649	CCGGTTTACCCCAAGACCTTGGGGTGGTGGTTCCAGTTTCAGCAATCATGGTTGG	708
Qy	624	ATTGTGAGTACCCCTTTCTTATTTATGGGGGTGTCATTTATTCACAGCAAGACATCAT	683
Db	709	CCTTATCCTCGCTGGTATTTGTCAATCCGTGTCCTGCTATTCATATTCATCTCCAAAGTC	768
Qy	684	GAAATGCCAAACATTAAATATCTGACCCCTTAAAGTTCTGCTCACAGTGGTAAZGT	743
Db	769	ACACTCCAAAGGCGCACCGAAGCGCAAGGCCCTTCAGAGCACAGTCATCTCATCTGGC	828
Qy	744	TTTCATTGTCACTCAACTGCTTTATAACATGTCAAGTTCTGCGAGCCATAGACATCAT	803
Db	829	TTTCTTGCGCTGGTGGCTGTGCTTACTACATGGGATCCAGATCGAATCCTTCATCTCTCT	888
Qy	804	CTACTCCCTGTATCCACAGCTGCACATGACAAACGCAATGCAATGCGATCCAAAGTCAAC	863
Db	889	GGAATCATCAAGCAAGGAGGTGATGTTTGAAACACTGTGCACAAAGTGATTTTCATATAC	948
Qy	864	AGAAAGCATGCGCACTCTTTACAGCTGCCCAACCCATCTTTATGTTTATGGAGAC	923
Db	949	CGAAGCCCTACCTTTCTTCCACGTGTGTCTGAACCCCATCTCTATGCTTTTCTTGGAGC	1008
Qy	924	ATCTTCAAAACT 937	
Db	1009	CAATTTAAACT 1022	

```

APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PFA4 Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ. ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-076-093A-3

Query Match 13.4%; Score 153.6; DB 1; Length 1737;
Best Local Similarity 49.6%; Pred. No. 6.8e-35;
Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;

QY 90 CTGTATCAAAAGATGTCAGAGATTGCAAGTTTCTCTCTATTTCTCAAT 139
DB 171 CTGTTCCGTGAAGAAATGCTAATTTCAATAAATCTCTGCCACATCTAATCCAT 230
QY 150 AGTTTGTGCTGACCTTGAGGCAATTCATGATGAGCAATTTATCTATTACA 209
DB 231 CATCTTCTTAAGTGGATGTCGATGATGATGATGATGATGATGATGATGATGAT 230
QY 210 GAAACAGAGACCAAAACAGATGTCATCTGATTTGGCTGTAGCAATTTACTCT 269
DB 291 GAAACTAGAGATGACGAGCAAGTACAGGCTGACCTGTAGTGGCCACCTCTCT 350
QY 270 TCTATTCATCTGCTTTTGGGCTGTTAATGAGTTCATGAGGCTTTTAAAGGAAAT 329
DB 351 TGTATCAAGCTTCTCTCTGAGGATGATGATGATGATGATGATGATGATGATGAT 410
QY 330 AATGTGCAAAATTAATTCAGCTTGTACACATTAATTTGTCTGTGGAATGAGTTCT 389
DB 411 CCTATGCAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 470
QY 390 GGGCTTGTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 449
DB 471 GGGCTTGTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 530
QY 450 GGGAAAC-----CATGCTGATCATCTGTTTCTGTTGCTGATGCTGCTGCTGCT 503
DB 531 AAGGAGCTGTTGGCTGAAAAAGGCTGATGATGATGATGATGATGATGATGATGAT 590

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QY 504 GAGATACCCGAGCTGTTTTTATAGATAAATGACATGCTAGTCATTCCTATTT 563
DB 591 GACTATTCGAGCTTATTTTGGCAAGCTCAGTACAGATGACATATATTTGTA 650
QY 564 CCCCCGCTACCTAGAACATCAATGAAAGATTGTAATGATGATGATGATGATGAT 623
DB 651 CCGCTTCTACCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 710
QY 624 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 683
DB 711 CCTATTCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 770
QY 684 GAGATGCAAAATTAATAATATCTGACCCCTAAAGTTCTGCTCAGTGTATAGT 743
DB 771 ACATTCGAAGGCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 830
QY 744 TTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 803
DB 831 TTTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
QY 804 CTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 863
DB 891 GGAATCATCAAGCAAGGAGTGTGAGTGTGAGAACCTGTGACAGATGATTTCCAT 950
QY 864 AGAAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 923
DB 951 CGAGGCTGATGTTTCTTCTCACTGTTGCTGATGATGATGATGATGATGATGAT 1010
QY 924 ATCTTTCAAAACT 937
DB 1011 CAAATTTAAACCT 1024

```

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RESULT 29
US-08-701-265-3
; Sequence 3, Application US/08701265
; Patent No. 5776457
; GENERAL INFORMATION:
; APPLICANT: Chunharapal, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PFA4 Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,265
; FILING DATE: 22-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 415/225-5530  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1737 nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
US-08-701-265-3

Query Match 13.4%; Score 153.6; DB 1; Length 1737;  
Best Local Similarity 49.6%; Pred. No. 6.8e-35;  
Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;

90 CTGTATCAAAAGATGTCAGAAATTTGCAAAAGTTTCTCCCTGATTCCTCAAT 149  
171 CTGTTCCGTGAGAAATGCTAATTAATCTCTCCGCAACATCTACTCAT 230  
150 AGTTTGTGATGGAATTCAGGCAATTCATGATGGAATTTATGCTTATCA 209  
231 CATCTTTAATGCAATTTGGGCAATGATGTCATCTGTCATGAGTTACAGAA 290  
210 GAAACAGAGAACCAAAACAGATGTCATCTGAATTTGGCTGTACAGATTTACTCT 269  
291 GAACTGAGAGATGACGAGCAAGTACAGGCTGACCTGTCACTGGCCGACCTCTCT 350  
270 TCTATTCCTGCTCTTTTGGGCTGTAAATGCACTTCAATGGGTTTATGAGAAAT 329  
351 TGTATCAACGCTTCTCTTGGGAGTTGATGCGTGGCAAACTTGATTTGGAACTT 410  
330 AATGTCAAATTAATCTGAGCTTGTACACACTAATTTGCTCTGGAATGCAATTTCT 389  
411 CCTATGCAAGGAGTCCATGTCATCTACAGTCACTCTACAGCAAGTGTCTCATCT 470  
390 GCGTTGATTCAGCATGACAGATATGTCAGTAACTTAACTCCCAAGCAATGAGAT 449  
471 GAGCTTATCATGTCAGTACGCTGACCTGATGCTGATGCTGCAACGCAACAGTCA 530  
450 GGGAAAC-----CATGCTGATCATCTGTTCTGTGTCGATGAGTGGTGCATCTGCT 503  
531 AAGGAAGCTGTTGGTGAAGAGTGTCTATGTTGGCTGTGAAATCCCTGCTCTGCT 590  
504 GAGCATACCCAGCTGATTTTATACAGTAATGACATGCTAGTGCATTTCCCATTTT 563  
591 GACATTTCCCACTTCACTTTTCCAGTCACTGATGAGGCAATGACATATATCTGGA 650  
564 CCCCCGCTACCTAGACATCATGAAAGATTGATTAATGCTAAGATCTGATTTGG 623  
651 CCGCTTACCCCAATGACTTGGGGTGTGTGTTCCAGTTTCAAGCATCATGATTTGG 710  
624 ATTGTAGTACCTCTTTCTTATTAAGGGGTGTGCTACTTATTCACAGAGAGACATCAT 683  
711 CCTTATCTGCTGATGATGTCATCTGCTGCTATGCAATTCATCTCAAGCTGTC 770  
684 GAAATGCAAAATTAATTAATCTGACCCCTAAAGTTTGTGCTCAGCTGTTATAGT 743  
771 AACTTCAGAGGCTCAGAGAGGCTCTCAAGACACAGTCAATCCCTCATCTGCGC 830  
744 TTTCAATGCTCACTGATGCTTATTAATGATGTCAGATTTGCGGAGCATGACATCAT 803  
831 TTTCTGCTGCTGCTGCTGCTTACTTACATTTGGATGCAATGCACTCTCATCTCTCT 890  
804 CTACTCCCTGATCAACACATGCAATGAGCAAAAGCATGAGCATGCAATGCAAGTAC 863  
891 GGAATTCATCAAGCAAGGCTGTGATGAGAACCTGTGCAAGATGAGATTTCAATAC 950  
864 AGAAAGCATGCACTCTTTCACAGCTGCTCAACCCCAATCCCTTATGTTTATGAGAGC 923  
951 GAGAGCCCTAGCTTCTTCTCACTGTTGTGTAAGAACCCCAATCCCTTATGCTTGGAGC 1010  
924 ATCTTTCAAAACT 937

Db 1011 CAATTTAAACCT 1024

RESULT 30  
US-08-284-586-3  
Sequence 3, Application US/08284586  
Patent No. 5840856  
GENERAL INFORMATION:  
APPLICANT: Chuntharapel, Anan  
APPLICANT: Lee, James  
APPLICANT: Hebert, Caroline  
APPLICANT: Jin Kim, K.  
TITLE OF INVENTION: Antibodies to Human p74 Receptors  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,586  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/076,093A  
FILING DATE: 11-Jun-1993  
APPLICATION NUMBER: 07/810782  
FILING DATE: 19-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/677211  
FILING DATE: 29-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET INFORMATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-5530  
TELEFAX: 415/952-9881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1737 nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
US-08-284-586-3

Query Match 13.4%; Score 153.6; DB 2; Length 1737;  
Best Local Similarity 49.6%; Pred. No. 6.8e-35;  
Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;

90 CTGTATCAAAAGATGTCAGAAATTTGCAAAAGTTTCTCCCTGATTCCTCAAT 149  
171 CTGTTCCGTGAGAAATGCTAATTAATCTCTCCGCAACATCTACTCAT 230  
150 AGTTTGTGATGGAATTCAGGCAATTCATGATGGAATTTATGCTTATCA 209  
231 CATCTTTAATGCAATTTGGGCAATGATGTCATCTGTCATGAGTTACAGAA 290  
210 GAAACAGAGAACCAAAACAGATGTCATCTGAATTTGGCTGTACAGATTTACTCTCT 269  
291 GAACTGAGAGATGACGAGCAAGTACAGGCTGACCTGTGATGAGCCGACCTCTCT 350  
270 TCTATTCCTGCTCTTTTGGGCTGTAAATGCACTTCAATGGGTTTATGAGAAAT 329  
351 TGTATCAACGCTTCTCTTGGGAGTTGATGCGTGGCAAACTGATCTTTGGAACTT 410

QY 330 AATGCGAAATACTTACGCTGTACACATACTTGTCTCTGGAATGACGTTCT 389  
DB 411 CCTATGCAAGGACATGATGATCTACACAGTCACTCACTTACAGAGTGTCTCATCT 470  
QY 390 GGGCTTGTATGACATAGACAGATATGTGGCAGTAACTAAAGTCCCGACCAATCAGAGT 449  
DB 471 GGGCTTATCATGTGTGACCGGCTACCTGCGCATGTCCAGGCCACCAAGTCAGAGGCC 530  
QY 450 GGGAAAC-----CATGCTGATCATCTGTTCTGTGTCTGATGCTGCTCATTTGCT 503  
DB 531 AAGGAAGCTGTGTGCTGAAAAGGTGCTATGTTGGGTCTGAGATCCCTGCTCCCTGCT 590  
QY 504 GAGATATCCAGCTGCTTTTATACAGTAATGACAAATGCTAGTGCATTCATTTT 563  
DB 591 GACTATTCCTGACCTTCTTCTTCCACAGTACAGTACAGATATATCTGTGA 650  
QY 564 CCCCCGCTACCTAGGAACATCAATGAAAGCATGATTCATTAATGCTAGAGATCTGCTTGG 623  
DB 651 CCGCTTACCCCAATGACTGTGTGGGTGTGTGTTCAGTTTACGACATCATGTTGG 710  
QY 624 ATTGTAGTACCTTCTTATTAATGAGGGGTGTCTACTTATACAGCAAGACATCTCAT 683  
DB 711 CCTATCTGCTGTGATGATGATCTGCTCTGCTATGATTCATTCATTCAGGCTGTC 770  
QY 684 GAAGATGCCAAATTAATAATATCTGACCCCTAAAGTTCTGCTACAGTCTTATAGT 743  
DB 771 ACATCCCAAGGCGCACGAAAGCGGAGCCCTCAAGACACAGTCACTCTCATCTGCGC 830  
QY 744 TTTGATGTCTACTCACTGCTTCTTAAATGTCATGTCAGTTCGCGGACCATAGACATCAT 803  
DB 831 TTTCTTGCGCTGTGGCTGCTTACTATGATGATGATGATGATGATGATGATGATGATGAT 890  
QY 804 CTACTCTCTGATACACAGCTGCAACATGAGCAAGCATGACATGCCCATCCAGTCTAC 863  
DB 891 GGAATATCATCAAGAGAGGTGTGAGTTGAGAACATGTCAGCAAGTGTGATTCATCAC 950  
QY 864 AGAAGATGCGACCTTCTTACAGCTGCTCAACCAATCCTTATGTTTATGGAGC 923  
DB 951 CGAGGCTTACTTCTTCTTCTGCTGTGTGATGATGATGATGATGATGATGATGATGATG 1010  
QY 924 ATCTTCAAAACT 937  
DB 1011 CAATTTAAACT 1024

RESULT 31  
US-08-805-478-3  
; Sequence 3, Application US/08805478  
; Patent No. 5874543  
; GENERAL INFORMATION:  
; APPLICANT: Chuncharapai, Anan  
; APPLICANT: Lee, James  
; APPLICANT: Hebert, Caroline  
; APPLICANT: Jin Kim, K.  
; TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/805,478  
; FILING DATE: 25-Feb-1997  
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/284586  
; FILING DATE: 10-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/076093  
; FILING DATE: 11-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/810782  
; FILING DATE: 19-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P0706P2P1C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5530  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1737 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
US-08-805-478-3

Query Match 13.4%; Score 153.6; DB 2; Length 1737;  
Best Local Similarity 49.6%; Pred. No. 6.8e-35;  
Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;

QY 90 CTGTATCAAAAGATGTGAGAAATTTGCAAAAGTTTCTCTCTGATTTCTTCAAT 149  
DB 171 CTGTTCCGTGAAGAAATGCTAATTTCAATAAATCTTCTGCCACATCTCATCTCAT 230  
QY 150 AGTTTTCGCTATGACTTGCAGGCAATTCAGTGTAGTGCATTTATGCTTAA 209  
DB 231 CATCTTCACTGACCTTGTGGGCAATGATGTGATCTCTGCTGATGCTTACGAA 290  
QY 210 GAAACAGAACCAAAAGATGTGATCATCTGATTTGCTGTAGAGATTTACTCT 269  
DB 291 GAAACTGAGAACAGACGACAGACATACAGGCTGACCTGTACAGGCGCACTCTCTT 350  
QY 270 TCTATTCATCTGCTTTTGGGCTGTGATGACGTTATGAGGAAAT 329  
DB 351 TGTATCAAGCTTCTCTCTGAGGAGTGTGATGCGTGAACATGCTTGTGGAACTT 410  
QY 330 AATGCGAAATACTTACGCTGTACACATACTTGTCTCTGGAATGACGTTCT 389  
DB 411 CCTATGCAAGGACATGATGATCTACACAGTCACTCACTTACAGACATGCTCATCT 470  
QY 390 GGGCTTGTATGACATAGACAGATATGTGGCAGTAACTAAAGTCCCGACCAATCAGAGT 449  
DB 471 GGGCTTATCATGTGTGACCGGCTACCTGCGCATGTCCAGGCCACCAAGTCAGAGGCC 530  
QY 450 GGGAAAC-----CATGCTGATCATCTGTTCTGTGTCTGATGCTGCTCATTTGCT 503  
DB 531 AAGGAAGCTGTGTGCTGAAAAGGTGCTATGTTGGGTCTGAGATCCCTGCTCCCTGCT 590  
QY 504 GAGCATATCCAGCTGCTTTTATACAGTAATGACAAATGCTAGTGCATTCATTTT 563  
DB 591 GACTATTCCTGACCTTCTTCTTCCACAGTACAGTACAGATATATCTGTGA 650  
QY 564 CCCCCGCTACCTAGGAACATCAATGAAAGCATGATTCATTAATGCTAGAGATCTGCTTGG 623  
DB 651 CCGCTTACCCCAATGACTGTGTGGGTGTGTGTTCAGTTTACGACATCATGTTGG 710  
QY 624 ATTGTAGTACCTTCTTATTAATGAGGGGTGTCTACTTATACAGCAAGACATCAT 683  
DB 711 CCTATTCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 770  
QY 684 GAAGATGCCAAATTAATAATATCTGACCCCTAAAGTTCTGCTACAGTCTTATAGT 743  
DB 771 ACATTCCAAGGCGCACGAAAGCGGAGCCCTCAAGACACAGTCACTCATCTCTGCGC 830

QY 744 TTTTCATGTCACCTGACCTTAAATTCAGATTCCTCCGAGCCATAGACATCAT 803  
DB 831 TTTCTTGCGCTGTTGGCTGCTTACTACTAGATGAGATGATCTTCAATCTCTCT 890  
QY 804 CTACTCCCTGATCCAGCTGCAACATGAGCAAGCATGACATGCCATCCAGTCCAC 863  
DB 891 GGAATATCATCAAGAGGCTGTGAGTTGAGAACATCTGTGACAAAGTGATTTCCATCAC 950  
QY 864 AGAAGATGACGACCTTTTCAAGCTGCTCAACCAATCTTATGTTTATGGAGAG 923  
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QY 924 ATCTTTCAAAAACCT 937  
DB 1011 CAAATTTAAACCT 1024

RESULT 32  
US-08-802-627A-3  
; Sequence 3, Application US/08802627A  
; Patent No. 5892017  
; GENERAL INFORMATION:  
; APPLICANT: Lee, James  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PFAA RECEPTOR  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/802,627A  
; FILING DATE: 19-Feb-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/284586  
; FILING DATE: 10-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/076093  
; FILING DATE: 11-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/810782  
; FILING DATE: 19-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P0706P2P1D2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5530  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1737 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; US-08-802-627A-3

Query Match 13.4%; Score 153.6; DB 2; Length 1737;  
Best Local Similarity 49.6%; Pred. No. 6.8e-35;  
Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;  
QY 90 CTGTATCAAAAGATGTCAGAGATTTCGAAAAGTTTCTCTCCCTGATTCCTCAGCAAT 149  
|||||

DB 171 CTGTTCCGTGAAGAAAATGCTAATTTCAATAAATCTTCTCCGCCACATCTACTCAT 230  
QY 150 AGTTTTCGTCATGAGTCTTGACAGCAATTCATGAGTATGAGCAATTTATGCTATTACAA 209  
DB 231 CATCTTCTTAATGGCATTTGTGGCAATGATGATGATCTCTGATGATGATGATGATG 290  
QY 210 GAAACAGAGAACCAAAACAGATGTGTATCATCTGTAATTTGGCTGTAGAGATTTACTCT 269  
DB 291 GAAACAGAGAACCAAAACAGATGTGTATCATCTGTAATTTGGCTGTAGAGATTTACTCT 350  
QY 270 TCTATTCATCTGCTCTTTTGGCTGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 329  
DB 351 TGTATCATGAGTCTTCTCTGAGGAGTGTATGAGTATGAGTATGAGTATGAGTATGAGT 410  
QY 330 AATGTCAAAATATACCTTACGCTTGTACACTTAATCTTGTCTGTGAGATGAGTATCT 389  
DB 411 CCTATGCAAGGAGTCATGATGATCTATACAGATGATGATGATGATGATGATGATGAT 470  
QY 390 GCGTGTATCAGCATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 449  
DB 471 GCGTGTATCAGCATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 530  
QY 450 GGGAAAC-----CATGCTGATCATCTGTTCTGTGCTGTGATGATGATGATGATGAT 503  
DB 531 AAGAGAGCTGTTGCTGAAAGAGTGTCTATGTTGCGTGTGATGATGATGATGATGATGAT 590  
QY 504 GAGCATATCCCAAGCTGTTTATATAGTAATGACATGATGATGATGATGATGATGATGAT 563  
DB 591 GACTATATCCCAAGCTGTTTATATAGTAATGACATGATGATGATGATGATGATGATGAT 650  
QY 564 CCGCGCTATCCTAGAGAACATCAATGAAAGATGATGATGATGATGATGATGATGATGAT 623  
DB 651 CCGCTTCAACCCCAATGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 710  
QY 624 ATTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 683  
DB 711 CTTATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 770  
QY 684 GAAAGTCCCAACATTTAAATATCTGACCCCTTAAAGTTCTGTCTACAGTGTATAGT 743  
DB 771 ACATCTCAAGGGCCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 830  
QY 744 TTTTCATGTCACCTGACCTTAAATTCAGATTCCTCCGAGCCATAGACATCAT 803  
DB 831 TTTCTTGCGCTGTTGGCTGCTTACTACTAGATGAGATGATCTTCAATCTCTCTCT 890  
QY 804 CTACTCCCTGATCCAGCTGCAACATGAGCAAGCATGACATGCCATCCAGTCCAC 863  
DB 891 GGAATATCATCAAGAGGCTGTGAGTTGAGAACATCTGTGACAAAGTGATTTCCATCAC 950  
QY 864 AGAAGATGACGACCTTTTCAAGCTGCTCAACCAATCTTATGTTTATGGAGAG 923  
DB 951 CGAGGCCCTGAGCTTTCTTCCACTGTGTGTGACCCCATCTCTATCTTCTTGAGAC 1010  
QY 924 ATCTTTCAAAAACCT 937  
DB 1011 CAAATTTAAACCT 1024

RESULT 33  
US-08-801-238-3  
; Sequence 3, Application US/08801238  
; Patent No. 5919896  
; GENERAL INFORMATION:  
; APPLICANT: Lee, James  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: PFAA RECEPTOR  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California

COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801,238  
FILING DATE: 19-Feb-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/284586  
FILING DATE: 10-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/076093  
FILING DATE: 11-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/810782  
FILING DATE: 19-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P0706P2P1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-5530  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1737 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
US-08-801-238-3

Query Match 13.4%; Score 153.6; DB 2; Length 1737;  
Best Local Similarity 49.6%; Pred. No. 6,8e-35;  
Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;

QY 90 CTGATCAAGAGATGTCAGAGAAATTTGCAAAAGTTTCTCCTGATTTCTTCAAT 149  
DB 171 CTGTTCCGTGAAGAAATGTAATTTCAATTAATCTTCCGCCACATCTCAT 230  
QY 150 AGTTTTCGATTTGACCTTGCAGGAAATTCCTAGTGGCAATTTATGCTTTAA 209  
DB 231 CATCTCTTAACTGCGCATTTGGGCAATGATGATGATCTGCTGATGGTTCAGAA 290  
QY 210 GAAACAGAGAACCAAAACAGATGTGTACATCTGTAATTTGGCTGAGCAGATTTACTCT 269  
DB 291 GAAACTGAGAGCATGACGAGCAAGTACAGGCTGACCTGTCAAGTGGCCGACCTCTCTT 350  
QY 270 TGTATCTACTGCTGCTTTTGGGCTGTAAAGCAATTCATGGGTGGTTTAAAGGAAAT 329  
DB 351 TGTCAATCAAGCTTCCCTCTGCGGAGTTGATGCCGTGCAAACTGTGTACTTTGGGAACTT 410  
QY 330 AATGCGAAAATAATCTTCACTTGTACACATAAATTTGTCTGTGAAGAGATTTCT 389  
DB 411 CCTATGCAAGGAGTCATGTCATCTACACAGTCAACCTCTACAGCAATGTCCTCATCTT 470  
QY 390 GGCTGTATCAGCATAGACAGATATGTGGCAGTAATAAGTCCCAAGCCATCAGAGT 449  
DB 471 GGCCTTCACTGATGTGAGACCGCTACTGCGCATCTGTCACGCCAACAAGTCAGAGGCC 530  
QY 450 GGGAAAC-----CATGCTGATCATCTGTTCTGTGTCTGATGAGTGGCTCATCTTCT 503  
DB 531 AAGGAGCTGTTGGCTGAAAGAGTGTGTATGTGTGGCGCTGATCCCTGCGCTCTCTCT 590  
QY 504 GAGCATACCCGAGCTGGTTTATATACAGTAATGACAAATGTAGTGCATTTCCATTTT 563  
DB 591 GACTATTTCCCGACTTCACTTTTGGCCAGCTCAGTGAAGCAATGACATATATCTTGGA 650  
QY 564 CCCCCTACTAGGAACATCAATGAAGCATTAATTAATGATGATCTGATGAG 623

DB 651 CCGCTTCAACCCCAATGACTGTGGGTGTGTGTCTCCAGTTTCAACATCATGATGGTGG 710  
QY 624 ATTGTAGTACCTTTCTTATATAGGGGTGTGTGCTACTTATACAGAGACACTAT 683  
DB 711 CCTATCTGCGCTGATTTGATCTGTCTGCTGATTTGATTAATCTTCAAGCTGTC 770  
QY 684 GAAGATGCCAAACATTAATAATCTGACCCCTAAAGTTCTGTCTACAGTGGTTATAGT 743  
DB 771 ACATCCAGAGGCGACCAAGAGCGAGGCCCTCAAGACCAAGTCAATCTCATCTGCG 830  
QY 744 TTTCAATGTCACTCAATGCTCTTATTAATTTCAATTTCAAGTTCTGCCAGCCATGATCAT 803  
DB 831 TTTCTTGCGCTGTGGCTGCTCTTACTACATTTGGAATCAGATGACCTCTTCATCTCTCT 890  
QY 804 CTACTCCCTGATACACAGCTGCAACATGAGCAAGCAATGACATGCGCATCAAGTAC 863  
DB 891 GGAATATCATCAAGCAAGGATGTGATTTAGAAACACTGTGCAAGTGGATTTTCAATCAG 950  
QY 864 AGAAGCATGCGACCTTTTCAAGAGCTGCTCAACCAATCTTTATGTTTATGGAGAC 923  
DB 951 CGAGGCCCTAGCTTTCTTCTTCACTGTTGTCTGAACCCATCTTATGCTTCTTGAGAC 1010  
QY 924 ATCTTCAAAACT 937  
DB 1011 CAAATTTAAACCT 1024

RESULT 34  
US-08-801-228-3  
Sequence 3, Application US/08801228  
Patent No. 5922541  
GENERAL INFORMATION:  
APPLICANT: Lee, James  
TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801,228  
FILING DATE: 19-Feb-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/284586  
FILING DATE: 10-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/076093  
FILING DATE: 11-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/810782  
FILING DATE: 19-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P0706P2P1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-5530  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1737 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
US-08-801-228-3

Query Match 13.4%; Score 153.6; DB 2; Length 1737;  
Best Local Similarity 49.6%; Pred. No. 6.8e-35;  
Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;

QY 90 CTGTATCAAGAGATGTCAGAGAAATTGCAAAAGTTTCTCCCTGATATCCACAAAT 149  
DB 171 CTGTTCCGTAGAGAAATGCTAATTTCAATTAATCTTCTGCGCACCATCTACAT 230  
QY 150 AGTTTCTGCTATGGAGCTTGAGGCAATTCATGGTAGTGCAATTATATGCGCTATTA 209  
DB 221 CATCTTTTAACTGGCATTTGGGGCAATGATGGTCACTCTGGTCAAGGGTTACAGAA 290  
QY 210 GAAACAGAGAACCAAAAGATGTTGATATCTGTAATTTGGCTGTAGAGATTTACTCT 269  
DB 291 GAAACTGAGAGATGACGACAAAGTACAGGCTGACCTGTCAAGTGGCGACCTCTCT 350  
QY 270 TCTATTTACTCTGCTTTTGGGCTGTTAATGCAATGATGGGTGGTTTATGGGAAAT 329  
DB 351 TGTCAATCAGCTTCTCTCTGCGAGTGTATGCGTGGCAAACTGTATTTGGAACTT 410  
QY 330 AATGCAAAATTAATCTGACCTGTACACATMAACTTTGCTCTGGAATGACGTTTCT 389  
DB 411 CCTATGCAAGGAGTCCATGTCATCTACAGTCACTCTACAGCAATGCTCTCATCTT 470  
QY 390 GCGTTGATCAGCATAGACAGATATGTCAGTAACTTAAAGTCCCGACCAATCAGAGT 449  
DB 471 GCGCTTCACTAGTGTGACCGCTACCTGCGCATGCTCCACGCAACAGTCAAGAGCC 530  
QY 450 GGGAAAC-----CATGCTGATATCTGTTCTGTCTGTGATGGTGGCATCTTCT 503  
DB 531 AAGGAGCTGTTGGTGAAGAGTGTATGTTGGCTGTGATGCTGCGCTCTGCT 590  
QY 504 GAGCATACCCAGCTGTTTATTAACAGTAAATGACAAATCTAGTGCATCTCCATTTT 563  
DB 591 GACTATTTCCCACTTCACTTTTCCCAAGTCACTGAGGCAATGACAGATATATCTGTA 650  
QY 554 CCCCCGCTACCTAGACATCATGAAAGCATGTGATCAAAATGCTAAGATCTGCAATTG 623  
DB 651 CCGCTTACCCCAATGACTGTGGGTGTGTGTTCCAGTTTCAAGCATCATGTTGG 710  
QY 624 ATTTGATGATCCCTTTTATTAATGAGGCTGTCTACTTATTCACAGAGAGACATCAT 683  
DB 711 CCTATCTGCTGCTGTGATGTCATCTGCTGCTATTTGATATCATCTTCAAGCTGTC 770  
QY 684 GAAATGCAAAATTAATATCTGACCCCTMAAAGTTTCTGCTACAGTCTTATAGT 743  
DB 771 ACATCTCAAGGGCCACGAGAGCGCAAGCCCTCAAGACCAAGTCACTCTCATCTGCG 830  
QY 744 TTTCAATTTCACTCACTGCTTATTAACATTTGCAAGTTTCCGAGCCATAGACATCAT 803  
DB 831 TTTCTGCGCTGTGGTGGCTTCACTACATTTGGATGAGATGCACTCTCTCATCTCT 890  
QY 804 CTACTCTGATCAGCAGCTGCAATGAGCAAGGCAATGACATGCGCATCTCAAGTAC 863  
DB 891 GGAATATCATCAAGCAAGGCTGTGAGTGTGAGAACATCTGTGACAAAGTGTTCATCAC 950  
QY 864 AGAAAGATGAGCATCTTTACAGCTGCTCAACCCATCTTATGTTTATATGGAGAC 923  
DB 951 CGAGGCTTCTGCTTCTTCTCACTGTGTCTGAGCCCATCTCTATGCTTCTTGAAGC 1010  
QY 924 ATCTTCAAAACT 937  
DB 1011 CAAATTTAAACT 1024

RESULT 35  
US-09-104-296-3

Sequence 3, Application US/09104296  
Patent No. 6087475  
GENERAL INFORMATION:  
APPLICANT: Lee, James  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: PFAA Receptors  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/104,296  
FILING DATE: 24-June-1998  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/701265  
FILING DATE: 22-AUG-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/664228  
FILING DATE: 06-JUN-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/076093  
FILING DATE: 11-JUN-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/810782  
FILING DATE: 19-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P0706P2C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-5530  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1737 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
US-09-104-296-3

Query Match 13.4%; Score 153.6; DB 3; Length 1737;  
Best Local Similarity 49.6%; Pred. No. 6.8e-35;  
Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;

QY 90 CTGTATCAAGAGATGTCAGAGAAATTGCAAAAGTTTCTCCCTGATATCCACAAAT 149  
DB 171 CTGTTCCGTAGAGAAATGCTAATTTCAATTAATCTTCTGCGCACCATCTACAT 230  
QY 150 AGTTTCTGCTATGGAGCTTGAGGCAATTCATGGTAGTGCAATTATATGCGCTATTA 209  
DB 221 CATCTTTTAACTGGCATTTGGGGCAATGATGGTCACTCTGGTCAAGGGTTACAGAA 290  
QY 210 GAAACAGAGAACCAAAAGATGTTGATATCTGTAATTTGGCTGTAGAGATTTACTCT 269  
DB 291 GAAACTGAGAGATGACGACAAAGTACAGGCTGACCTGTCAAGTGGCGACCTCTCT 350  
QY 270 TCTATTTACTCTGCTTTTGGGCTGTTAATGCAATGATGGGTGGTTTATGGGAAAT 329  
DB 351 TGTCAATCAGCTTCTCTCTGCGAGTGTATGCGTGGCAAACTGTATTTGGAACTT 410  
QY 330 AATGCAAAATTAATCTGACCTGTACACATMAACTTTGCTCTGGAATGACGTTTCT 389

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Db 411 CCTATGCAAGGACATGTCATGATCAAGTCAACCTCTTACAGACAGTGTCTCATCT 470
Qy 390 GCCTGTATACGATAGACATATATGTGGCACTAAAGTCCCAACCATAGAGAGT 449
Db 471 GGCCTTCATCACTGACGACCGCTACCTGCGCATCTCCACGCAACACATGAGAGCC 530
Qy 450 GGGAAAC-----CATGTGATCATCTGTTCTGTCTGATGAGTGGTGCATCTTGTCT 503
Db 531 AAGGAAGCTGTTGGCTGAAAGAGTGTCTATTTGGCTCTGATCCCTGCTCTCTCT 590
Qy 504 GAGCATACCCCAAGCTGTTTTTATACAGTAATGACAATGCTAGTGCATTTCCATTTT 563
Db 591 GACTATTCGCACTTCATCTTTGCCAAGTCAGTGAGCAAGATGACAGATATATCTGGA 650
Qy 564 CCCCCGCTACCTAGGACATCAATGAAAGCATTTGATTAATGCTAGATCTGATTTGG 623
Db 651 CCGCTTCAACCCCAATGACTTGTGGTGTGTGTTCAGTTTCAGACATCATGTTGG 710
Qy 624 ATTTGATGACCTTTCTTATATGAGGGGTGTGCTACTTTATCAAGAGAAGACATCAT 683
Db 711 CCTATCTGCTGCTGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 770
Qy 684 GAAGATGCAACATTAATAATATCTGACCCCTTAAAGTTCTCTCAAGTGTATAGT 743
Db 771 ACATTCGAAGGGCACACAGAGGCAAGGCGCTCAAGACACAGTCATCTCATCTGCG 830
Qy 744 TTTTATTTGCTCACTCACTGCTTTATTAATCACTTGTCAAGTTTGGCGCATAGACATAT 803
Db 831 TTTCTTGGCTGTGGCTGCTGCTTACTACATGGAATGACATGCACTCTCTCTCTCTCT 890
Qy 804 CTACTCCCGATCAACAGCTGCAATGAGCAAGCAAGCATGAGCATGCGCATCAAGTAC 863
Db 891 GGAATATCAACAGAGGATGATGATTGAGAACTGTGACAGTGCACAGATTTTCATAC 950
Qy 864 AGAAGCATGCACTCTTTTCAAGCTGCTCAACCCCATCTTTATGTTTTTATGGAGC 923
Db 951 CGAGGCGCTAGCTTCTTCTTCACTGTTGTGTGAACCCCATCTCTATGCTTCTTGAGC 1010
Qy 924 ATCTTCAAAACT 937
Db 1011 CAATTTAAACCT 1024

```

RESULT 36  
PCT-US94-06380-2  
Sequence 2, Application PC/TUS9406380

GENERAL INFORMATION:

APPLICANT: Chunharapai, Anan

APPLICANT: Lee, James

APPLICANT: Hebert, Caroline

APPLICANT: K. Jin Kim

APPLICANT: Genentech, Inc.

TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY DISORDERS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/06380

FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/076093

```

ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-06380-2

Query Match 13.4%; Score 153.6; DB 5; Length 1737;
Best Local Similarity 49.6%; Pred. No. 6.8e-35;
Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;

Qy 90 CTGTATCAAAAGAGATGTCAGAAATTTGCAAAAGTTTCCCTCCGTATTCACAAAT 149
Db 171 CTGTATCCGTAAGAAATGCTAATTTCAATAAATCTTCTGCGCCACCATCTACTCAT 230
Qy 150 AGTTTCGTATGACCTTGACAGGCAATTCATGATGAGCAATTTATGCTATTAACA 209
Db 231 CATCTTCTTACCTGGCATTTGTGGCAATGATTTGATCATCTGTGATGAGTTTACAGA 290
Qy 210 GAAACAGAACCAAAACAGATGTGACATCTGAAATTTGGCTGTAGCAATTTACTCT 269
Db 291 GAAACAGAACGATACGACAGCAAGATGACAGCTGACCTGTGATGAGCGACCTCTCT 350
Qy 270 TCTATTCACCTGCTGCTTTTGGCTGTTAATGCAATTCATGAGGTGGCTTTAGGAAAT 329
Db 351 TGTATACCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 410
Qy 330 AATGCAAAATTAATCTTACGCTTTGTACACACTTAACTTTGTCTGTGAATGACATTTCT 389
Db 411 CTATGCAAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 470
Qy 390 GCCTGTATACGATAGACATATATGTGGCACTTAAATGTCCTCCAGCAATCAGAGAT 449
Db 471 GGCCTTATACGATGACGACGCTACCTGCGCATCTGCAAGCCACCAAGTCAAGAGCC 530
Qy 450 GGGAAAC-----CATGTGATCATCTGTTCTGTCTGATGAGTGGTGCATCTTGTCT 503
Db 531 AAGGAAGCTGTTGGCTGAAAGAGTGTCTATTTGGCTCTGATCCCTGCTCTGCT 590
Qy 504 GAGCATACCCCAAGCTGTTTTTATACAGTAATGACAATGCTAGTGCATTTCCATTTT 563
Db 591 GACTATTCGCACTTCATCTTTGCCAAGTCAGTGAGCAAGATGACAGATATATCTGGA 650
Qy 564 CCCCCGCTACCTAGGACATCAATGAAAGCATTTGATTAATGCTAGATCTGATTTGG 623
Db 651 CCGCTTCAACCCCAATGACTTGTGGTGTGTGTTCAGTTTCAGACATCATGTTGG 710
Qy 624 ATTTGATGACCTTTCTTATATGAGGGGTGTGCTACTTTATCAAGAGAAGACATCAT 683
Db 711 CCTATCTGCTGCTGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 770
Qy 684 GAAGATGCAACATTAATAATATCTGACCCCTTAAAGTTCTCTCAAGTGTATAGT 743
Db 771 ACATTCGAAGGGCACACAGAGGCAAGGCGCTCAAGACACAGTCATCTCATCTGCG 830
Qy 744 TTTTATTTGCTCACTCACTGCTTTATTAATCACTTGTCAAGTTTGGCGCATAGACATAT 803
Db 831 TTTCTTGGCTGTGGCTGCTTACTACATGGAATGACATGCACTCTCTCTCTCTCT 890
Qy 804 CTACTCCCGATCAACAGCTGCAATGAGCAAGCAAGCATGAGCATGCGCATCAAGTAC 863
Db 891 GGAATATCAACAGAGGATGATGATTGAGAACTGTGACAGTGCACAGATTTTCATAC 950
Qy 864 AGAAGCATGCACTCTTTCAAGCTGCTCAACCCCATCTTTATGTTTTTATGGAGC 923

```



Db 951 CGAGCCCTTCTTCACCTGTTGTCGACCCCATCTTATCTTCTTGAGC 1010  
QY 924 ATCTTCAAAACT 937  
Db 1011 CAATTAAACT 1024

## RESULT 37

US-08-153-848-23

Sequence 23, Application US/08153848

Patent No. 5759804

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.

APPLICANT: Schweikart, Vicki L.

TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &amp;

ADDRESS: Bicknell

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/153,848

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 5759804and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 2751 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: intron

LOCATION: 1..691

FEATURE:

NAME/KEY: exon

LOCATION: 692..1771

FEATURE:

NAME/KEY: CDS

LOCATION: 692..1768

FEATURE:

NAME/KEY: polyA\_signal

LOCATION: 2341..2348

US-08-153-848-23

Query Match 13.3%; Score 152.2; DB 1; Length 2751;  
Best Local Similarity 49.9%; Pred. No. 2.2e-34;  
Matches 478; Conservative 0; Mismatches 458; Indels 21; Gaps 3;

QY 39 TGAGGAATGAAATGAGCACTTATGACGTCATATGAACTGATCTGTCAA 98

Db 721 TGACTACATCGCGAGAAATVCCAGGTGACTACACCTGTAGCGTGTCTTCAA 780  
QY 99 AGAAGATGACAGAAATTTTCCCTGCTATTCACAAATAGTTTGGT 158  
Db 781 GAAAGATGCGGAACTTTAAGGCTGTTCTGCTCTCAATATTCGATCTGGCT 840  
QY 159 CATTGACTTGGAGCAATTCATGAGTGAATTTATGCTTATTAAGAAACAGAG 218  
Db 841 CGTGGGCTGCTGGCAAGGGCTGTGATCTAGCATCATCTATTCAAGAGCTCAA 900  
QY 219 AACCAAAAGATGTATCATCTGAAATTTGGCTGATGAGATTTACCTCTATTCAC 278  
Db 901 GACCATGAGGATACCTTACCTCTCAACCTGCGGAGACATCTTTCTCTTAAT 960  
QY 279 TCTGCTTTTGGGCTGTTAATGACATGAGTGGGTTTGAAGAAATATGAGCA 338  
Db 961 TCTTCTCTTCTGGGCTTACAGGAAAGCCAGTCTGATCTTTGGGCTGATCTGTGA 1020  
QY 339 AATTACTGAGCTTGTACACATTAACCTTTGTCTGTGAATGACGTTTCTGCTTAT 398  
Db 1021 GGGCATCTTGGCATCTATAAGTTAAGTTCTTCAAGCGGAGTGTGCTCTTATGCA 1080  
QY 399 CAGCATGACATATCT-----GGCAGTAACTAAAGTCCAGCAATCAG 446  
Db 1081 CAGCATGACCTGTACATGACATGCTCAAGGCTGTGCTCATGCGACCGGCGG 1140  
QY 447 AGTGGGAAACATGCTGATCATCTGTTCTGTGTGTGATGCTGCACTTGTGAG 506  
Db 1141 CGTCTTTCATACGACAGCTGCTGTGAGGCACTGAGATGCTGCTCTCTCTC 1200  
QY 507 CATACCCAGCTGTTTATTAAGTAAATGACATGCTAGTGTATCCATTTTCC 566  
Db 1201 CATCCGAGCTGCTTACAGCGGCTCCAGAAAGACAGCGGAGACAGCTGATG 1260  
QY 567 CCGCTACTGGAACATCATGAAAGATGATTAATGCTG-----AGATGTCAT 620  
Db 1261 CTACCTGTAGTGGCCAGTGGAGGCTTGTATCACCATTCAGAGTGGCCAGATGTTT 1320  
QY 621 TGATTTGTAGTACCTTTCTTATTAAGGAGTGTGCTTATTCACAGCAAGCACT 680  
Db 1321 TGGTTCCTAGTGGCTTATGCTGCTATGAGTTTCTGCTCATATATCATCTGACT 1380  
QY 681 CATGAGATGCCAAACATTAATAATCTGACCCCTTAAAGTTCTGCTCAGCTGTTAT 740  
Db 1381 GCTCAGGACAGCAACTTGTAGCGGAAAGGCAATCAAGTATATGCGCTGTGGT 1440  
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US-09-299-843A-23  
Sequence 23, Application US/09299843A  
Patent No. 6107475  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schweikart, Vicki L.  
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 66

RESPONSE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/299,843A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/088,337  
FILING DATE: 01-JUN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/153,848  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Jill E. Uhl  
REGISTRATION NUMBER: 43,213  
REFERENCE/DOCKET NUMBER: 27866/32059B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX:  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2751 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
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NAME/KEY: intron  
LOCATION: 1..691  
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LOCATION: 2341..2348  
US-09-299-843A-23  
Query Match 13.3%; Score 152.2; DB 3; Length 2751;  
Best Local Similarity 49.9%; Pired. No. 2.2e-34;  
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; Sequence 23, Application US/09088337B  
; Patent No. 6348574  
; GENERAL INFORMATION:  
; APPLICANT: Godiska, Ronald  
; Gray, Patrick W.  
; Schweikart, Vicki L.  
; TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS





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2044.760 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1077652

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 135 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1130.6	98.6	2156	10	US-09-765-994-3 Sequence 3, Appli
3	1113	97.0	1113	10	US-09-796-338A-7 Sequence 7, Appli
4	1053	91.8	1053	10	US-09-796-338A-9 Sequence 9, Appli
5	551.8	48.1	821	9	US-09-989-442-36 Sequence 36, Appli
6	551.8	48.1	821	9	US-10-073-863-32 Sequence 32, Appli
7	551.8	48.1	821	9	US-09-764-853-164 Sequence 164, App
8	305.8	26.7	381	10	US-09-960-352-1604 Sequence 1604, Ap
9	164.8	14.4	2577	9	US-09-966-755-1 Sequence 1, Appli
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14	153.6	13.4	1737	9	US-09-104-063-3 Sequence 3, Appli
15	152	13.3	1102	9	US-09-870-759-143 Sequence 143, App
16	143	12.5	1487	10	US-09-789-482-3 Sequence 3, Appli
17	143	12.5	1487	10	US-09-789-486-3 Sequence 3, Appli
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19	143	12.5	3100	10	US-09-954-456-945 Sequence 945, App

20	143	12.5	3100	10	US-09-954-456-1588 Sequence 1588, Ap
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22	129.4	11.3	1607	9	US-09-764-413-19 Sequence 19, Appli
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86	56	4.9	1414	9	US-10-098-841-312 Sequence 312, App
87	55.6	4.8	362	9	US-10-100-178-7 Sequence 7, Appli
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91	52.4	4.6	1408	10	US-09-914-904-5 Sequence 5, Appli
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93 51 4.4 514 9 US-09-764-413-5  
 94 49.4 4.3 823 12 US-10-044-090-598  
 95 48.8 4.3 1087 9 US-10-044-070A-1  
 96 48 4.2 1910 10 US-09-944-807-1  
 97 47.8 4.2 1301 9 US-10-024-484-7  
 98 46 4.0 476 10 US-09-864-761-2944  
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 100 45.8 4.0 1050 10 US-09-912-025-1  
 101 44.8 3.9 1083 10 US-09-852-156-7  
 102 44.6 3.9 1062 9 US-10-083-168-1  
 103 43.8 3.8 421 9 US-09-796-692-2611  
 104 43.6 3.8 484 10 US-09-864-761-5741  
 105 43.4 3.8 1377 10 US-09-822-830A-588  
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 107 42.6 3.7 1041 9 US-10-094-417-7  
 108 42.6 3.7 1041 10 US-09-862-274-1  
 109 42.6 3.7 1041 10 US-09-942-374-3  
 110 42.6 3.7 1194 10 US-09-942-374-1  
 111 42.6 3.7 58985 9 US-09-901-152-3  
 112 42.4 3.7 2183 10 US-09-925-302-309  
 113 41.6 3.6 1083 10 US-09-852-156-11  
 114 41.4 3.6 1753 12 US-10-084-206-1  
 115 40.6 3.5 370 10 US-09-728-446-223  
 116 40 3.5 1083 10 US-09-852-156-9  
 117 39.8 3.5 1892 9 US-09-900-699A-1  
 118 39.6 3.5 583 10 US-09-864-761-20772  
 119 39.6 3.5 1959 10 US-09-864-761-4012  
 120 39.4 3.4 1014 9 US-10-023-775B-1  
 121 39.4 3.4 1014 9 US-10-270-144-1  
 122 39.4 3.4 1014 10 US-09-943-798-3  
 123 39.4 3.4 1313 10 US-09-728-422-1  
 124 39.4 3.4 9905 9 US-10-270-144-3  
 125 38.8 3.4 439 10 US-09-864-761-20174  
 126 38.8 3.4 1307 9 US-10-007-343-1  
 127 38.6 3.4 546 10 US-09-812-102-64  
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 ; TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR  
 ; FILE REFERENCE: GH-70225-C1  
 ; CURRENT APPLICATION NUMBER: US/09/765,994  
 ; CURRENT FILING DATE: 2001-01-19  
 ; PRIOR APPLICATION NUMBER: 60/055,895  
 ; PRIOR FILING DATE: 1997-08-15  
 ; PRIOR APPLICATION NUMBER: 08/962,922  
 ; PRIOR FILING DATE: 1997-10-27  
 ; NUMBER OF SEQ ID NOS: 4  
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 ; SEQ ID NO 1  
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 ; TYPE: DNA  
 ; ORGANISM: HOMO SAPIENS  
 ; US-09-765-994-1

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 Best Local Similarity 99.8%; Pred. No. 4.9e-300;

Matches 1136; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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 QY 781 TTCTGCCGAGCCATGACATCTACTCCCTGATCAGAGTCCATGAGCAAAAGC 840  
 Db 1029 TTCTGCCGAGCCATGACATCTACTCCCTGATCAGAGTCCATGAGCAAAAGC 1088  
 QY 841 ATGACATGCGCATCTCAAGTACAGAAAGATGGACCTTTTACAGTGGCTCAACCA 900  
 Db 1089 ATGACATGCGCATCTCAAGTACAGAAAGATGGACCTTTTACAGTGGCTCAACCA 1148  
 QY 901 ATCTCTTATGTTTATGAGAGCATCTTCAAAATAGCTTATGAAGTGGCAAGAA 960  
 Db 1149 ATCTCTTATGTTTATGAGAGCATCTTCAAAATAGCTTATGAAGTGGCAAGAA 1208  
 QY 961 TATGGTCTGTAGAGAGCAAGAGCAAAAGTGTGAGAGTTTCTTTTGAATTCAGAGGT 1020  
 Db 1209 TATGGTCTGTAGAGAGCAAGAGCAAAAGTGTGAGAGTTTCTTTTGAATTCAGAGGT 1268  
 QY 1021 CCTACAGAGCCAACTGATCTTTTATGCAATTTAAAGTTAAAGTCTGCTTTGCTTG 1080  
 Db 1269 CCTACAGAGCCAACTGATCTTTTATGCAATTTAAAGTTAAAGTCTGCTTTGCTTG 1328

QY 1081 GATACATATGATGATGCTTCCCTCAATTAACATCTGCTTATCTGAAAAAA 1140  
Db 1329 GATACATATGATGATGCTTCCCTCAATTAACATCTGCTTATCTGAAAAAA 1388

## RESULT 2

US-09-765-994-3  
; Sequence 3, Application US/09765994  
; Patent No. US20010016336A1  
; GENERAL INFORMATION:  
; APPLICANT: ELLIS, CATHERINE  
; TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR  
; TITLE OF INVENTION: (HEFA041)  
; FILE REFERENCE: GH-70225-C1  
; CURRENT APPLICATION NUMBER: US/09/765,994  
; CURRENT FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/055,895  
; PRIOR FILING DATE: 1997-08-15  
; PRIOR APPLICATION NUMBER: 08/962,922  
; PRIOR FILING DATE: 1997-10-27  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 2156  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-765-994-3

Query Match 98.6%; Score 1130.6; DB 10; Length 2156;  
Best Local Similarity 99.6%; Pred. No. 3.1e-299;  
Matches 113; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GCTTTGGAACAGAACCACTCAAGATTTATTTATGAGAAATGAATGAGCACT 63  
Db 1 GCTTTGGAACAGAACCACTCAAGATTTATTTATGAGAAATGAATGAGCACT 60  
QY 64 TATGACTACAGCAATATGAACTGATCTGATCAAGAAAGATGAGAAATTTGCAAA 123  
Db 61 TATGACTACAGCAATATGAACTGATCTGATCAAGAAAGATGAGAAATTTGCAAA 120  
QY 124 GTTTCCTCCTGATATCTCTCAATAGTTTGTGATTTGAGCACTTGCAATTCATG 183  
Db 121 GTTTCCTCCTGATATCTCTCAATAGTTTGTGATTTGAGCACTTGCAATTCATG 180  
QY 184 GTAGTGGCAATTTATGCTCATTAAGAAAGAGAAACCAAGATGAGTGAATCCTG 243  
Db 181 GTAGTGGCAATTTATGCTCATTAAGAAAGAGAAACCAAGATGAGTGAATCCTG 240  
QY 244 AATTGGCTGTAGCAATTTACTCTCTTATCACTGCTCTTTTGGGCTGTATGCA 303  
Db 241 AATTGGCTGTAGCAATTTACTCTCTTATCACTGCTCTTTTGGGCTGTATGCA 300  
QY 304 GTTCATGAGTGGGTTTATGAGAAATATGCAAAATTAATCTTACCTTGACACATA 363  
Db 301 GTTCATGAGTGGGTTTATGAGAAATATGCAAAATTAATCTTACCTTGACACATA 360  
QY 364 AACTTGTCTGAGATGAGTTTGTGCTGTATGAGATGAGATGAGATGAGATG 423  
Db 361 AACTTGTCTGAGATGAGTTTGTGCTGTATGAGATGAGATGAGATGAGATG 420  
QY 424 ACTAAGTCCCAAGCCATCAGAGTGGGAAACCATGCTGATCATCTGTTCTGTGTC 483  
Db 421 ACTAAGTCCCAAGCCATCAGAGTGGGAAACCATGCTGATCATCTGTTCTGTGTC 480  
QY 484 TGGATGGCTGCACTTTCTGAGACATACCCGAGCTGTTTTTATATGAGTAAATG 543  
Db 481 TGGATGGCTGCACTTTCTGAGACATACCCGAGCTGTTTTTATATGAGTAAATG 540  
QY 544 GGTAGGATGATCCATTTTCCCGCTACCTAGAAACATCAATGAAGCATTTGATCA 603  
Db 541 GGTAGGATGATCCATTTTCCCGCTACCTAGAAACATCAATGAAGCATTTGATCA 600

QY 604 ATGCTAGAGATCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 663  
Db 601 ATGCTAGAGATCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 660  
QY 664 ATCAGCAAGGACACTATGAGAGTGGCAACATTTAAATATCTCGAACCCCTAAAGTT 723  
Db 661 ATCAGCAAGGACACTATGAGAGTGGCAACATTTAAATATCTCGAACCCCTAAAGTT 720  
QY 724 CTGCTCAGAGTGGTATATGATTTGATTTGATTTGATTTGATTTGATTTGATTT 783  
Db 721 CTGCTCAGAGTGGTATATGATTTGATTTGATTTGATTTGATTTGATTTGATTT 780  
QY 784 TGGCGAGCCATGACATCTTCTGAGACATCTGATTTGATTTGATTTGATTTGATTT 843  
Db 781 TGGCGAGCCATGACATCTTCTGAGACATCTGATTTGATTTGATTTGATTTGATTT 840  
QY 844 GACATGCGCATCCAGTTCAGAGAGATGAGATGAGATGAGATGAGATGAGATG 903  
Db 841 GACATGCGCATCCAGTTCAGAGAGATGAGATGAGATGAGATGAGATGAGATG 900  
QY 904 CTTTATGTTTTTATGAGACATCTTTCAAAAATGATGATGATGATGATGATGAT 963  
Db 901 CTTTATGTTTTTATGAGACATCTTTCAAAAATGATGATGATGATGATGATGAT 960  
QY 964 GGGTCTGAG 1023  
Db 961 GGGTCTGAG 1020  
QY 1024 ACAGAGCAACAGTCTTTTATGATTTTAAAGTAAACCTGCTGCTTTGCTTGAT 1083  
Db 1021 ACAGAGCAACAGTCTTTTATGATTTTAAAGTAAACCTGCTGCTTTGCTTGAT 1080  
QY 1084 ACATATGATGATGCTTTTCCCTCAATTAACATCTGCTTATTTGAAAAAAA 1140  
Db 1081 ACATATGATGATGCTTTTCCCTCAATTAACATCTGCTTATTTGAAAAAAA 1137

## RESULT 3

US-09-796-338A-7  
; Sequence 7, Application US/09796338A  
; Patent No. US20020061522A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND  
; TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR  
; FILE REFERENCE: 10448-020001  
; CURRENT APPLICATION NUMBER: US/09/796,338A  
; CURRENT FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: US 60/186,059  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1113  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1050)  
US-09-796-338A-7

Query Match 97.0%; Score 1113; DB 10; Length 1113;  
Best Local Similarity 100.0%; Pred. No. 1.4e-294;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTTTGGAACAGAACCACTCAAGATTTATTTATGAGAAATGAATGATGCG 60  
Db 1 ATGCTTTGGAACAGAACCACTCAAGATTTATTTATGAGAAATGAATGATGCG 60  
QY 61 ACTTATGATCACTACATATGAACTGATCTGTATCAAAAGATGTCAGAAATTTGCA 120  
Db 61 ACTTATGATCACTACATATGAACTGATCTGTATCAAAAGATGTCAGAAATTTGCA 120

QY 121 AAAAGTTTCTCCCTGATATCTCAATAGTTTTCGATTTGAGCTTGACGAATTTCC 180  
DB 121 AAAAGTTTCTCCCTGATATCTCAATAGTTTTCGATTTGAGCTTGACGAATTTCC 180  
QY 181 ATGGTAGTGGCAATTTATGCTATATACAGAAACAGAAACCAAAACAGATGTATAC 240  
DB 181 ATGGTAGTGGCAATTTATGCTATATACAGAAACAGAAACCAAAACAGATGTATAC 240  
QY 241 CTGAATTTGGCTGATGAGATTTACTCTCTTATTCATCTGCTGCTTTTGGCTGTAT 300  
DB 241 CTGAATTTGGCTGATGAGATTTACTCTCTTATTCATCTGCTGCTTTTGGCTGTAT 300  
QY 301 GCAGTTTCATGGGTGGGTTTATGGGAAATATATGTCACAAATATCTAGCCTGTACACA 360  
DB 301 GCAGTTTCATGGGTGGGTTTATGGGAAATATATGTCACAAATATCTAGCCTGTACACA 360  
QY 361 CTAAACTTTGCTCTGGAATGAGTTTCTGGCTGTATCAGCATATAGCAGATATGTGCA 420  
DB 361 CTAAACTTTGCTCTGGAATGAGTTTCTGGCTGTATCAGCATATAGCAGATATGTGCA 420  
QY 421 GTAATTAAGTCCCAAGCAATCAGAGTGGGAAACCATGCTGATCATCTTTCTGT 480  
DB 421 GTAATTAAGTCCCAAGCAATCAGAGTGGGAAACCATGCTGATCATCTTTCTGT 480  
QY 481 GTCTGATGGGCTGCATCTGTGATGATCCCAAGCTGCTTTTATPACAGTAATGAC 540  
DB 481 GTCTGATGGGCTGCATCTGTGATGATCCCAAGCTGCTTTTATPACAGTAATGAC 540  
QY 541 AATGCTAGGTCATTTCCCATTTTCCCGCTATCTAGGACATCAATGAAAGCATTTGAT 600  
DB 541 AATGCTAGGTCATTTCCCATTTTCCCGCTATCTAGGACATCAATGAAAGCATTTGAT 600  
QY 601 CAATGCTAGGATCTGATTTGATTTAGTACCTTTCTTATTTATGAGGGGTGTCTAC 660  
DB 601 CAATGCTAGGATCTGATTTGATTTAGTACCTTTCTTATTTATGAGGGGTGTCTAC 660  
QY 661 TTATACAGAGGACACTCATGATGATGATGACCAATTAATATCTCGAAGCTGTAC 720  
DB 661 TTATACAGAGGACACTCATGATGATGATGACCAATTAATATCTCGAAGCTGTAC 720  
QY 721 GTTCTGCTCAGAGTCTGATATGATTTTCAATGTCATCACTCACTGCTTAAATTTGCA 780  
DB 721 GTTCTGCTCAGAGTCTGATATGATTTTCAATGTCATCACTCACTGCTTAAATTTGCA 780  
QY 781 TTTCGCGAGGCAATGACATGATCTACTCCCTGATCAACAGCTGCAATGAGAAACGC 840  
DB 781 TTTCGCGAGGCAATGACATGATCTACTCCCTGATCAACAGCTGCAATGAGAAACGC 840  
QY 841 ATGACATCGCCATCCAAAGTCAAGAAAGCATGCTCTTTCACAGCTGCTCAACCA 900  
DB 841 ATGACATCGCCATCCAAAGTCAAGAAAGCATGCTCTTTCACAGCTGCTCAACCA 900  
QY 901 ATCTTTATGTTTTTATGGAGATCTTTCAAAAATGATGTAAGAAAGTGGCCAAAGAA 960  
DB 901 ATCTTTATGTTTTTATGGAGATCTTTCAAAAATGATGTAAGAAAGTGGCCAAAGAA 960  
QY 961 TATGGTCTCTGGAATAAACAAGATGAGAGATTTCTTTGATTTGAGGGT 1020  
DB 961 TATGGTCTCTGGAATAAACAAGATGAGAGATTTCTTTGATTTGAGGGT 1020  
QY 1021 CCTACAGAGCAACAGATCTTTAGCATTTAAAGTAAACCTGCTGCTTTTGGCTTG 1080  
DB 1021 CCTACAGAGCAACAGATCTTTAGCATTTAAAGTAAACCTGCTGCTTTTGGCTTG 1080  
QY 1081 GATACATATGATGATGCTTTCCCTCAAAATTA 1113  
DB 1081 GATACATATGATGATGCTTTCCCTCAAAATTA 1113

RESULT 4  
US-09-796-338A-9  
; Sequence 9, Application US/09796338A  
; Patent No. US20020061522A1

; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND  
; TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USBS THEREFOR  
; FILE REFERENCE: 10448-020001  
; CURRENT APPLICATION NUMBER: US/09/796,338A  
; PRIORITY FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: US 60/186,059  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1053  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-796-338A-9  
Query Match 91.8%; Score 1053; DB 10; Length 1053;  
Best Local Similarity 100.0%; Pred. No. 3,6e-278;  
Matches 1053; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCTTTGGAAACAGAACCAATGATTAATTAATGAGAAATGAATGAATGAGC 60  
DB 1 ATGGCTTTGGAAACAGAACCAATGATTAATTAATGAGAAATGAATGAATGAGC 60  
QY 61 ACTTATGACTACAGTCAATATGATGATCTGTATCAAAAGAGATGTCAGAAATTTGCA 120  
DB 61 ACTTATGACTACAGTCAATATGATGATCTGTATCAAAAGAGATGTCAGAAATTTGCA 120  
QY 121 AAAAGTTTCTCCCTGATATCTCAATAGTTTTCGATTTGAGCTTGACGAATTTCC 180  
DB 121 AAAAGTTTCTCCCTGATATCTCAATAGTTTTCGATTTGAGCTTGACGAATTTCC 180  
QY 181 ATGGTAGTGGCAATTTATGCTATATACAGAAACAGAAACCAAAACAGATGTATAC 240  
DB 181 ATGGTAGTGGCAATTTATGCTATATACAGAAACAGAAACCAAAACAGATGTATAC 240  
QY 241 CTGAATTTGGCTGATGAGATTTACTCTCTTATTCATCTGCTGCTTTTGGCTGTAT 300  
DB 241 CTGAATTTGGCTGATGAGATTTACTCTCTTATTCATCTGCTGCTTTTGGCTGTAT 300  
QY 301 GCAGTTTCATGGGTGGGTTTATGGGAAATATATGTCACAAATATCTAGCCTGTACACA 360  
DB 301 GCAGTTTCATGGGTGGGTTTATGGGAAATATATGTCACAAATATCTAGCCTGTACACA 360  
QY 361 CTAAACTTTGCTCTGGAATGAGTTTCTGGCTGTATCAGCATATAGCAGATATGTGCA 420  
DB 361 CTAAACTTTGCTCTGGAATGAGTTTCTGGCTGTATCAGCATATAGCAGATATGTGCA 420  
QY 421 GTAATTAAGTCCCAAGCAATCAGAGTGGGAAACCATGCTGATCATCTTTCTGT 480  
DB 421 GTAATTAAGTCCCAAGCAATCAGAGTGGGAAACCATGCTGATCATCTTTCTGT 480  
QY 481 GTCTGATGGGCTGCATCTGTGATGATCCCAAGCTGCTTTTATPACAGTAATGAC 540  
DB 481 GTCTGATGGGCTGCATCTGTGATGATCCCAAGCTGCTTTTATPACAGTAATGAC 540  
QY 541 AATGCTAGGTCATTTCCCATTTTCCCGCTATCTAGGACATCAATGAAAGCATTTGAT 600  
DB 541 AATGCTAGGTCATTTCCCATTTTCCCGCTATCTAGGACATCAATGAAAGCATTTGAT 600  
QY 601 CAATGCTAGGATCTGATTTGATTTAGTACCTTTCTTATTTATGAGGGGTGTCTAC 660  
DB 601 CAATGCTAGGATCTGATTTGATTTAGTACCTTTCTTATTTATGAGGGGTGTCTAC 660  
QY 661 TTATACAGAGGACACTCATGATGATGATGACCAATTAATATCTCGAAGCTGTAC 720  
DB 661 TTATACAGAGGACACTCATGATGATGATGACCAATTAATATCTCGAAGCTGTAC 720  
QY 721 GTTCTGCTCAGAGTCTGATATGATTTTCAATGTCATCACTCACTGCTTAAATTTGCA 780  
DB 721 GTTCTGCTCAGAGTCTGATATGATTTTCAATGTCATCACTCACTGCTTAAATTTGCA 780



Qy 781 TTCTGCCAGCCATAGACATCATCTACTCCCTGATACACAGCTGCAACATGAGCAACGC 840  
Db 781 TTCTGCCAGCCATAGACATCATCTACTCCCTGATACACAGCTGCAACATGAGCAACGC 840  
Qy 841 ATGACATGCGCATTCAGATCAAGAGAGAGATGCGACTCTTTCAAGCTGCTCAACCCA 900  
Db 841 ATGACATGCGCATTCAGATCAAGAGAGAGATGCGACTCTTTCAAGCTGCTCAACCCA 900  
Qy 901 ATCTTTTATGTTTTATGAGGAGCATCTTTCAAAAACCTAGCTATGAAAGTGGCCAAAGAA 960  
Db 901 ATCTTTTATGTTTTATGAGGAGCATCTTTCAAAAACCTAGCTATGAAAGTGGCCAAAGAA 960  
Qy 961 TATGGGTCCTGAGAGAGACAGAGACAAAGTGTGAGAGAGATTCTTTTGAATTCGAGGAT 1020  
Db 961 TATGGGTCCTGAGAGAGACAGAGACAAAGTGTGAGAGAGATTCTTTTGAATTCGAGGAT 1020  
Qy 1021 CCTACAGAGCCACCACTGACTTTTATGACTTTAA 1053  
Db 1021 CCTACAGAGCCACCACTGACTTTTATGACTTTAA 1053

RESULT 5  
US-09-989-442-36/c  
; Sequence 36, Application US/09989442  
; Publication No. US20030013649A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P0208  
; CURRENT APPLICATION NUMBER: US/09/989,442  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/225,757  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/226,868  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/216,647  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,267  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/216,880  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,270  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/251,869  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/235,834  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/234,274  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/234,223  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/228,924  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/224,518  
; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/236,369  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/224,519  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,964  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/241,809  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/249,299  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/236,327  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/241,785  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/244,617  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 60/225,268  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,368  
; PRIOR FILING DATE: 2000-09-29  
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; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/251,868  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/229,344  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/234,997  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: 60/229,343  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,345  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,287  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,513  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/231,413  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/229,509  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/236,367  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/237,039  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,038  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/236,370  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/236,802  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,037  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,040  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/240,960  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/239,935  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/239,937  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/241,787  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,474  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/246,532  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/249,216  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,210  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/226,681  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,759

PRIOR FILING DATE: 2000-08-14	60/225, 213
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PRIOR FILING DATE: 2000-08-14	60/227, 182
PRIOR APPLICATION NUMBER: 60/227, 182	
PRIOR FILING DATE: 2000-08-22	60/235, 214
PRIOR APPLICATION NUMBER: 60/235, 214	
PRIOR FILING DATE: 2000-08-14	60/235, 836
PRIOR APPLICATION NUMBER: 60/235, 836	
PRIOR FILING DATE: 2000-09-27	60/230, 438
PRIOR APPLICATION NUMBER: 60/230, 438	
PRIOR FILING DATE: 2000-09-06	60/235, 135
PRIOR APPLICATION NUMBER: 60/235, 135	
PRIOR FILING DATE: 2000-06-30	60/225, 266
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PRIOR FILING DATE: 2000-08-14	60/249, 218
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PRIOR FILING DATE: 2000-11-17	60/249, 208
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PRIOR APPLICATION NUMBER: 60/249, 211	
PRIOR FILING DATE: 2000-11-17	60/249, 215
PRIOR APPLICATION NUMBER: 60/249, 215	
PRIOR FILING DATE: 2000-11-17	60/249, 264
PRIOR APPLICATION NUMBER: 60/249, 264	
PRIOR FILING DATE: 2000-11-17	60/249, 214
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PRIOR FILING DATE: 2000-11-17	60/249, 297
PRIOR APPLICATION NUMBER: 60/249, 297	
PRIOR FILING DATE: 2000-11-17	60/232, 400
PRIOR APPLICATION NUMBER: 60/232, 400	
PRIOR FILING DATE: 2000-09-14	60/231, 242
PRIOR APPLICATION NUMBER: 60/231, 242	
PRIOR FILING DATE: 2000-09-08	60/232, 081
PRIOR APPLICATION NUMBER: 60/232, 081	
PRIOR FILING DATE: 2000-09-08	60/232, 080
PRIOR APPLICATION NUMBER: 60/232, 080	
PRIOR FILING DATE: 2000-09-08	60/231, 414
PRIOR APPLICATION NUMBER: 60/231, 414	
PRIOR FILING DATE: 2000-09-08	60/231, 244
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PRIOR FILING DATE: 2000-09-08	60/233, 054
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PRIOR FILING DATE: 2000-09-14	60/233, 053
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PRIOR FILING DATE: 2000-09-14	60/232, 399
PRIOR APPLICATION NUMBER: 60/232, 399	
PRIOR FILING DATE: 2000-09-14	60/232, 401
PRIOR APPLICATION NUMBER: 60/232, 401	
PRIOR FILING DATE: 2000-09-14	60/241, 786
PRIOR APPLICATION NUMBER: 60/241, 786	
PRIOR FILING DATE: 2000-10-20	60/241, 221
PRIOR APPLICATION NUMBER: 60/241, 221	
PRIOR FILING DATE: 2000-10-20	60/246, 475
PRIOR APPLICATION NUMBER: 60/246, 475	
PRIOR FILING DATE: 2000-11-08	

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; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14

Query Match          48.1%; Score 551.8; DB 9; Length 821;
Best Local Similarity 95.1%; Pred. No. 4,5e-141;
Matches 597; Conservative 2; Mismatches 24; Indels 5; Gaps 3;

OY 520 GTTTTATATACGTAATATGACATGCTAGGTGACATTCCTCCATTTTCCCGCTACCTAGGA 579
    |||||
Db 820 GTGGTATTTATCCNGTAATATGACAAATCTGTGTF--CATCCATTTTCCCGCTACCT-GGN 765
    |||||

OY 580 ACATCAATGAAGACATATGATTCAAATGCTAGAGATCTGCATTTGGATTTTGTAGTACCTTT 639
    |||||
Db 764 ACATCAATGAAGACATATGATTC--AATGCTAAGATCTGCATTTGGATTTTGTAGTACCTTT 706
    |||||

OY 640 CTATATATGGGGGTGTGCTACTTTTATCAACAGCAAGACACTCATGAAGATGCCAAACATT 699
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Db 705 CTATATATGGGGGTGTGCTACTTTTATCAAGAAAGACACTCATGAAGATGCCAAACATT 646
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OY 700 AAAATATCTGACCCCTAAAAAGTTTGTCTCACTGCTGTATAGTTTTCATTTGTCACTCAA 759
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Db 645 AAAATATCTGACCCCTAAAAAGTTTGTCTCACTGCTGTATAGTTTTCATTTGTCACTCAA 586
    |||||

OY 760 CTGGCTTATATACATTTGTCAAGTTCTGCGGACGCATAGACATCATCTACTCCGTATCACC 819
    |||||
Db 585 CTGGCTTATATACATTTGTCAAGTTCTGCGGACGCATAGACATCATCTACTCCGTATCACC 526
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OY 820 AGCTGCACATGACAGCAACGACATGACATGCGCATCCAAATCCAAATGACAGAAAGATGCACTC 879
    |||||
Db 525 AGCTGCACATGACAGCAACGACATGACATGCGCATCCAAATCCAAATGACAGAAAGATGCACTC 466
    |||||

OY 880 TTTGACAGCTGCTCAACCCATTCCTTTATGTTTTATGGAGAGATTTTCAAAAATCTAC 939
    |||||
Db 465 TTTGACAGCTGCTCAACCCATTCCTTTATGTTTTATGGAGAGATTTTCAAAAATCTAC 406
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OY 940 GTTATGAAGATGGCCAAAGAAATATGAGTCTCTGGAGAAAGACAGAGACAAATGTGAGAGAG 999
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Db 405 GTTATGAAGATGGCCAAAGAAATATGAGTCTCTGGAGAAAGACAGAGACAAATGTGAGAGAG 346
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OY 1000 TTTTCCTTTGATTTCTGAGGGTCTTACAGAGCCAAACAGTACTTTTAGCATTTAAAGGTAA 1059
    |||||
Db 345 TTTTCCTTTGATTTCTGAGGGTCTTACAGAGCCAAACAGTACTTTTAGCATTTAAAGGTAA 286
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OY 1060 AACTGCTCTGCTTTTGTCTGTGATATCATATGAATGATGCTTTCCCTCAATATAAACATTC 1119
    |||||
Db 285 AACTGCTCTGCTTTTGTCTGTGATATCATATGAATGATGCTTTCCCTCAATATAAACATTC 226
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OY 1120 TGCCTTATTTCTGAAAAAATTTTTTTTTTTT 1147
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Db 225 TGCATTTATTTGAACTCAAAAAAATTTT 198
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RESULT 6
US-10-073--865-32/C
; Sequence 32, Application US/10073865
; Publication No. US20030044904A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: RJ209C1
; CURRENT APPLICATION NUMBER: US/10/073,865
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

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1 LOCATION: (58)
2 OTHER INFORMATION: n equals a,t,g, or c
3 NAME/KEY: misc feature
4 LOCATION: (109)
5 OTHER INFORMATION: n equals a,t,g, or c
6 NAME/KEY: misc feature
7 LOCATION: (335)
8 OTHER INFORMATION: n equals a,t,g, or c
9 NAME/KEY: misc feature
10 LOCATION: (765)
11 OTHER INFORMATION: n equals a,t,g, or c
12 NAME/KEY: misc feature
13 LOCATION: (759)
14 OTHER INFORMATION: n equals a,t,g, or c
15 NAME/KEY: misc feature
16 LOCATION: (773)
17 OTHER INFORMATION: n equals a,t,g, or c
18 NAME/KEY: misc feature
19 LOCATION: (808)
20 OTHER INFORMATION: n equals a,t,g, or c
21
22 JS-10-073-865-32

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Db 405 GTTATGAAGAGTGGCCAGAAATATGGTCTCTGGAGAGACAGACAAAGTGTGGAGAG 346  
QY 1000 TTTCCCTTTGATTTGAGAGGTCTCTACAGAGCCAACTACTTTTATGATTTAAAGTAA 1059  
Db 345 TTTCCCTTTGATTTGAGAGGTCTCTACAGAGCCAACTACTTTTATGATTTAAAGTAA 286  
QY 1060 AACTGCTGCTGCTTTGCTTGTGATACATATGATGCTTTCCCTCAAAATTAACATC 1119  
Db 285 AACTGCTGCTGCTTTGCTTGTGATACATATGATGCTTTCCCTCAAAATTAACATC 226  
QY 1120 TGCCTTATTTCTGAAAAAAM 1147  
Db 225 TGCATTTATTTCTGAAACTCAAAAAA 198

## RESULT 8

US-09-960-352-1604  
; Sequence 1604, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 1604  
; LENGTH: 381  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; OTHER INFORMATION: Clone ID: 07-LIB34-081-Q1-E1-B3  
US-09-960-352-1604

Query Match 26.7%; Score 305.8; DB 10; Length 381;  
Best Local Similarity 87.7%; Pred. No. 6.2e-74;  
Matches 334; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 208 AAGAAACAGAGAACCAAAACAGATGTACATCTGAAATTTGGCTGACAGATTTACTC 267  
Db 1 AAAAAAGAGCGCAACCAAAACAGATGTACATCTGAAATTTGGCGAGTTCGATTTATTC 60  
QY 268 CTTCATTCACCTGCTGCTTTTGGCTGTTAATGACATTCATGCTGCTTTTGGGAAA 327  
Db 61 CTTCATTCACCTGCTGCTTTTGGCTGTTAATGACATTCATGCTGCTTTTGGGAAA 120  
QY 328 ATATGTCACAAATTAATTCAGCTTGTACACACTTAACCTTGTCTGGAATGCACTTT 387  
Db 121 ATCATGTCAAAAGTACCTTACAGCTTGTACACAGTCAATTTTGTGTCTGGAATGCACTTT 180  
QY 388 CTGCTTTATTCAGATACAGATATGTGCACTTAATTAATGCTTCCCAAGCAATACAGA 447  
Db 181 CTGCTTTATTCAGATACAGATATGTGCACTTAATTAATGCTTCCCAAGCAATACAGA 240  
QY 448 GTGGGAAAACATGCTGATCATCTGCTTCTGTCTGGAATGCTGCTGCTGCTGCTGCTG 507  
Db 241 GTGGGAAAACATGCTGATCATCTGCTTCTGTCTGGAATGCTGCTGCTGCTGCTGCTG 300  
QY 508 ATACCCCACTGCTTTTATATACAGTAATGACATGCTGATGCTGCTGCTGCTGCTGCTG 567  
Db 301 ATCCCTGAGTGTGTTTTTATACAGTAATGACATGCTGATGCTGCTGCTGCTGCTGCTG 360  
QY 568 CGTACTGAGAACATCAATG 588  
Db 361 TACCACTTACGACATCAATG 381

RESULT 9  
US-09-966-755-1  
; Sequence 1, Application US/09966755

; Publication No. US20030022238A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew, David P.  
; APPLICANT: Zabel, Brian A.  
; APPLICANT: Ponach, Paul D.  
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF  
; TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION  
; FILE REFERENCE: LK98-16  
; CURRENT APPLICATION NUMBER: US/09/966,755  
; CURRENT FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US/09/266,464  
; PRIOR FILING DATE: 1999-03-11  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 2577  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (58)...(1131)  
US-09-966-755-1

Query Match 14.4%; Score 164.8; DB 9; Length 2577;  
Best Local Similarity 51.0%; Pred. No. 6.2e-35;  
Matches 481; Conservative 0; Mismatches 442; Indels 21; Gaps 3;

QY 52 ATGAATGGCACTTATGACTACAGTCAATATGACATGATCTGATCAAGAGATGTCAGA 111  
Db 94 ATGAAGACTACGTTAACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 153  
QY 112 GAATTTGCAAAAGTTTCTCCCTGATTTCTCACAATGATTTGCTATTTGCACTTGA 171  
Db 154 CAGTTTGCAGACATTTCTCCACCTTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 213  
QY 172 GGCATTCAGTGTAGTGGCAATTTATGCTTATTAAGAAACAGAGAACCAAAACAGAT 231  
Db 214 GGCACAGCTTGTATCTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACT 273  
QY 232 GTGTATATCTGTAATTTGGCTGATGACATTTATCTCTTCTTATCTGCTGCTTTTGG 291  
Db 274 ATGTTCTTTTGAATTTGGCAATGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 333  
QY 292 GCTGTTATGACATTCATGCTGCTGCTTTTGAAGAAATTAATGCAAAATTAATCACTC 351  
Db 334 GCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 393  
QY 352 TTGTACACATAAATCTTGTCTGGAATGCAATTTGCTGCTTGTATGACATACAGA 411  
Db 394 ATGTACAGATGAATCTTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 453  
QY 412 TATGTGCGAGTACATAAGTCCCGAG-----CCAAACAGAGTGGGAAACCAT----- 460  
Db 454 TACATTTGCATTTGCCAGCCATGAGACACATACCTTGAAGGAGAAAGCTTTTGTAC 513  
QY 461 -GCTGATCATCTGTTTCTGTTCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519  
Db 514 AGCAAAATGTTTCTTTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 573  
QY 520 GTTTTATACAGTAATGA-----CAATGCTGATGCTTCCATTTTCCCGCC 570  
Db 574 TTATACAGCAATATCAAGAGGAATCCGCAATGCTGCTGCTGCTGCTGCTGCTGCTG 633  
QY 571 TACCTAGAAACATCAATGAAGCATTTAAATGCTGATGCTGCTGCTGCTGCTGCTG 630  
Db 634 GATGAGAGCAACCAACTGAAGTCACTGCTTGAAGGCTGCTGCTGCTGCTGCTGCTG 693  
QY 631 GTACCTTTCTTATGAGGCTGCTGCTGCTTATACAGCAAGGACCTGATGAAGATG 690  
Db 694 CTTCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 753  
QY 691 CCAAACTTAAATATCTGACCCCTAAAGTCTGCTGACAGTCTGTTATGTTTCAAT 750

Db 754 AAGAAGTCTTCACAGCAAAAGCCCTAAAGTACACACTGCTGACCGCTTTGTC 813  
 QY 751 GTCACCTAACCTCTTATACATGTCAGTTCTGCGAGCCATAGACATCATCTTACC 810  
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 QY 811 CTGATCACACCTGCAACATAGAGCAAGCAAGCATGCGCATCCAGTCAAGAAAGC 870  
 Db 874 TTCACTCTCAACCTGCGCTTTCACCAACATGACATCTGCTTCCAGGTACCCAGAC 933  
 QY 871 ATGCACTCTTTCACAGCTGCTCAACCCAACTCTTATGTTTTATGGAAGCATCTTTC 930  
 Db 934 ATGCGCTCTTTCACAGCTGCTGCAACCTGCTTCTATGTTTTGTTGGTGAAGATTC 993  
 QY 931 AAAAAGTCTTATGAAAGTGCGCAAGAAATATGGGTCTGAG 974  
 Db 994 CGCCGGATCTCGTGAAGAAACCTGGAAGAACTGGGTTCATCAG 1037

RESULT 10  
 ; US-09-903-377-1  
 ; Sequence 1, Application US/09903377  
 ; Patent No. US20020116727A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Allen, Keith D.  
 ; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHEMOKINE  
 ; FILE REFERENCE: R-365  
 ; CURRENT APPLICATION NUMBER: US/09/903,377  
 ; PRIOR FILING DATE: 2001-07-10  
 ; PRIOR APPLICATION NUMBER: US 60/217,255  
 ; PRIOR FILING DATE: 2000-07-10  
 ; PRIOR APPLICATION NUMBER: US 60/221,483  
 ; PRIOR FILING DATE: 2000-07-27  
 ; PRIOR APPLICATION NUMBER: US 60/262,113  
 ; PRIOR FILING DATE: 2001-01-16  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 2577  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Targeting vector  
 ; US-09-903-377-1

Query Match 14.4%; Score 164.8; DB 10; Length 2577;  
 Best Local Similarity 51.0%; Pred. No. 6.2e-35;  
 Matches 481; Conservative 0; Mismatches 442; Indels 21; Gaps 3;  
 QY 52 ATGAAATGGCACTTATGACTACAGTCAATATGAACTGATCTGATCAAGAAAGATGTCAGA 111  
 Db 94 ATGGAAGACTACGTTAATCACTTCACTGACTTCTGAGAGAAACAATGTCAG 153  
 QY 112 GAATTTGCAAAAGTTTCTCCCTGATTCCTACAAATAGTTTTGCTCATTTGACCTTGA 171  
 Db 154 CAGTTTGCAAGCAATTTCTCCACCTGTAATGCTGCTGTGTATATGCTGGGCTTG 213  
 QY 172 GGCATTTCCATGCTAGTGGCAATTTATGCTTATTAACAAGAAACAGAAACCAAGT 231  
 Db 214 GGCACAGCTTGTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 273  
 QY 232 GTGTACATCTGTAATTTGGTGTAGAGATTTATCTCTTCTATTCCTGCTGCTTTTGG 291  
 Db 274 ATGTTCCTTTGAAATTTGGCAATTTGCTGACCTCTCTTCTTCTGCTGCTTCTGCTG 333  
 QY 292 GCTGTTATGCACTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 351  
 Db 334 GCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 393  
 QY 352 TTGTACACACTAACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 411  
 Db 394 ATGTACAGATGAATCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453

QY 412 TATGTGACAGTAATAAGTCCCGAG-----CCATACAGAGTGGAAAAACAT----- 460  
 Db 454 TACATTTGCCATTTGCCAGGCCCATAGAGACATATCTTGAGAGGAGAAAAAGCTTTGTAC 513  
 QY 461 -GCTGATCATCTGTTTCTGTGTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519  
 Db 514 AGCAAAATGTTGCTTTTCCATCTGGGATTTGGAGAGCTGCTCTGTGATCCAGAAATTC 573  
 QY 520 GTTTTTTATACAGTAATAA-----CAANGCTAGGTGATTCCTCATTTTCCCGCGC 570  
 Db 574 TTATACAGCAAAATCAAGAGAAATCCGCAATTTGCTATTTGACATGATTTTACCTTAC 633  
 QY 571 TACCTAGAAACATCAATGAAAGATTTCAATAGCTAGAGATCTGATTTGATTTGTA 630  
 Db 634 GATGAGAGACCAAACTGAAGTACAGTGTCTGACCTGAAAGTCAATCTGGGGTCTTC 693  
 QY 631 GTACCTTTCTTATTTATGCGGGTGTCTTCTTATACAGCAAGACATCTGAAAGATG 690  
 Db 694 CTTCCTTGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 753  
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 QY 751 GTCACCTAACCTCTTATACATTTGCAAGTTCTGCGAGCCATAGACATCATCTTACC 810  
 Db 814 TTGCTCAGTTTCCCTACACACTGATTTGTTGGTGCAGACATGACCGCTATGCGATG 873  
 QY 811 CTGATCACACCTGCAACATAGAGCAAGCAAGCATGCGCATCCAGTCAAGAAAGC 870  
 Db 874 TTCACTCTCAACCTGCGCTTTCACCAACATGACATCTGCTTCCAGGTACCCAGAC 933  
 QY 871 ATGCACTCTTTCACAGCTGCTCAACCCAACTCTTATGTTTTATGGAAGCATCTTTC 930  
 Db 934 ATGCGCTCTTTCACAGCTGCTGCAACCTGCTTCTATGTTTTGTTGGTGAAGATTC 993  
 QY 931 AAAAAGTCTTATGAAAGTGCGCAAGAAATATGGGTCTGAG 974  
 Db 994 CGCCGGATCTCGTGAAGAAACCTGGAAGAACTGGGTTCATCAG 1037

RESULT 11  
 ; US-09-952-385-1  
 ; Sequence 1, Application US/09952385  
 ; Patent No. US20020119504A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Andrew, David P.  
 ; APPLICANT: Zabel, Brian A.  
 ; APPLICANT: Ponath, Paul D.  
 ; TITLE OF INVENTION: ANTI-GRP-9-6 ANTIBODIES AND METHODS OF  
 ; FILE REFERENCE: LKS98-16  
 ; CURRENT APPLICATION NUMBER: US/09/952,385  
 ; PRIOR FILING DATE: 2001-09-13  
 ; PRIOR APPLICATION NUMBER: 09/266,464  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 2577  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (58)...(1131)  
 ; US-09-952-385-1

Query Match 14.4%; Score 164.8; DB 10; Length 2577;  
 Best Local Similarity 51.0%; Pred. No. 6.2e-35;  
 Matches 481; Conservative 0; Mismatches 442; Indels 21; Gaps 3;  
 QY 52 ATGAAATGGCACTTATGACTACAGTCAATATGAACTGATCTGATCAAGAAAGATGTCAGA 111

Db 94 ATGGAAGCTACGTTAACTTCACTCACTGACTTCTACTGTGAGAAAACAAAGTCAGG 153  
Qy 112 GAATTTGCAAAAGTTTCTCTCCGTATCTCTCAACATAGTTTTCGTATGGAATTGCA 171  
Db 154 CAGTTTGAGACCAATTCCTCCACCCCTTGTATCGGTCTGTTTCATCGTGGGCGCTTG 213  
Qy 172 GGCATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 231  
Db 214 GGCACAGCTCTTGTATCTTGTCTACTGTACTGTAACAGAGAGAGAGAGAGAGAGAG 273  
Qy 232 GTGATACCTCTGAATTTGGCTGAGACATTTACTCTCTTATCTACTCTCTCTTTTG 291  
Db 274 ATGTTCTCTTTGAATTTGGCAATTTGCACTCTCTCTCTCTCTCTCTCTCTCTCTG 333  
Qy 292 GCTGTATGAGATTTCAAGGTGGGTTTGAAGAAAATATATGTCAAATATATCTTACCC 351  
Db 334 GCAATGCTGCTGTGACGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 393  
Qy 352 TTGTACACACTAAATCTTGTCTGTGAGATGAGATTTCTGCTGTATCAGCATAGACAGA 411  
Db 394 ATGTACAGATGAACTTCTCAAGCTGTGTGTCTGTATCATGTGATCAGAGGAGAGAG 453  
Qy 412 TATGTGCACTAACTAAAGTCCAG-----CCAATCAGAGTGGGAAACCAT----- 460  
Db 454 TACATTCGATTCGCCAGGACCATGAGAGACATCTTGAAGGAGAGAGAGAGAGAGAG 513  
Qy 461 -GCTGATCATCTGTTCTGTGTCTGTGATGAGTGGTCCATCTTGTGAGACATACCCAGCTG 519  
Db 514 AGCAAAATGTTGCTTCACTCATCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGATC 573  
Qy 520 GTTTTATACAGTAATGA-----CAATGCTAGTGCATTTCCATTTTCCCGCG 570  
Db 574 TTATACAGCCAAATCAAGAGAGAGATCCGGCATTTGTATCTGACACATGTTTACCTAGC 633  
Qy 571 TACCTAGAACATCAATGAAGAGATTAATCAAAATGCTAAGATCTGATGATGATTTGA 630  
Db 634 GATGAGAGACCAAACTGAGATGAGTGTGTGACCTGAGAGAGAGAGAGAGAGAGAGATC 693  
Qy 631 GTACCTCTCTTATTTATGAGGAGTGTGCTACTTTATCAACAGAGAGAGAGAGAGAGATG 690  
Db 694 CTTCCTCTCTGTCATAGGCTGTGCTATACATCAATCAATCAACCTGATACAGAGCC 753  
Qy 691 CCAAACTAAATATCTCGACCCCTAAAGTTCTGCTCAAGTCTTATAGTTTTCAT 750  
Db 754 AAGAAGCTTCCAAAGCAAAAGCCCTAAAGTGAACATCTGCTGAGCCGCTTTGTC 813  
Qy 751 GTCACTCACTGCTTATTAACATTTGCAAGTTCTGCCGAGCCATAGACATCACTCTCC 810  
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Qy 811 CTGATCAGAGCTGACATGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870  
Db 874 TTCACTCTCACTGTGCGCTTTCACCAACATTTGATCTTCCAGGTACCCAGACC 933  
Qy 871 ATGCACTCTTTCACAGCTGCTCAACCCATCTTATGTTTATAGGAGCATCTTTC 930  
Db 934 ATGCGCTTCTTCCACAGATGCTGAAACCTGTCTATGTTTGTGGGTGAGAGATTC 993  
Qy 931 AAAAATCACTTATGAAG 974  
Db 994 CGCGGATCTCGTGAAG 1037

RESULT 12  
US-10-000-759A-1

; Sequence 1, Application US/10000759A  
; Patent No. US2002014191A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew, David P.  
; APPLICANT: Zabel, Brian A.  
; APPLICANT: Bonath, Paul D.  
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF

; TITLE OF INVENTION: IDENTIFYING MODULATORS OF GPR-9-6 FUNCTION  
; FILE REFERENCE: 1855.1064-003  
; CURRENT APPLICATION NUMBER: US/10/000,759A  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US/09/522,752  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: US 09/266,464  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2577  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (58) ... (1131)  
US-10-000-759A-1

Query Match 14.4%; Score 164.8; DB 12; Length 2577;  
Best Local Similarity 51.0%; Pred. No. 6.2e-35; Indels 21; Gaps 3;  
Matches 481; Conservative 0; Mismatches 442;

Qy 52 ATGAATGGCACTTATGACTACAGTCAATATGATCTGTATCAAGAAAGAGAGAGAGATGTCAGA 111  
Db 94 ATGGAAGCTACGTTAACTTCACTCACTGACTTCTACTGTGAGAAAACAAAGTCAGG 153  
Qy 112 GAATTTGCAAAAGTTTCTCTCCGTATCTCTCAACATAGTTTTCGTATGGAATTGCA 171  
Db 154 CAGTTTGAGACCAATTCCTCCACCCCTTGTATCGGTCTGTTTCATCGTGGGCGCTTG 213  
Qy 172 GGCATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 231  
Db 214 GGCACAGCTCTTGTATCTTGTCTACTGTACTGTAACAGAGAGAGAGAGAGAGAGAGAG 273  
Qy 232 GTGATACCTCTGAATTTGGCTGAGACATTTACTCTCTTATCTACTCTCTCTTTTG 291  
Db 274 ATGTTCTCTTTGAATTTGGCAATTTGCACTCTCTCTCTCTCTCTCTCTCTCTCTG 333  
Qy 292 GCTGTATGAGATTTCAAGGTGGGTTTGAAGAAAATATATGTCAAATATATCTTACCC 351  
Db 334 GCAATGCTGCTGTGACGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 393  
Qy 352 TTGTACACACTAAATCTTGTCTGTGAGATGAGATTTCTGCTGTATCAGCATAGACAGA 411  
Db 394 ATGTACAGATGAACTTCTCAAGCTGTGTGTCTGTATCATGTGATCAGAGGAGAGAG 453  
Qy 412 TATGTGCACTAACTAAAGTCCAG-----CCAATCAGAGTGGGAAACCAT----- 460  
Db 454 TACATTCGATTCGCCAGGACCATGAGAGACATCTTGAAGGAGAGAGAGAGAGAGAGATC 513  
Qy 461 -GCTGATCATCTGTTCTGTGTCTGTGATGAGTGGTCCATCTTGTGAGACATACCCAGCTG 519  
Db 514 AGCAAAATGTTGCTTCACTCATCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 573  
Qy 520 GTTTTATACAGTAATGA-----CAATGCTAGTGCATTTCCATTTTCCCGCG 570  
Db 574 TTATACAGCCAAATCAAGAGAGAGATCCGGCATTTGTATCTGACACATGTTTACCTAGC 633  
Qy 571 TACCTAGAACATCAATGAAGAGATTAATCAAAATGCTAAGATCTGATGATGATTTGA 630  
Db 634 GATGAGAGACCAAACTGAGATGAGTGTGTGACCTGAGAGAGAGAGAGAGAGAGAGATC 693  
Qy 631 GTACCTCTCTTATTTATGAGGAGTGTGCTACTTTATCAACAGAGAGAGAGAGAGAGATG 690  
Db 694 CTTCCTCTCTGTCATAGGCTGTGCTATACATCAATCAATCAACCTGATACAGAGCC 753  
Qy 691 CCAAACTAAATATCTCGACCCCTAAAGTTCTGCTCAAGTCTTATAGTTTTCAT 750  
Db 754 AAGAAGCTTCCAAAGCAAAAGCCCTAAAGTGAACATCTGCTGAGCCGCTTTGTC 813  
Qy 751 GTCACTCACTGCTTATTAACATTTGCAAGTTCTGCCGAGCCATAGACATCACTCTCC 810

Db 814 TTGTCACGTTTCCCTACACTGCAATTTTGTGGGACAGACCATTAAGCGCTATGCCATG 873  
 QY 811 CTGATACCACTGCAACATGAGAAACGATGACATGCCATCCAGTCAAGAAAGC 870  
 Db 874 TTCAATCTCAACTGCGCGTTTCCACCAACATGACATCTGCTTCCAGGTCCACAGCC 933  
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 Db 934 ATGCGCTTCTTCCACAGTGGCTGACACCTGTTCTATGTTTTTGGGGAGAGATTC 993  
 QY 931 AAAAAGTACGTTATGAAGTGGCCAGAAATATAGGTCCTGAG 974  
 Db 994 CGCGGAGATCTCGTGAAGAAACCTGGAAGAACTGGGTGCATCAG 1037

RESULT 13  
 US-09-880-107-2143  
 ; Sequence 2143, Application US/09880107  
 ; Patent No. US20020142981A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Horne, Darci T.  
 ; APPLICANT: Vockley, Joseph G.  
 ; APPLICANT: Scheif, Uwe  
 ; APPLICANT: Gene Logic, Inc.  
 ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
 ; FILE REFERENCE: 44921-5028-WO  
 ; CURRENT APPLICATION NUMBER: US/09/880,107  
 ; CURRENT FILING DATE: 2001-06-14  
 ; PRIOR APPLICATION NUMBER: US 60/211,379  
 ; PRIOR FILING DATE: 2000-06-14  
 ; PRIOR APPLICATION NUMBER: US 60/237,054  
 ; PRIOR FILING DATE: 2000-10-02  
 ; NUMBER OF SEQ ID NOS: 3950  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 2143  
 ; LENGTH: 1670  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE: Homo sapiens  
 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L06797  
 US-09-880-107-2143

Query Match 13.4%; Score 153.6; DB 10; Length 1670;  
 Best Local Similarity 49.6%; Pred. No. 5.8e-32;  
 Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;  
 QY 90 CTGATCAAAAGAGATGTCAGAAATTGCAAAAGTTTCTCCTGTAATTCCTCAAT 149  
 Db 153 CTGTTCCGTGAAGAAATGCTAATTTCAATAAAATCTTCCGACCACCATCTCAT 212  
 QY 150 ACTTTTCCGATTCGACCTGAGGCAATTCAGAGTGGCAATTTATGCTATTACAA 209  
 Db 213 CATCTTCTTAACGCGATGTCGAGATGATGATGTCATCTGTCATGAGGTTACCAAA 272  
 QY 210 GAAACAGAGAACCAAAACAGATGTGTACATCTGAAATTTGGCTGAGCAGATTATCTCT 269  
 Db 273 GAAACAGAGAGATGTCAGCAAGAGAGGCTGACCTGTGACAGCGCACTCTCTT 332  
 QY 270 TCTATTCACTGCTCTTTTGGGCTGTATAGCAGTTCATAGGTTGGGTTTGGGAAAT 329  
 Db 333 TGTCAATCAGGCTTCTTCTGCGCAGTGTATGCGGCAAACTGGTACTTTGGAACTT 392  
 QY 330 AATGCAAAATTAATTCAGCCTGTGACACACTAACTTGTCTCGAATGCAATTTCT 389  
 Db 393 CCTATGCAAGGAGTCATATGTATCTACACAGTCAACCTCTACAGAGTGTCTCATCT 452  
 QY 390 GAGCTTATCAGATACAGATATGTGGCAGTAACATAAGTCCCAAGCAATCAGAGT 449  
 Db 453 GGCCTTCATCAGTCTGAGCGGTAACCTGCGCATCTGCAAGCAACAGTCAAGAGCC 512  
 QY 450 GGGAAAAA-----CATGCGATCATCTGTTCTGTCGTGGATGGCGCATCTGCT 503  
 Db 513 AAGGAAGCTGTTGGTGAAGAAAGGTGTATATGTTGGCGTCTGATCTCTGCTCTGCT 572

QY 504 GAGCATACCCAGCTGTTTTTTATACAGTAATGACAATGCTAGTGCATTCCTCAATTT 563  
 Db 573 GACTATTCCTCCAGCTTCATCTTTTCCAGAGTCAAGTGAAGGAGATGACAGATATATCTGGA 632  
 QY 564 CCCCCGTAACCTAGGAACATCAATGAAGCATTTGATTCAAATGCTAGAGATCTGCATTGG 623  
 Db 633 CGGCTTCTACCCCAATGACTTGTGGTGTGTGTGTTCCAGTTTCAGCATCATGATGTTGG 692  
 QY 624 ATTGTAGTACCTTTCTTATATAGGGGGTGTGCTACTTATACAGCAAGACATCAT 683  
 Db 693 CTTATCTGCTGCTGATATGTCATCTGCTCTCTATTTGATTCATCTCAAGTGTGC 752  
 QY 684 GAAGATGCCAAACATTAATAATCTGACCCCTAAAGTTTCTGCTACAGTCTTATAGT 743  
 Db 753 ACAGTCCAAAGGGCACAGAGAGGCAAGGCCCTCAAGACACAGTATCTCATCTGTGC 812  
 QY 744 TTTGATTTGCTACCACTGCTCTTATTAACATTTGCAAGTTCTGCGCAGCATGACATCAT 803  
 Db 813 TTTCTTGCGCTGTGTGGCTGCTTACTACATTTGGATCAGATCAGACTCTTCACTCTCT 872  
 QY 804 CTACTCCCTGATCACCAGCTGCAACATGAGCAAAAGCATGACATGCGCATCCCAAGTCA 863  
 Db 873 GGAATCATCAGCAAGGCTGTGATTTAGAAACAATGTCACAAAGTGAATTTCCATCAG 932  
 QY 864 AGAAGCATGCACTCTTTCACAGCTGCTCAACCCATCTTATGTTTATGAGGAGC 923  
 Db 933 CGAGGCGCTGATCTTCTTTCACATGTTGTCTGAACCCCATCTCTATGCTTCTTGGAGC 992  
 QY 924 ATCTTTCAAAACT 937  
 Db 993 CAAATTTAAACCT 1006

RESULT 14  
 US-09-104-063-3  
 ; Sequence 3, Application US/09104063  
 ; Patent No. US20020168356A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lee, James  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Pf4A Receptors  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; City: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/104,063  
 ; FILING DATE: 24-June-1998  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/701265  
 ; FILING DATE: 22-AUG-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/664228  
 ; FILING DATE: 06-JUN-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/076093  
 ; FILING DATE: 11-JUN-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/810782  
 ; FILING DATE: 19-DEC-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659  
 REFERENCE/DOCKET NUMBER: P0706P2C2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-5530  
 TELEFAX: 415/952-9881  
 TELEEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1737 base pairs  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 US-09-104-063-3

Query Match 13.4%; Score 153.6; DB 9; Length 1737;  
 Best Local Similarity 49.6%; Pred. No. 5.9e-32;  
 Matches 424; Conservative 0; Mismatches 424; Indels 6; Gaps 1;

90 CTGTATCAAGAGATGTCAGAGATTTGCAAAAGTTTCTCCCTGATTTCTCACAAT 149  
 171 CTGTTCCGTGAAGAAATGCTAATTTCAATAAATCTCTGCGCAACATCTACTCAT 230  
 150 AGTTTTCGTCATTTGACTGACGCAATTCATGATGAGCAATTTATGCTATTACA 209  
 231 CATCTTCTTAATCTGCAATTTGGGCAATGATGTGTCATCTGTCATGGGTTACAGAA 230  
 210 GAACAGAGAACCAAAACAGATGTCATCTGATTTGGCTGTACAGATTTACTCCT 269  
 291 GAACCTGAGAGCATGACGAGCAAGTACAGCTCACTGTCAGTGGCCGACCTCTCTT 350  
 270 TCTATTCATCTGCTTTTGGGCTGTTAATGCAATTCATGGTGGGTTTAAAGAAAT 329  
 351 TGTATCATCGCTTCCCTCTGCGGAGTTGATGCGTGGCAACCTGTACTTTGGAACTT 410  
 330 AATGTGCAAAATTAATCTGACCTGTGTACACTAACTTTGTCTTGGAATGCAATTTCT 389  
 411 CTTATGCAAGGCAATTCATCTATCTACAGTCAACCTCTACAGAGTGTCTTCACTCT 470  
 390 GGCCTTATCAGATPAGACATATGTCAGTAATTAAGTCCCGCAATCAGAGAT 449  
 471 GGCCTTATCAGTGTGAGCCGCTACCTGCGCATCTGCAAGCAACAGTCAAGAGCC 530  
 450 GGGAAAC-----CATGCTGATCATCTGTTCTGTGTGTGATGAGTGGCTGCCATCTTGTCT 503  
 531 AAGGAAGCTGTGCTGAAAAAGGTGATCTATGTTGGGCTGTGATCTCCCTCTGCT 590  
 504 GAGATACCCAGCTGCTGTTTATACAGTAATGACATGCTAGTGTCTCCCATTTT 563  
 591 GACTATTTCCGACTTCACTTTTGGCAAGTCAAGTGAAGAGATGACAGATATATCTGTGA 650  
 564 CCCCCTACCTAGAGACATCAATGAAAGCATTTGATCAATGCTAGAGATGCAATTTG 623  
 651 CCGCTTACCCCAATGACTTGTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 710  
 624 ATTGTGATACCTTTCTTATATGAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 663  
 711 CTTATCTGTGCTGTATTTGATCTGCTGCTATTTGATATATCTCAAGCTGTC 770  
 684 GAAGATGCCAAACATTAATATCTGACCCCTAAAGTTCTGCTCAAGCTCTTATAGT 743  
 771 ACACCTCAAGGGCCACAGAGAGGCAAGGCCCTCAAGACAGTCACTCTCTGAG 830  
 744 TTTTATGTACATCACTGCTTATTAACATTTGCAAGTTTGTGCGAGCCATACATCAT 803  
 831 TTTTCTGCTGT 890  
 804 CTACTCCCTATATCAACGCTGCAACATGAGCAAAAGCATGAGATGCAATCCCACTGAC 863  
 891 GGAATATCAAGAGAGGAGTGTGAGTTGAGAAACATGTCACAGAGTGTATTCATCAC 950  
 864 AGAAGATGCACTCTTTTACAGCTGCTCAACCCCAATCTTTATGTTTATGAGGAGC 923  
 951 CGAGGCTTGTGCTTTTCACTGTGTGTGTGAACCCCATCTCTATGCTTTCTTGTGAGCC 1010

QY 924 ATCTTCAAAACCT 937  
 DB 1011 CAAATTTAAACCT 1024

RESULT 15  
 US-09-870-759-143  
 Sequence 143, Application US/09870759  
 Patent No. US20020177551A1  
 GENERAL INFORMATION:  
 APPLICANT: TERMAN, David S  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
 FILE REFERENCE: 870759  
 CURRENT APPLICATION NUMBER: US/09/870,759  
 CURRENT FILING DATE: 2002-01-14  
 PRIOR APPLICATION NUMBER: US 60/208,128  
 PRIOR FILING DATE: 2000-05-30  
 NUMBER OF SEQ ID NOS: 166  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 143  
 LENGTH: 1102  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (44)..(1102)  
 OTHER INFORMATION:  
 US-09-870-759-143

Query Match 13.3%; Score 152; DB 9; Length 1102;  
 Best Local Similarity 49.5%; Pred. No. 1.3e-31;  
 Matches 423; Conservative 0; Mismatches 425; Indels 6; Gaps 1;

90 CTGTATCAAGAGATGTCAGAGATTTGCAAAAGTTTCTCCCTGATTTCTCACAAT 149  
 124 CTGTTCCGTGAAGAAATGCTAATTTCAATAAATCTTCTGCGCAACATCTACTCAT 183  
 150 AGTTTTCGTCATTTGACTGACGCAATTCATGATGAGCAATTTATGCTATTACA 209  
 184 CATCTTCTTAATCTGCAATTTGGGCAATGATGTGTCATCTGTCATGGGTTACAGAA 243  
 210 GAACAGAGAACCAAAACAGATGTCATCTGATTTGGCTGTACAGATTTACTCCT 269  
 244 GAACCTGAGAGCATGACGAGCAAGTACAGCTCACTGTCATGGGCGACCTCTCTT 303  
 270 TCTATTCATCTGCTTTTGGGCTGTTAATGCAATTCAGTGTGAGGTTTAAAGAAAT 329  
 304 TGTATCATCGCTTCCCTCTGCGGAGTTGATGCGTGGCAAACTGTATTTGGAACTT 363  
 330 AATGTGCAAAATTAATCTGACCTGTGTACAGCTTAACTTTGTCTGGAATGCAATTTCT 389  
 364 CTTATGCAAGGCACTGATCTATCTATACAGTCAACCTCTACAGCAAGTGTCTCATCT 423  
 390 GGCCTTATCAGATPAGACATATGTCAGTAATTAAGTCCCGCAATCAGAGAT 449  
 424 GGCCTTATCAGTGTGAGCCGCTACCTGCGCATTTGTCAGGCCAACAGTCAAGAGCC 483  
 450 GGGAAAC-----CATGCTGATCATCTGTTCTGTGTGTGATGAGTGGCTGCCATCTTGTCT 503  
 484 AAGGAAGCTGTGCTGAAAAAGGTGATCTATGTTGGGCTGTGATCTCCCTGCTCTGCT 543  
 504 GAGCATACCCAGCGGCTTTTATACAGTAATGACATGCTAGTGTGATTTCCCATTTT 563  
 544 GACTATTTCCGACTTCACTTTTGGCAAGCTGAGGAGAGATGACAGATATATCTGTGA 603  
 564 CCCCCTACCTAGAGACATCAATGAAAGCATTTGATTAATGCTAGAGATCTGCAATTTG 623  
 604 CCGCTTACCCCAATGACTTGTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 663  
 624 ATTGTGATACCTTTCTTATATGAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 683  
 664 CTTATCTGCTGTGTATGTGTCATCTGCTGCTATTTGATATATCATCTTCAAGCTGTC 723



QY 684 GAGATGCCAATTAATAATATCTGACCCCTAAAGTTGCTCACAGTGGTAAAT 743  
 Db 724 AACCTCCAAAGGCGCACGAGAGCGAGCCCTCAAGACCAATATCAATCCCATCTG 783  
 QY 744 TTTCATGTCACCTCACTGCTTATTAATGTCAGTTCGCGGAGCCATAGACATCAT 803  
 Db 784 TTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843  
 QY 804 CTACTCCCTGATCAGCTGCAACATGAGCAAGCATGACATGCGCATTCAGTCA 863  
 Db 844 GGAATATCATCAAGCAAGGCTGAGTTGAGAACTGTCAGCAAGTGGATTTCCATC 903  
 QY 864 AGAAGCATGCACTCTTTCACAGCTGCTCAACCAATCTTTATGTTTATGGAGC 923  
 Db 904 CAGGCGCTTACGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 963  
 QY 924 ATCTTCAAAACT 937  
 Db 964 CAATTTAAACT 977

RESULT 16  
 US-09-789-482-3  
 ; Sequence 3, Application US/09789482  
 ; Patent No. US20020054875A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koch, Alisa E.  
 ; APPLICANT: Ruth, Jeffrey H.  
 ; APPLICANT: Rottman, James B.  
 ; TITLE OF INVENTION: Therapeutic Methods That Target  
 ; FILE REFERENCE: 3238.1000-003  
 ; CURRENT APPLICATION NUMBER: US/09/789,482  
 ; PRIOR FILING DATE: 2001-02-20  
 ; PRIOR APPLICATION NUMBER: US 60/183,568  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1487  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (46)...(1113)  
 US-09-789-482-3

Query Match 12.5%; Score 143; DB 10; Length 1487;  
 Best Local Similarity 49.6%; Pred. No. 4.3e-29;  
 Matches 455; Conservative 0; Mismatches 450; Indels 12; Gaps 3;  
 QY 51 AATGAATGCACTTATGACTACATCAATATGAATGATGATCAAGAGATGTCAG 110  
 Db 66 AGTACAGAAAATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 125  
 QY 111 AGAATTTGCAAAAGTTTCTCCCTGATTCCTCAAGATGTTTGTGATGATGATG 170  
 Db 126 GGTCTTTGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185  
 QY 171 AGGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 230  
 Db 186 GGGAAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 245  
 QY 231 TGTGTACATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 290  
 Db 246 CATTTACCTCTGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 305  
 QY 291 GGGCTTAAATGCACTTATGATGATGATGATGATGATGATGATGATGATGATG 350  
 Db 306 GACTCACAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 365  
 QY 351 CTGTACACTAACTTTGCTGTGATGATGATGATGATGATGATGATGATGATGAT 410

Db 366 CTTCCTTCATGAGCTTTTGGAGCAATTTCTTACATCCCTGATCAAGATTATAG 425  
 QY 411 ATATGAGCAGTAACTAAAGTCCAGC-----CAATAGAGTGGGAAAACATGCTG 464  
 Db 426 GTACCTGACCATGCTCTGCGCCCACTCAATGACAAACCCGAGCTGAGATGCG 485  
 QY 465 GATCATCTGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 524  
 Db 486 CACCATAGCTTGGGCTGTGGGACAGCATTTTGGGAGCAGCCCAAGTTCAATGTT 545  
 QY 525 TTATACGTAAATGACATGCTAGTGCATTTTCCCGGCTACCTAGAACATC 584  
 Db 546 CACAAAGCAGAAAAGT---AATGCTTGTGACTACCCGAGTCTTACAGAAAT 602  
 QY 585 AATGAAGCACTTATGATCAATGCTAGAGATCTGATGATTTGTAGTACCTTTCT 644  
 Db 603 CTGCGCCCTGCTCGCATGTGAGAAACAAATTTCTGGCTTCTACTCCCTGCTCAT 662  
 QY 645 TATGGGGTGTGCTTATATCAAGACAGACATCATAGATGCAAACTTAAAT 704  
 Db 663 TATGATTTATGCTACTTCAAGATCATCCAGAGCTGTTTCTGCAAGAACAGAA 722  
 QY 705 ATCTGACCCCTAAAGTGTGCTCAAGCTGCTTATAGTTTCACTGACCTGAC 764  
 Db 723 AGCCAAAGCATTAACTGATCTTCTGTGTGATGATGATTTCTCTTCTGAGAC 782  
 QY 765 TTATACATTTGCAAGTTCGCGAGCAGCATAGACATCATCTCTCTGATCAAGCTG 824  
 Db 783 CTACAC---GTATGATTTTCTGAGAGAGCTTAAGCTTATAGACTCTTCTCCAGTTG 839  
 QY 825 CAACATGAGCAAGCATGATGATGATGATGATGATGATGATGATGATGATGAT 884  
 Db 840 TGACATGAGGAAGATCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899  
 QY 885 CAGTGTCTTCAACCATCTTATGTTTATGAGGAGCATCTTCAAAACTAGTTAT 944  
 Db 900 TTGTTGCTGATCTCTCTCATATGATTTGCTGGGAGAAAGTTCAAGAAATACCTT 959  
 QY 945 GAAATGGCCAAAGAT 961  
 Db 960 CCACCTGATGGAAT 976

RESULT 17  
 US-09-789-486-3  
 ; Sequence 3, Application US/09789486  
 ; Patent No. US2002005456A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koch, Alisa E.  
 ; TITLE OF INVENTION: Therapeutic Methods That Target  
 ; FILE REFERENCE: 3238.1000-004  
 ; CURRENT APPLICATION NUMBER: US/09/789,486  
 ; PRIOR FILING DATE: 2001-02-20  
 ; PRIOR APPLICATION NUMBER: US 60/183,568  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1487  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (46)...(1113)  
 US-09-789-486-3

Query Match 12.5%; Score 143; DB 10; Length 1487;  
 Best Local Similarity 49.6%; Pred. No. 4.3e-29;  
 Matches 455; Conservative 0; Mismatches 450; Indels 12; Gaps 3;  
 QY 51 AATGAATGCACTTATGACTACATCAATATGAATGATGATCAAGAGATGTCAG 110

Db 66 AGTACAGAAAAGCTTGAAGTATGATGCTGAGGCGCTGTTATATGTTGGGACATCGT 125  
Qy 111 AGAATTTGCAAAAGTTTCCCTCCCTGATTTCTCAACAATAGTTTTCGTCATTGACATTGC 170  
Db 126 GGTCTTTGGGACTGTGTTCCCTGATATTTCTACTCCCTCATCTTTTGCATTTGGCTGGT 185  
Qy 171 AGCAATTCATGAGTATGAGCAATTTATGCTATTACAGAAACAGAAACCAAAAGCA 230  
Db 186 GGGAAATTTGTTGGTATGTTTGGCTTACCAACAGCAAGAGCCCAAGAGTGTACCGA 245  
Qy 231 TGTGTACATCTGATTTGGCTGATAGCAATTTACTCTTCTATCTACTGCTTTTGG 290  
Db 246 CATTTACCTCTGAAACCTGGCTTGTCTGATCTGCTGTTGTATGACCACTTTGCCCTTCTG 305  
Qy 291 GGTCTTTATGACATTTCTGAGTGGTGGTATTAGGAAATATATGCAAAATTAATTAGC 350  
Db 306 GACTCACTATTTGATTAATGAAAGGGCTTCCACAAATGCGCAATGCAATTTCACTACCGC 365  
Qy 351 CTGTGACACATTAACCTTTGCTCTGAAATGCAATTTCTGGCTTGTATCAGATAGACAG 410  
Db 366 CTTCTTTCTTCACTGGCTTTTGTGAGACATATTTCTTATCAGCGTCACTCAGCATTTAG 425  
Qy 411 ATATGTGGCACTAACTAAAGTCCCGAC-----CAATCAGAGTGGGAAACCATGCTG 464  
Db 426 GTACCTGGCCATCGTCTGGCCGCAACTCCATGACACACCGGACGTCAGATGGCGT 485  
Qy 465 GATCATCTGTTCTGTGTCGATAGTGGCTGATCTGCTGATGAGTATACCCAGCTGGTTT 524  
Db 486 CACCATCAGCTAGGCGCTGGGAGAGAGCCATTTTGTGGAGACACCCAGTTCATGTT 545  
Qy 525 TTATACAGTAATGACATGCTAGTGCATTTCCATTTTCCCGGCTACTAGGAACATC 584  
Db 546 CACAAGAGAAAATAATG---AATGCTTTGGTACTACCCGAGGTCTTTGACGAAAT 602  
Qy 585 AATGAAGCATTTGATTAATGCTAGAGATCTGATTTGATTTGATTTGATTTGATTTGAT 644  
Db 603 CTGGCCCGTGTCTCGCAATGTGAAACAAATTTTCTGGCTCTACTCCCGCTGCTCAT 662  
Qy 645 TATGGGGGTGTACTTTTATCAGAGAGACATGATGAAGTGCAGAAATTAAT 704  
Db 663 TATAGTTATTTGCTACTTCAAGATCATCCAGACGCTTTTCTGCAAGAACCAAGAA 722  
Qy 705 ATCTGACCCCTAAAGTTCTGCTCAGAGTCTGATATTTTATTTTCTGCTCACTGACC 764  
Db 723 AGCCAAAGCATTTAACTGATCTTCTGTGTGATGATGTTTCTCTTCTGACACC 782  
Qy 765 TTATTAATTTGCTAAGTTCTGCGGAGCCATAGACATCATCTTCTCTGATCCAGCTG 824  
Db 783 CTACACAC---GTTATGATTTTCTCGAGAGCGTTAAGCTTATGACTTTTCCAGTTG 839  
Qy 825 CAACATGAGCAAGCATGAGCATCCGATCCAGTCCAGTACAGAAAGCATGSCATCTTTCA 884  
Db 840 TGACATAGAGAAAGATCTGAGGCTGCGCTCAGTGTACAGAGCGGTGATTTAGCCA 899  
Qy 885 CAGTGGCTCAACCATCTTTATTTTATTTTATGAGAGCATCTTTCAAAATACATTTAT 944  
Db 900 TTGTTGCTGAATCTCTCATATGATGATTTTGTGGGAGAAAGTTTCAAGAAATACCTTTA 959  
Qy 945 GAAAGTGGCCAAAGAT 961  
Db 960 CCACCTGTATAGGAAAT 976

RESULT 18  
US-09-954-456-267  
; Sequence 267, Application US/09954456  
; Patent No. US20020115057A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc  
; TITLE OF INVENTION: Sets  
; FILE REFERENCE: 689290-76

; CURRENT APPLICATION NUMBER: US/09/954,456  
; CURRENT FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US/60/233,617  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,052  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,923  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,134  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,637  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US/60/235,638  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US/60/235,711  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,720  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,840  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,863  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 2276  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 267  
; LENGTH: 3100  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-954-456-267

Query Match 12.5%; Score 143; DB 10; Length 3100;  
Best Local Similarity 49.6%; Pred. No. 6.3e-29;  
Matches 455; Conservative 0; Mismatches 450; Indels 12; Gaps 3;

Qy 51 AATGATGGCACTTATGACTACATGATGAACTGATCTGATCAAGAGATGCTAG 110  
Db 108 AGTACAGAAAAGCTTGAAGTATGATGATTTGGCTGAGGCTGTTATATTTGGGACATCGT 167  
Qy 111 AGAATTTGCAAAAGTTTCCCTCCCTGATTTCTGACAAATGTTTTCGTCATTGACATTGC 170  
Db 168 GGTCTTTGGAGTGTGTTCTGCTGCTCATTTTCTACTCGTCACTTTTGCATTTGGCTGGT 227  
Qy 171 AGCAATTCATGAGTATGAGCAATTTATGCTATTACAGAAACAGAAACCAAAAGCA 230  
Db 228 GGGAAATTTGTTGGTATGATTTTGGCTTACCAACAGCAAGAGCCCAAGAGTGTACCGA 287  
Qy 231 TGTGTACATCTGATTTTGGCTGATAGATTTACTCTCTTATTTCACTGCTTTTGG 290  
Db 288 CATTTACCTCTGAAACCTGGCTTGTGATCTGCTGTTGTATGACCACTTTGCGCTTCTG 347  
Qy 291 GGTCTTTATGACATTTCAATGAGTGGTGGTTTTAGGAAATATATGCAAAATTAATTGACG 350  
Db 348 GACTCACTATTTGATTAATGAAAGGGCTTCCACAAAGCCATGTGCAAAATTTCACTACCGC 407  
Qy 351 CTGTGACACATTAACCTTTGCTCTGAAATGCAATTTCTGGCTTGTATCAGATAGACAG 410  
Db 408 CTTCTTTCTTCACTGGCTTTTGTGAGACATATTTCTTATCAGCGTATCAGATTTAG 467  
Qy 411 ATATGTGGCACTAACTAAAGTCCCGAC-----CAATCAGAGTGGGAAACCATGCTG 464  
Db 468 GTACCTGGCCATGCTGCTGGCCGCAACTCCATGACAAACCGGACCGTGCAGATGGCGT 527  
Qy 465 GATCATCTGTTCTGTGTCGATAGTGGCTGATCTTGTGAGATATACCCAGCTGGTTT 524  
Db 528 CACCATCAGCTAGGCGCTGGGAGAGAGCCATTTTGTGGAGACACCCAGTTCATGTT 587  
Qy 525 TTATACAGTAATGACATGCTAGTGCATTTCCATTTTCCCGGCTACTAGGAACATC 584  
Db 588 CACAAGAGAAAATAATG---AATGCTTTGGTACTACCCGAGGTCTCTCCAGAAAT 644  
Qy 585 AATGAAGCATTTGATTAATGCTAGAGATCTGATTTGATTTGATTTGATTTGATTTGAT 644  
Db 645 CTGGCCCGTGTCTCGCAATGTGAAACAAATTTTCTTGTCTTACTCTCCCGCTGCTCAT 704

QY 645 TATGGGGGTGCTACTTATACAGCAAGACACTGAGAGCCAAATTAAAT 704  
 DB 705 TATGGTTATTTGCTACTTACATATATCCAGCGCTTTTCCGCAAGAACCAAGAA 764  
 QY 705 ATCTGACCCCTTAAAGTTCTGCTCAAGTCGTATATGTTTCACTGCTCACTGCTC 764  
 DB 765 AGCCAAAGCATTAACATGATCTCTGCTGCTGATCGTGTCTTCTTCTGCAAC 824  
 QY 765 TTATACATTTGCTCAAGTTCTGCTGCAAGCATATGATCTTACCTGCTGCTGCTG 824  
 DB 825 CTACAAAC---GTTATGATTTTCTGAGAGCGTTTAACTTATGATCTTCTTCCAGTTG 881  
 QY 825 CAACATGAGCAAGCATGAGCATGCTCAAGTCAAGAAAGCATGCTCTTTCA 884  
 DB 882 TGACATGAGAAAGATCTGAGGCTGCGCTCATGTTGATGAGAGGTTGATTTAGCA 941  
 QY 885 CAGCTGCTCAACCCATCTTATGTTTATGAGAGCATCTTTCAAAACATAGTTAT 944  
 DB 942 TTGTTGCTGATCTCTCATCTATGATTTGCTGGGAGAAAGTTCAAGAAATACCTTTA 1001  
 QY 945 GAAAGTGGCCAAAGAT 961  
 DB 1002 CCACCTGTATGGAAAT 1018

## RESULT 19

US-09-954-456-945  
 ; Sequence 945, Application US/09954456  
 ; Patent No. US20020115057A1  
 ; GENERAL INFORMATION:

; APPLICANT: Young, Paul  
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand  
 ; FILE REFERENCE: 689290-76  
 ; CURRENT APPLICATION NUMBER: US/09/954, 456  
 ; CURRENT FILING DATE: 2001-09-18  
 ; PRIOR APPLICATION NUMBER: US/60/233, 617  
 ; PRIOR FILING DATE: 2000-09-18  
 ; PRIOR APPLICATION NUMBER: US/60/234, 052  
 ; PRIOR FILING DATE: 2000-09-20  
 ; PRIOR APPLICATION NUMBER: US/60/234, 923  
 ; PRIOR FILING DATE: 2000-09-25  
 ; PRIOR APPLICATION NUMBER: US/60/235, 134  
 ; PRIOR FILING DATE: 2000-09-25  
 ; PRIOR APPLICATION NUMBER: US/60/235, 637  
 ; PRIOR FILING DATE: 2000-09-26  
 ; PRIOR APPLICATION NUMBER: US/60/235, 638  
 ; PRIOR FILING DATE: 2000-09-26  
 ; PRIOR APPLICATION NUMBER: US/60/235, 711  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: US/60/235, 720  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: US/60/235, 840  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: US/60/235, 863  
 ; PRIOR FILING DATE: 2000-09-27  
 ; NUMBER OF SEQ ID NOS: 2276  
 ; SOFTWARE: Patentin version 3.0  
 ; SEQ ID NO 945  
 ; LENGTH: 3100  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-954-456-945

Query Match 12.5%; Score 143; DB 10; Length 3100;  
 Best Local Similarity 49.6%; Pred. No. 6.3e-29;  
 Matches 455; Conservative 0; Mismatches 450; Indels 12; Gaps 3;

QY 51 AATGAAATGACACTTATGATCAGTCAATATGAACTGATCTGATCAAGAGATGTCAG 110  
 DB 108 AGTGACGAAAACTTGTGATGATGATTTGGCTGAGGCTGTATATATTGGGACATCGT 167

QY 111 AGAATTTGCAAAAGTTTCTCCCTGATTTCTCCACAAATAGTTTTCATTTGACCTTGC 170  
 DB 168 GGTCTTTGGGAACTGTGTCTCTGATATTTTACATCCGATCTTTGCTATTTGGCTGCT 227  
 QY 171 AGCCATTTCCATGATGATGAGCAATTTATGCTATTATCAAGAAACAGAGAACCAAAACAGA 230  
 DB 228 GGGAAATTTGTTGATGATTTTGGCTTCCCTCAACCAAGCAAGAGAGAGTGTACCGA 287  
 QY 231 TGTGATATCTGATATTTGCTGATGAGATTTTACTCTTCTTATTTACTCTGCTTTTGG 290  
 DB 288 CATTTACCTCTGAACTGCGCTTGTCTGATCTGCTGTTTGTAGCACTTTGCCCTTCTG 347  
 QY 291 GGTCTTTATGATGATGATGAGGTTGTTTGGGAAATTAATGTAATTAATTTCACTGAC 350  
 DB 348 GACTCACTATTGATTAAGAAAGGCGCTCAATGCAATGCAATGCAATGCAATGCAATG 407  
 QY 351 CTGTTGACACCTTAACTTTGCTCTGAAATGAGTTTCTGCTGTTATGATGATGACAG 410  
 DB 408 CTCTCTTCTGATGCTGCTTTTGGAAAGCATTTCTTCAACCGTATGATGATGATG 467  
 QY 411 ATATGTCAGTAACTTAAAGTCCGAGC-----CAATGAGAGTGGGAAACCATGCTG 464  
 DB 468 GTACCTGGCATCTGCTGCGCGCAATTCATGAAACCGGACCGTGCAGATGCGCT 527  
 QY 465 GATCATCTGTTTCTGTGTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524  
 DB 528 CACCATGAGCTGAGGCTGCGGACAGCATTTTGTGTCAGCAGCCCAAGTTCATGTT 587  
 QY 525 TTATACGTAATGACAAATGCTAGTGCATTTCCATTTTCCCGCTGCTGAGAAATC 584  
 DB 588 CACAAAGCAAAAGAAATG--AATGCTTGTGATCTACCCGAGGTCTCCAGAAAT 644  
 QY 585 AATGAAAGCATTTGATCAATGCTAGAGATCTGATGATTTGATGATCTTTTCTTAT 644  
 DB 645 CTGGCCGCTGCTCGCAATGTAAGAAATTTCTTGGCTTCTTCTGCTGCTGCTGCT 704  
 QY 645 TATGGGGGTGCTACTTATATCAAGCAAGAGACATCAAGAAATGCAAACTTAAAT 704  
 DB 705 TATGATGATTTGCTACTTCAAGATCAATCCAGAGCTGTTTCTGCAAGAAACCAAGAA 764  
 QY 705 ATCTGACCCCTTAAAGTTCTGCTCAAGTCGTATATGTTTCTATTTGCTCACTGAC 764  
 DB 765 AGCCAAAGCATTAATGATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 824  
 QY 765 TTATACATTTGCTCAAGTTCTGCTGCAAGCATGATCTTCTGCTGCTGCTGCTGCT 824  
 DB 825 CTACAAAC---GTTATGATTTTCTGAGAGCTTAACTTATGATCTTCTTCCAGTTG 881  
 QY 825 CAATATGAGCAAGCATGAGCATGCTGCAAGTCAAGTCAAGAAAGCATGCTCTTTCA 884  
 DB 882 TGACATGAGAAAGATCTGAGGCTGCGCTCAAGTGTGATGAGAGGTTGATTTAGCCA 941  
 QY 885 CAGCTGCTCAACCCATCTTATGTTTATGAGAGCATCTTTCAAAACATAGTTAT 944  
 DB 942 TTGTTGCTGATCTCTCATCTATGATTTGCTGGGAGAAAGTTCAAGAAATACCTTTA 1001  
 QY 945 GAAAGTGGCCAAAGAT 961  
 DB 1002 CCACCTGTATGGAAAT 1018

## RESULT 20

US-09-954-456-1588  
 ; Sequence 1588, Application US/09954456  
 ; Patent No. US20020115057A1  
 ; GENERAL INFORMATION:

; APPLICANT: Young, Paul  
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc  
 ; FILE REFERENCE: 689290-76  
 ; CURRENT APPLICATION NUMBER: US/09/954, 456  
 ; CURRENT FILING DATE: 2001-09-18  
 ; PRIOR APPLICATION NUMBER: US/60/233, 617



Matches 444; Conservative 0; Mismatches 416; Indels 25; Gaps 4;

```

OY 91 TGTATCAAAAGAGATGTAGAGAAATTTGCAAAAGTTTCCCTCCCTGTATCCACATA 150
Db 267 TGCACCAAAAGAGCATCAAGCATTTGGGAGCTCTCCGCCCCCACTGATTTCTTG 326
OY 151 GTTTTCGTCATTGACCTTGACGCAATTCATGTTAGTGGCAATTTATGCTTATCAAG 210
Db 327 GTTTTGTATTTGGTCTGCTGGAATTTCTGTTGTTGTTGTTGTTGTTGTTGTTG 386
OY 211 AAACAGAGAACCAAAAGATGTGTACATCTGAATTTGGCTGTAGAGATTTATCTCT 270
Db 387 CGGCTCAGAGTCATGATGTGTACCTGCTCAACTTGGCATCTGGATCTGCTCTTC 446
OY 271 CTATTCATCTGCTTTTGGGCTGTAAAGATTCATGTTAGTGGTGGTTTAAAGGAATA 330
Db 447 GTGTTTCCCTCCCTTTTGGGCTACTATGACAGACCAAGTGGGTTTGGGCTAGGT 506
OY 331 ATGTGCAAAATTAATCTTGACCTTTGACACATAAACTTTGCTGTGAATGCAAGTTCTG 390
Db 507 CTGTGCAAGATGATTTCTGTGATGTACTTGTGGGCTTTTACATGGGATATTTCTTGTG 566
OY 391 GCTTGTATCAGCATAGACAGATGTGTGAGTAACTAAAGTCCCAATCAAGAGTG 450
Db 567 ATGCTCATGAGCATGTATGATACCTGGCAGATAGACAG--CGGTGTTTCTTGAAGG 624
OY 451 GGAAGAACCATGCTGATCATCTGTTCTGTGTGTGTGATGCTGCTCATCTTGTAGCATA 510
Db 625 CAAGGACCTTGACTTATGAGGCTCATACCAAGTTGGCTACATGTGCTAGTGTGTG 684
OY 511 CCCCAGCTGT-----TTTTATACAGTAATGACATGCTAGTGCA 553
Db 685 CTTCCCTTCTGCTGCTTCTGTTGACACATTTGTATATGACGACGACATATCTTGTGCA 744
OY 554 TTCCCATTTTCCCGCTACCTAGAGACATCAATGAAAGATGATTAATTAATGCTAGAGA 613
Db 745 AAACCAAGTACTCTCAACTCC--ACGAGTGGAAGTTCTCAGCTCCCTGGAATACTA 801
OY 614 TCTGATTTGATTTTATGATCCCTTTTATATATGAGGAGTGTGTCTACTTATCAAGAGA 673
Db 802 ACATTTCTGAGTGTGTATCCCTTGAAGATCATGCTGTTTGTACATCCATGATCATCA 861
OY 674 GGACACTATGAAGATGCAAAATTAATAATATCTGACCCCTTAAAGATTTGCTGACAG 733
Db 862 GGACCTTGACATTTGTAAATATGAAAGAGACAAAGCGGTGAAGTATCTTTGCG 921
OY 734 TCGTATATGTTTCACTGCTCACTCACTGCTTATATACATTTGTCTGCGAGCA 793
Db 922 TGGTGTCTCTCTCTTGGGTTCTGGAACCTTACATATAGT--GCTCTTCTAGAGA 978
OY 794 TAGACATCTACTCTGCTGATCAGCAGTGTGAATAGAGCAAGCATGACATCGCA 853
Db 979 CCTGTGTAGCTAGAGATGCTTCAAGACTGCACTTGAAGATATCTTGAATGCA 1038
OY 854 TCCAGTCAAGAAAGCATGCACTCTTTCAAGCTGCTCAACCAATCTTATGTTT 913
Db 1039 TCCAGGCCACAAAGCTGCTGCTTTTGTTCATCTGCTGCTTATCTCAATCTACTT 1098
OY 914 TTATGGAGCATCTTTCAAAACATACGTTATGAAAGTGGCCAGA 958
Db 1099 TTCTGGGAGAAATTTGGCAAGTACATCTTCAAAA 1143

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RESULT 22  
US-09-764-413-19  
; Sequence 19, Application US/09764413  
; Publication No. US20020187930A1  
GENERAL INFORMATION:  
APPLICANT: Wells, Timothy N.C.  
Power, Christine A.  
TITLE OF INVENTION: A CHEMOKINE RECEPTOR ABLE TO BIND TO  
MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES  
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHIVE P.C.  
STREET: 1100 NO. US20020187930A1th Glebe Rd. 8th floor  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201-4741  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/764,413  
FILING DATE: 19-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/875,573  
FILING DATE: <Unknown>  
APPLICATION NUMBER: GB 9501683.8  
FILING DATE: 27-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mary J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1430-172  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1607 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 183..1262  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-764-413-19

Query Match 11.3%; Score 129.4; DB 9; Length 1607;  
Best Local Similarity 50.2%; Pred. No. 2.4e-25;  
Matches 444; Conservative 0; Mismatches 416; Indels 25; Gaps 4;

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OY 91 TGTATCAAAAGAGATGTAGAGAAATTTGCAAAAGTTTCCCTCCCTGTATCCACATA 150
Db 267 TGCACCAAAAGAGCATCAAGCATTTGGGAGCTCTTCTGCCCCCACTGATTTCTTG 326
OY 151 GTTTTCGTCATTGACCTTGACGCAATTCATGTTAGTGGCAATTTATGCTTATCAAG 210
Db 327 GTTTTGTATTTGGTCTGCTGGAATTTCTGTTGTTGTTGTTGTTGTTGTTGTTG 386
OY 211 AAACAGAGAACCAAAAGATGTGTACATCTGAATTTGGCTGTAGAGATTTATCTCT 270
Db 387 CGGCTCAGAGTCATGATGTGTACCTGCTCAACTTGGCATCTGGATCTGCTCTTC 446
OY 271 CTATTCATCTGCTTTTGGGCTGTAAAGATTCATGTTAGTGGTGGTTTAAAGGAATA 330
Db 447 GTGTTTCCCTCCCTTTTGGGCTACTATGACAGACCAAGTGGGTTTGGGCTAGGT 506
OY 331 ATGTGCAAAATTAATCTTGACCTTTGACACATAAACTTTGCTGTGAATGCAAGTTCTG 390
Db 507 CTGTGCAAGATGATTTCTGTGATGTACTTGTGGGCTTTTACATGGGATATTTCTTGTG 566
OY 391 GCTTGTATCAGCATAGACAGATGTGTGAGTAACTAAAGTCCCAATCAAGAGTG 450
Db 567 ATGCTCATGAGCATGTATGATACCTGGCAGATAGACAG--CGGTGTTTCTTGAAGG 624
OY 451 GGAAGAACCATGCTGATCATCTGTTCTGTGTGTGTGATGCTGCTCATCTTGTAGCATA 510
Db 625 CAAGGACCTTGACTTATGAGGCTCATACCAAGTTGGCTACATGTTGCTAGTGTGTG 684

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QY 511 CCCAGCTGCT-----TTTTATACAGTAATGACATGCTAGTGCA 553  
Db 685 CCGCTAGGCTCCAGCTTTCTGTTACAGCACTTGTATACAGGAGCAACCATCTACTGCA 744  
QY 554 TTCCCATTTTCCCGCTTACCTAGGACATCAATGAAGCATTTGATTCATAAATGCTAGAGA 613  
Db 745 AACCAAGTACTCTCTCAACTCC--ACGACGTGAAGGTCTCAGCTCCCTGGAATCA 801  
QY 614 TCTGATGAGATTGTGTAACCTTTCTTATATGAGGGGTGTGCTACTTTATCAACAGAA 673  
Db 802 ACATTTCTGATGTGTATCCCTTTAGGATCATGCTGTTTGTCTACTCCATGATCAATCA 861  
QY 674 GGACATCATGAGATGCAAAATTAATAATATCTGACACCCCTAAAGTTCTGCTACAG 733  
Db 862 GGACCTTCACACATTTGTAAATAAGAAAGAAACAAGGGGTGAAGATGATCTTTGCCG 921  
QY 734 TCGTTATGTTTTCATTTCTACTCACTGCTTTTAACTTTGTAAGTTTGTCCGAGCCA 793  
Db 922 TGGGTGCTCTCTCTGTTGGGTCTGACACCTTACACATGAT--GCTCTCTTAGAGA 978  
QY 794 TAGACATCATCTCCCTGATACACAGCTGCAACATGAGCAACGATGAGACATGSCCA 853  
Db 979 CCTGTGTGAGCTAGAACTCTTACAGCATGACCTTTGAAAGATCTTGAATATGCA 1038  
QY 854 TCCAAGTACAGAAAGCATGCACTTTTCAAGCTGCTTCAACCAATCCTTTATGTTT 913  
Db 1039 TCCAGGCCACAGAAACTGTGGCTTTTGTCTACTGCTGCTTAATCCCATCATCTACTTT 1098  
QY 914 TTATGGAGCATCTTTCAAAACTAGCTTATGAAGTGGCCAAAG 958  
Db 1099 TTCTGGGGAGAAATTTGCAAGTACATCTCAAGCTCTTCAAAA 1143

RESULT 23  
US-09-837-446-1  
; Sequence 1, Application US/09837446  
; Patent No. US20020019341A1  
; GENERAL INFORMATION:  
; APPLICANT: Butcher, Eugene C.  
; APPLICANT: Campbell, James J.  
; APPLICANT: Rottman, James B.  
; APPLICANT: Wu, Lijian  
; TITLE OF INVENTION: Modulation of Systemic Memory T Cell  
; FILE REFERENCE: STAN-110CON  
; CURRENT APPLICATION NUMBER: US/09/837,446  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 09/232,878  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1677  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (183) .. (1265)  
; OTHER INFORMATION: CCR4, Chemokine receptor coding sequence  
US-09-837-446-1

Query Match 11.3%; Score 129.4; DB 10; Length 1677;  
Best Local Similarity 50.2%; Pred. No. 2.4e-25;  
Matches 444; Conservative 0; Mismatches 416; Indels 25; Gaps 4;

QY 91 TGTATCAAGAAAGATGTGAGAAATTTGCAAAAGTTTCTCTGATTCCTCAATA 150  
Db 267 TGCACCAAGAAAGCATCAAGGATTTGGGAGCTTTCTGCCCCACATGATTCCTTG 326  
QY 151 GTTTTGTGATGATGCTGACGAGCATTTCCATGTAGTGCATTTATGCTTATCAAG 210  
Db 327 GTTTTGTATTTGCTGCTGTGAAATTTGTGTGTGTTCTGTGCTGTTCATCAACAG 386

QY 211 AAACAGAGAACCAAAACAGATGTATACATCTGAAATTTGGCTGTAGCATTTACTCTT 270  
Db 387 CGGCTAGGCTCATGATGATGTATACCTGCTCAACCTTGCATCTCGGATCTGCTTTC 446  
QY 271 CTATTCATCTGCTTTTGGGCTGTATAGTATTCATGGGTGGTTTTAGGAAAAATA 330  
Db 447 GTGTTTCCCTCCCTTTTGGGGCTACTATGACAGACACAGTGGTTTTTGGGCTAGT 506  
QY 331 AATGCAAAATTAATCTCAAGCTTTTACACATTAACCTTTGTCTGGAATGCAAGTTTG 390  
Db 507 CTGTGCAATATATTTCTGATGATCTTGTGGGCTTTTACAGTGGCATATTTCTTTGTC 566  
QY 391 GCTTGTATGAGATAGACAGATATGTGCAATTAAGTCCCAAGCAATCAGAGTG 450  
Db 567 ATGCTCATGAGATGATGATGATACCTGGGATAGTACAG--CGGTGTTTCTTGAAGG 624  
QY 451 GGAAGAACATGCTGATCATCTGTTCTGTGTGTGATGCGTCCATTTGCTAGACTA 510  
Db 625 CAAGGACCTTGAATTAAGGGATCACACAGTTGGCTACATGTGCAAGTGGCTGTGTCG 684  
QY 511 CCCAGCTGCT-----TTTTATACAGTAATGACAAATGCTAGTGCA 553  
Db 685 CTTCCCTTCTGCTGCTTTCTGTTCAAGCACTTGTATATCTGAGCGCAACCATACTGCA 744  
QY 554 TTCCCATTTTCCCGCTACCTAGGACATCAATGAAGATTTGATAATGCTAGAGA 613  
Db 745 AACCAAGTACTCTCTCAACTCC--ACGACGTGAAGTTCTGAGCTCCCTGGAATCA 801  
QY 614 TCTGATTTGATTTGTATGATCCCTTTCTTATATATGGGGTGTGCTACTTTATCACAGAA 673  
Db 802 ACATTTCTGATTTGTATGATTTCCCTTAGGATCATGCTTTTGTCTACTCATGATCATCA 861  
QY 674 GGACATCATGAGATGCAAAATTAATAATATCTGACACCCCTAAAGTTCTGCTCAG 733  
Db 862 GGACCTTGCAGCATTTGTAAATAAGAAAGAAACAAGCGGTGAAGTATCTTTGCCG 921  
QY 734 TCGTTATAGTTTTCATTTGCTCACTCACTGCTTATTAACATTTGCAAGTTCTGCCAGCA 793  
Db 922 TGTGTGCTCTCTCTTCTTGGGTCTGGAACCTTACAAATGAT--GCTCTCTTAGAGA 978  
QY 794 TAGACATCATCTCTCTGATACACAGCTGCAACATGACAAAGCATGACATGCGCA 853  
Db 979 CCTGTGTGAGCTAGAACTCTTCAAGACTGACCTTTGAAAGATCTTGAACATATGCA 1038  
QY 854 TCCAAGTACAGAAAGCATGCACTTTTCAAGCTGCTTCAACCAATCCTTTATGTTT 913  
Db 1039 TCCAGGCCACAGAACTGTGGCTTTTGTCTACTGCTGCTTAATCCCATCATCTACTTT 1098  
QY 914 TTATGGAGCATCTTTCAAAACTAGCTTATGAAGTGGCCAAAG 958  
Db 1099 TTCTGGGGAGAAATTTGCAAGTACATCTCAAGCTCTTCAAAA 1143

RESULT 24  
US-09-917-800A-1445  
; Sequence 1445, Application US/09917800A  
; Patent No. US20020119462A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Casstle, Arthur  
; APPLICANT: Elashoff, Michael  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5038-US  
; CURRENT APPLICATION NUMBER: US/09/917,800A  
; PRIOR FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: US 60/222,040  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: US 60/222,880  
; PRIOR FILING DATE: 2000-11-02  
; PRIOR APPLICATION NUMBER: US 60/290,029

PRIOR FILING DATE: 2001-05-11  
 PRIOR APPLICATION NUMBER: US 60/290,645  
 PRIOR FILING DATE: 2001-05-15  
 PRIOR APPLICATION NUMBER: US 60/292,336  
 PRIOR FILING DATE: 2001-05-22  
 PRIOR APPLICATION NUMBER: US 60/295,798  
 PRIOR FILING DATE: 2001-06-06  
 PRIOR APPLICATION NUMBER: US 60/297,457  
 PRIOR FILING DATE: 2001-06-13  
 PRIOR APPLICATION NUMBER: US 60/298,884  
 PRIOR FILING DATE: 2001-06-19  
 PRIOR APPLICATION NUMBER: US 60/303,459  
 PRIOR FILING DATE: 2001-07-09  
 NUMBER OF SEQ ID NOS: 1740  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 1445  
 LENGTH: 1318  
 TYPE: DNA  
 ORGANISM: Rattus norvegicus  
 FEATURE:  
 OTHER INFORMATION: Genbank Accession No. US20020119462A1 U04808  
 US-09-917-800A-1445

Query Match 11.1%; Score 126.8; DB 10; Length 1318;  
 Best Local Similarity 48.6%; Pred. No. 1.1e-24;  
 Matches 443; Conservative 0; Mismatches 457; Indels 12; Gaps 3;

64 TATGACTACGATCAATATGACTGATCTGTATCAAAAGAGATGTCAGAGATTGGCAAAA 123  
 104 TTGAGTATGATGACTCTGCTGAGGCTGTATTGCGTGATCGTGGCCCTGGAGCC 163  
 124 GTTTCCTCCCTGATCTCTCAATAGTTTTCGATCTGAGCTTGACGGCAATTCATG 183  
 164 ATCTTCATATTAATTTTCACTCCCTGCTTCACTGCTGCTGCTGCTGCTGCTGCTG 223  
 184 GTATGAGCAATTTATGCTTATTAAGAAACAGAGAACCAAAACAGATGTGATCTCTG 243  
 224 GTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 283  
 244 AATTGGCTGATGACGATTTACTCTCTTATTAATCACTGCTGCTGCTGCTGCTGCTGCTG 303  
 284 AACCTGCTTGGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 343  
 304 GTTCAAGGATGGGTTTATGAGAAATATGTCGCAAAATTAATCTTCAAGCTTGTACACTA 363  
 344 ATGAGCATGAGGCTTCCACAAAGCCATGTGCAAGCTCAACAGCTCTTCTTCTTCAAT 403  
 364 AACTTGTCTGGAATGAGATTTCTGCTTGTATGAGATGACATGATATGTGCACTA 423  
 404 GGCTTCTTGGGGGCAATTTCTTCAACCGTCACTGAGATGACCGGTAACCTGCGCATC 463  
 424 ACTAAGTCCCAAC-----CATCAGAGATGGGAAAAACATGCTGATCAATGTTTC 477  
 464 GTCTGCGCCCACTTCATGAACACCGAGAGTSCAACACGCGCTCAACATCACTGCTG 523  
 478 TGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 537  
 524 GGGGCTGGGGGCGGCACTTATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 583  
 538 GACATGCTAGTGCATTTCCATTTTCCCGCTACCTTGAAGAAATCAATGAAGCATTTG 597  
 584 GACACAG--AATGTTGGGTGATTAACCCGAGGTCTGACGAGAAATCTGGCCCGTCTC 640  
 598 ATTCAATGCTAGATCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 657  
 641 CGCAACTGAGATCAATCTGAGGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 700  
 658 TACTTATCAAGCAAGACATCATGAGATGCAAAATTAATATCTGACCCCTA 717  
 701 TACTTCCGATCTGCTGAGGCTGCTTCTGCAAGAAACGGAAGGCAAGGCAATTT 760  
 718 AAGTCTGCTACAGTCTGATTTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777

Db 761 AGGCTCATCTCTGGTGGTGTGTCTTCTTCTTCTGAGCCCTTACAACTGCG 820  
 Qy 778 AAGTCTGCGGAGCAATAGATCATCTACTCCATGATCAGAGTGCACATGAGCAAA 837  
 Db 821 ATTTT---CTGAGACTCTGAATTTTCAACCTTCTCCATGTTGAGCAATGAGG 877  
 Qy 838 CGCATGACATGCGCATTCACAGTGCAGAAAGATGCACTTTTCAACAGCTGCTCAAC 897  
 Db 878 GACCTGAGGTGGGCTTGTGTGACGAGACATGGGCTTTAGCCACTGCTGCTCAAC 937  
 Qy 898 CCAATCTTATGTTTATTTGAGAGCATCTTCAAAATCACTATGAAAGTGCACAG 957  
 Db 938 CCTTATCTAGCTTCTGCTGCGGAAAGTTCAAGAGTACTGAGACCTGTATCAAC 997  
 Qy 958 AATATGAGTCC 969  
 Db 998 AAGTCTGCTGCC 1009

## RESULT 25

US-09-967-768A-316  
 Sequence 316, Application US/09967768A  
 Patent No. US20020150877A1  
 GENERAL INFORMATION:  
 APPLICANT: Augustus, Meena  
 TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatur  
 TITLE OF INVENTION: Sets  
 FILE REFERENCE: 689290-72  
 CURRENT APPLICATION NUMBER: US/09/967,768A  
 CURRENT FILING DATE: 2001-09-28  
 PRIOR APPLICATION NUMBER: US/60/236,109  
 PRIOR FILING DATE: 2000-09-28  
 PRIOR APPLICATION NUMBER: US/60/236,034  
 PRIOR FILING DATE: 2000-09-28  
 PRIOR APPLICATION NUMBER: US/60/236,111  
 PRIOR FILING DATE: 2000-09-28  
 NUMBER OF SEQ ID NOS: 325  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 316  
 LENGTH: 143068  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-967-768A-316

Query Match 9.8%; Score 112.8; DB 10; Length 143068;  
 Best Local Similarity 49.1%; Pred. No. 8e-20;  
 Matches 421; Conservative 0; Mismatches 422; Indels 15; Gaps 4;

Qy 90 CTGTATCAAAAGATGTCAGAAATTTGCAAAAGTTTCTCCCTGATTTCTCAAT 149  
 Db 46198 CTGTATCAAAATTTGAGCGTGAAGCAAAATTTGGGCCCAACTCTGCTCCGCTTACCTGCT 46257  
 Qy 150 AGTTTGGTCAATGAGCTTGAGGCAATTCATGATGAGCAATTTATGCTATTAACA 209  
 Db 46258 GGTGTATCTTTGGTGTGTTGAGGCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 46317  
 Qy 210 GAAACAGAAACCAAAACAGATGTGTATCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTG 269  
 Db 46318 AAGCTGAAGTCTGACTGACATTTTACCTGCTCAACCTGCGCACTCTGATCTGCTTTT 46377  
 Qy 270 TCTATTCATCTGCTTTTGGGCTGTTAATGACATGATGAGTGGGTTTATGGGAAAT 329  
 Db 46378 TCTATTCATCTGCTTTTGGGCTGTTAATGACATGATGAGTGGGTTTATGGGAAAT 46437  
 Qy 330 AATGCAAAATTAATTCAGGCTTGTACACATTAATCTTGTCTGGAATGAGCTTTCT 389  
 Db 46438 AATGCAAAATTAATTCAGGCTTGTATCAATGATGAGTGGGTTTATGGGAAATCTTCTCAT 46497  
 Qy 390 GGCTTGTATGACATGACATATATGAGGAGT-----AATCAAGTCCCAAGCAATC 443  
 Db 46498 CATCTCTGACAAATGATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 46557  
 Qy 444 AGAGTGGGAAACCATGCTGATCATCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 503

Db	4658	CAGAGCGTCACTTTGGGGTGGAGCAAGTGCATCCTGGTTGGTGGCTGTGTTTG	4661
Qy	504	GACATATACCCAGCTGGTTTTTTATACAGTAATGACATGCTAGGTGCATTTCCATTTT	563
Db	46618	TTCTGTCCAGGAATATCTTTTCTAAATGCGAGAAAGAAAGATTCGTTATGTCTGTGG	46777
Qy	564	CCCCCCTACTAGGAACATCATGAAAGCATTGATTCAAATGCTAGATTCGCATTGG	623
Db	46678	CCCTTATTTTCCACGAGATGGAATTAATTTCCACACAAATATAGGAACATTT---TGGG	46734
Qy	624	ATTTGTAGTACCTTTCTTAATTAATGGGGGTGTGCTACTTATTCACGAAAGACACTCAT	683
Db	46735	GCTGTCTGCGCGCTGCTCATATGTCATCTGTCTCTGCGGAATCTGAAAACCTGTGT	46794
Qy	684	GAAAGATGCCAAGC--ATTATAATATCTGACCCCTTAAAGTTTGTCTCAAGTGGTAT	740
Db	46795	TGCGTGTCAAAAGAGAAAGAGGAGATGGGAGAGAAAGTATCTTACATCATCATAT	46854
Qy	741	AGTTTTCATTGTCAATCAACGTGCTTATAATTTGCATGTCAGTTCTGGCGAGCATAGACAT	800
Db	46855	TGTTTACTTTCTTTCTTGTGACATCTCTATTAACATTTGCTATCTTGAAACCTTTCAGGA	46914
Qy	801	CATCTACTCCCTGATCACCAGCTGCACAATGAGCAACCATGACATCGCCATCCAAAT	860
Db	46915	ATTCTTGGGCTGAGTAATCTGTAAAGCACAGTCAAC---TGGACCAAGCCACGCAAGT	46971
Qy	861	CACAGAAAGCATGCACCTTTTCAACGTTGCTCAACCCCAATCTTATATGTTTTATGGG	920
Db	46972	GACAGAGACTCTTGGGATGATCACTGCTGCATCAATCCATCATCTATGCTGTGGTGG	47031
Qy	921	AGCATCTTCAAAAACATA 938	
Db	47032	GGAGAAATTCAGAAAGATA 47049	

```

RESULT 26
US-10-083-168-3
; Sequence 3, Application US/10083168
; Publication No. US20030023069A1
; GENERAL INFORMATION:
; APPLICANT: Liaw, Chen W.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Maciejewski-Lenior, Dominique
; APPLICANT: Leonard, James N.
; APPLICANT: Ortuno, Daniel
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Acti
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0320
; CURRENT APPLICATION NUMBER: US/10/083,168
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1029
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-083-168-3

```

Query Match	9.7%	Score 111.2	DB 9	Length 1029
Best Local Similarity	49.2%	Pred. No. 1.8e-20		
Matches 433	Conservative 0	Mismatches 413	Indels 33	Gaps 4
QY 101	AAGATGCAAGAAATTTGCAAAAGTTTCTCCCGTATATTCCTACAATAGATTTCGTCA	160		
Db 71	AAGCTTCTCGCAATTTCAGCAAGGCTCTTCTGCCCCGTCATGACTGCTGGTGTGTGTCT	130		
QY 161	TTGACTTTGAGGCAATTCATGATGATGGCAATTTATGCTATTACAAGAAACAGAA	220		
Db 131	GTGGTCTGGTGGGGAACCTCTCTGGTCTGTGTATATTCATCTTCTTACCATTAGTTGGAGA	190		

OY	221	CCAAAACAGATGTGACATCCGGAATTTGGCTGAGACGATTTTACTCCTTATTAATC	28
Db	191	GCTGACGGAATGTGTTCTCGTGAACCTAACCCCTGCTGACCTGGTGTGTTCCTGACTC	25
OY	281	TGSCCTTTTGGGCTGTTAATGCAAGTTTCATGGGATGGGTTTATGGGAAAATAATGTGCAAA	34
Db	251	TGCCCCCTTGGGGCTATGAGAGGCATCATGATGGGTGTGGCCAGGTGATGTGCAAA	31
OY	341	TAACTTCAGCCTTGTACACACTAACTTTGTCTCGAATGCAAGTTTCTGGCTGTATCA	40
Db	311	GCCTAATGGGCACTTACACTATTAACCTTCAAGTCCATCCTCATCTCACTGCATCA	37
OY	401	GCATGACAGATATGTGACAGTAACATAAGTCCCGACCAATTCAGAGTGGGAAAACAT	46
Db	371	CTGTGATGCTTTACTATTGTATGGTTAAAG--CCACCAAGGCTTACACACAGAACCA	42
OY	461	GCTGATCATCTGTTCTGTGTCTGATGAGCTGCATCTTGCTGAGATACCCAGCTGG	52
Db	428	AGAGGATGACCTGGGGGCAAGGTCAACAGCTTGTCATCTGGGTG--ATATCCCTGGCTGG	48
OY	521	TTTTTTATACGATTAATGACAAATGCTAGGTGATTTCCATTTTCCCC-----GCT	57
Db	485	TTTTCTTCCCCCAATTATCTATGGCAATGTCTTAAATTCGCAGACCTAATATGTGTT	54
OY	572	ACCTGAGAACATCATGAAACATTTGATTCAAATGTCAAGATGTGATTTGTAG	63
Db	545	ACCATGACGAGGCAATTTCCACTGTGTTCTTGCCACCCAGATATACACTGGGTTCTTCT	60
OY	632	TACCTTTCTTATTAATGGGGGTGTGCTACTTTATCAGACGAGACACTATGAAGATG	69
Db	605	TGCCACTCTCACCATGATTTGTGTCTATTCAGTCAATATCAAAACACTGGTTCATGCTG	66
OY	692	CAAAATTTAAATATCTGCACCCCTTAAAGTTGTGCTCAAGTGTATATGTTTCAATG	75
Db	665	GAGGTTTCCAAAGACACAGATCTTAAAGATCATCTTCTGGTGTATGGCTGTCTCTGC	72
OY	752	TCACTCAACTCCTTTATTAACATGTCAAGTTCTGSCGAGCATGTGACATCATCACTCCC	81
Db	725	TGACCCAGATGCTCTTCAACTCATGTAAGTTTCACTCCGACAGACACACTGGGAATATCATG	78
OY	812	TGATATCACCAGCTGCACAGATGAGCAAAAGCATGACATGCGCATTCACAGTCAAGAAAGCA	87
Db	785	CCATGACCAAGCT-----TTGACTACACATCATGATGTGACAGAGCCA	82
OY	872	TTCGACTCTTTCAAGCTGCTCAACCAATCTTTATGTTTTATGGAACATCTTTCA	91
Db	827	TTCGATATCTGAGGGCCTGCTTAACTGCTGTATGCTCTTTGTTCAGCCTGAAGTTTC	88
OY	932	AAAACATGTTATGAAGTGGGCCAAGAAATATGGGTCC	96
Db	887	GAAGAAGTTCTGAAACTTGTGTGAGGACATTTGGTTGC	92

```

RESULT 27
US-09-940-063-1
: Sequence 1, Application US/09940063
: Patent No. US20020090657A1
: GENERAL INFORMATION:
: APPLICANT: Briskin, Michael J.
: APPLICANT: Murphy, Kristine E.
: APPLICANT: Wilbanks, Alyson M.
: APPLICANT: Wu, LiJun
: TITLE OF INVENTION: No. US20020090657A1el Antibodies and Ligands for "Bonzoi"
: TITLE OF INVENTION: Chemokine Receptor
: FILE REFERENCE: 1855.1070-000
: CURRENT APPLICATION NUMBER: US/09/940,063
: CURRENT FILING DATE: 2001-08-27
: PRIOR APPLICATION NUMBER: 09/445,437
: PRIOR FILING DATE: 1999-11-24
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 1029

```





Db 750 TGTACTTCTCTCTGAGCTCCCTATATATATGTCATCTCTGGAACCTTCAGGA 809  
 QY 801 CATCTACTCCCTGATATCAGCTGCAATGAGCAAGCATGAGCATGCACTTCAAGT 860  
 Db 810 ATTCTTGGCTGAGTATCTGTGAAAGCAACGATCAGC--TGACCAAGCAGCAGGT 866  
 QY 861 CACAAAAGCATCCGACTCTTTACAGCTGCTCAACCAATCTTATGTTTATGAG 920  
 Db 867 GACAGAGCTCTGGAGATGACTGCTGTCATCATCCATCATCTATGCTTCTGG 926  
 QY 921 AGCATCTTCAAACTA 938  
 Db 927 GGAGAGTTCCAGAGTA 944

## RESULT 29

US-09-104-792-1  
 Sequence 1, Application US/09104792  
 Patent No. US20020019026A1  
 GENERAL INFORMATION:  
 APPLICANT: Soppe, Daniel R.  
 APPLICANT: Yi, Li  
 APPLICANT: Ruben, Steven M.  
 APPLICANT: Rosen, Craig A.  
 TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
 ADDRESS: STUART & OLSTEIN  
 STREET: 6 Becker Farm Road  
 CITY: Roseland  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/104,792  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/461,244  
 FILING DATE: 05-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ferraro, Gregory D.  
 REGISTRATION NUMBER: 36,134  
 REFERENCE/DOCKET NUMBER: 325800-445  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1586 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 431..1495  
 US-09-104-792-1

Query Match 9 7%; Score 111; DB 10; Length 1586;  
 Best Local Similarity 48.9%; Pred.No. 2.6e-20;  
 Matches 421; Conservative 0; Mismatches 425; Indels 15; Gaps 4;

QY 117 TGCAAAAGTTTCTCCCTGATATCTTCAATAGTTTGTGATGAGCTTGACAGGCAA 176  
 Db 529 TGGCAAGTGTCTCTGCTGCTTTATGCTCTGTTTATTCAGTCTTCTGGAAA 588

QY 177 TTCCATGAGTGGCAATTTATCTATTAAGAAACAGAAACCAAAACAGATGTGA 236  
 Db 589 CAGCTGTGATCTGCTGCTGTGTGTGCAAGAGCTGAGAGCATCAGAGATGATA 648  
 QY 237 CATCTGAATTTGGCTGAGAGATTTATCTCTTATTTCACTGCTTTTGGCTGT 296  
 Db 649 CCTCTTGAACCTGGCCGCTGTGACCTGCTTTTGTCTTCTTCCCTTTACAGCTA 708  
 QY 297 TATGCACTTCAATGGGTGGTTTGGGAAAATATGTGCAAAATTAATTGACCTTGA 356  
 Db 709 CTATCTGTGACCAAGTGGGTGTTGGGACCTGTATGTGCAAAAGGTGTCTGCTTTTA 768  
 QY 357 CACACTAACTTTGTCTGGAATGACAGTTTCTGGCTGTATGACATAGACATATGT 416  
 Db 769 TTACATTTGCTTTCTACAGACATGTTTATCATCCTCATAGATGTGACAGTACT 828  
 QY 417 GGCAGTAACTAAAGTC--CCAGCCMATCAGAGTGGGAAAACCATGCTGATCTGT 474  
 Db 829 GAGCTGTGTCATGCGCGTATGTCCTTAAAGTGGAGCATCAGATGGGCAACAGCT 888  
 QY 475 TTCTGTGCTGATGAGTCT--GCCATTTGCTGAGCATACCCAGCTGTTTATAC 530  
 Db 889 GTGCTGGCAGATGCTTACCCGCAATATGCTTACATCCATGCTAGTGTATGCA 948  
 QY 531 AGTAATGACAATGCTAGTGCATTTCCATTTTCCCGCTACCTAGGAACATCAATGAA 590  
 Db 949 AGTGCCCTGAAGATGATGTCTTACAGTGTATTTATTTACATCAACAGCTTTGAA 1008  
 QY 591 AGCATTTGATTC-----AAATGCTAGAGATCTGCATTGATTTGTAGTACCTTTCTAT 644  
 Db 1009 GTGMAAGATCTTCAACAACTTCAAAATGAATTTAGCTGTGTATCCATTCACCAT 1068  
 QY 645 TATGGGGGTGTGCTACTTATACAGACAGACACTATGAAGTGCACAACTTAAT 704  
 Db 1069 CTTATGTTCTGCTACATTAATTCCTGACACAGCTAAGAGGTGTAACCAACAA 1128  
 QY 705 ATCTGACCCCTTAAAGTGTGCTCAGAGTGTATAGTTTCTATGCTCACTCACTGCC 764  
 Db 1129 GACCAAGGCCATCAGGTGTGGTGTCTATGTTGTGATTTGATTTTCTTGGGCTCC 1188  
 QY 765 TTATTAATTTGTCAAGTTTGTGCGAGGCATAGACATCTACTCTCTGTATCAGAGTGG 824  
 Db 1189 ATTCAAGCTGTGTTCTTCTCTCACTTCTTGACAGATACATCTTGGATG--GATG 1245  
 QY 825 CAACATGAGCAAGACAGACATGCCATCCCAAGTACAGAAAGATGCCACTTTTCA 884  
 Db 1246 TAGCATTAAGCCACAGCTGACTTATGCAACCATGTCAGAAATCATTTCTTTACTCA 1305  
 QY 885 CAGCTGCTCAACCCAACTCTTATGTTTATGGAGCATCTTTCAAAATACATGTTAT 944  
 Db 1306 CTGCTGTGTGAACCTGTATATGTTTGTGGGAAAGTTCAAGAAACACCTCTC 1365  
 QY 945 GAAAGTGCCCAAGAAATATGG 965  
 Db 1366 AGAAATATTTCCAGAAAAGTGG 1386

## RESULT 30

US-09-104-063-1  
 Sequence 1, Application US/09104063  
 Patent No. US20020168356A1  
 GENERAL INFORMATION:  
 APPLICANT: Lee, James  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Pf4A Receptors  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winpatin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/104,063  
 FILING DATE: 24-June-1998  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/701265  
 FILING DATE: 22-AUG-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/664228  
 FILING DATE: 06-JUN-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/076093  
 FILING DATE: 11-JUN-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/810782  
 FILING DATE: 19-DEC-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Love, Richard B.  
 REGISTRATION NUMBER: 34,659  
 REFERENCE/DOCKET NUMBER: P0706P2C2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-5530  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1933 base pairs  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 US-09-104-063-1

Query Match 9.6%; Score 110.6; DB 9; Length 1933;  
 Best Local Similarity 48.2%; Pred. No. 3.6e-20;  
 Matches 382; Conservative 0; Mismatches 399; Indels 12; Gaps 2;

149 TAGTTTGGTCACTTGGAGTTCAGGCAATTCATGATGAGCAATTATGCTATTACA 208  
 193 TAGTGTCTCTGAGCCTGCGGAAACTCCCTGTATGCTGATCTTATACACAGA 252  
 209 AGAAACAGAGAAACAAACAGATGTGTACATCTGAATTTGGCTTACAGATTACTCC 268  
 253 GGATGGCGCGCTCCGCTACCTGATGTCTTACCTGTGAACCTGGCTTGGCCGACTACTCT 312  
 269 TTCTATTCACTGCTTTTGGGCTGTTAATGCAATTCATGGTGGGTTTGGGAAA 328  
 313 TTGCTGTGACCTTGGCCATCTGGGCGCTCCAGGTGAATGGCTGATTTTGGCACT 372  
 329 TAATGTCAAAATTAACCTGAGCTTGTACACATAAATTGTCTGTGATGACGTTTC 388  
 373 TCTGTGCAAGGTGTCTCACTCTGAGAGAGTCAACTTTACAGTGGCATCTGCTGT 432  
 389 TGGCTGTATGACATAGACAGATATGTGGCAGTAACTAAATC---CCGACCAATGAG 445  
 433 TGGCCTGACATGATGTGAGCCGTTTACCTGGCCATTGTCAATGACACACCAACGACCC 492  
 446 GATGTGGAAACATGCTGATCATCTGTTTGTGTCTGATGAGCTGACATCTTGCTGA 505  
 493 AGAAGGTCACTTGTGCAAGTTTGTCTTGTGCTGCTGGGAGCTGTATGAATCTGT 552  
 506 GATATCCCAAGCTGTTTATACAGTAATGACAAATGCTAGTGCATTTCCATTTTCC 565  
 553 CCTGACCTTCTTCTTCCGCAAGCTTACCATCAAAATTCAGTCCAGTTTGTCT 612  
 566 CCGGCTACCTAGAAATCAATGAAGCAT-----TGATTCAATGCTAGAGATCT 616  
 613 ATGAGTCTGGGAAATGACAGCAAAATGGGAGATGTGTGCGGATCTCTCCACACA 672

617 GCATTGATTTGTAGTACCTTTCTTATTATGAGGGGTGTCTACTTTATACAGCAAGA 676  
 673 CTTTGGCTTATGCTGCGCTGTTTGTGATGCTGTTCTGTATGATGATCAACCTGCGTA 732  
 677 CACTATGAAATGCGCAAAATTAATATCTGACCCCTAAAGTTTGTGCTCAGTGC 736  
 733 CACTGTTTAAAGCCCAATGGGGCAGAGCAACCGACCATAGAGGTATCTTTGTGTGC 792  
 737 TTAATGTTTCAATTTGTCACTCACTGACCTTTAATCAATTTGCAAGTTTGTGCGAGCATAG 796  
 793 TCTTATCTTCTGCTTTGTGCTGCGCTCAACCTGCTCTGCTGACAGACACCTCA 852  
 797 ACATCATCTACTCCTGTATCACCAGCTGACATAGCAAAAGCATGACATCGCATCC 856  
 853 TGAGAGCCAGGTGATTCAGAGAGACCTGTGAGCCGCGAACAATGCGCGGCTGG 912  
 857 AAGTACAGAAAGCATCGGACCTTTCAAGTGGCTCAACCCATCTTTATGTTTAA 916  
 913 ATGCCACTGAGATTCTGGGATTTCTCCATAGCTGCTCAACCCCATCATACGCTTCA 972  
 917 TGGAGCATCTTT 929  
 973 TCGGCCAAATTT 985

RESULT 31  
 US-09-131-827A-19  
 Sequence 19, Application US/09131827A  
 Patent No. US20020038469A1  
 GENERAL INFORMATION:  
 APPLICANT: Dean, Michael  
 APPLICANT: O'Brien, Stephen J.  
 APPLICANT: Smith, Michael  
 APPLICANT: Carington, Mary  
 TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A  
 TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE  
 FILE REFERENCE: 14014.0333  
 CURRENT APPLICATION NUMBER: US/09/131,827A  
 CURRENT FILING DATE: 1998-08-10  
 PRIOR APPLICATION NUMBER: 60/055,659  
 PRIOR FILING DATE: 1997-08-14  
 NUMBER OF SEQ ID NOS: 20  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 19  
 LENGTH: 1083  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-131-827A-19

Query Match 9.6%; Score 109.6; DB 10; Length 1083;  
 Best Local Similarity 48.8%; Pred. No. 5.1e-20;  
 Matches 419; Conservative 0; Mismatches 424; Indels 15; Gaps 4;

90 CTGTATCAAGAGATGTCAAGATTTGCAAAAGTTTCTCCCTGATTTCTCAAT 149  
 93 CTGTCAATTAATTTGCTGAGCAAAATTTGGGCGCAACTCTGCTCGCTCACTGCT 152  
 150 AGTTTGTCAATGAGCTTGGGCAATTCATGATGATGAGCAATTTATGCTATTACAA 209  
 153 GTGTATCATCTTGTGTTTGGGCAACATGCTGTGATCTCATCTTAATTAACGCAA 212  
 210 GAAACAGAAACCAAAACAGATGTGTACATCTGCAATTTGGCTGTACAGATTACTCT 269  
 213 AAAGTGAAGTGTGACTGACATTTTACCTGCTCAACCTGGCATCTGTATCTGCTTT 272  
 270 TCTATTCACTGCTTTTGGGCTGTTAAATGCAAGTTATGAGTGGTTTATGAGAAAT 329  
 273 TCTATTACTCTCCATTTGTGGCTCACTGCTGCAAAATGAGTGGTCTTTTGGAAATGC 332  
 330 AATGTCAAAATTAATTCAGCTTGTACACACTAACTTTGTCTCTGGAATGAGATCT 389  
 333 AATGTCAAAATTAATTCAGAGGCTGTATCAATGATGTTTATTTGGGGAATCTTCTTCT 392

QY 390 GGCTTGATGACATAGACAGATATGTGGAGT-----AACTAAGTCCCCAGCCCATC 443  
 Db 393 CATCTCTGCAATGCAATGATACCTGGCTATGTCCATGCTGTGTGTTTAAAGC 452  
 QY 444 AGAGTGGGAAACCATGCTGATCATCTGTTCTGTGTGATGGCTCCACTTGTCT 503  
 Db 453 CAGGACGGTCACTTTGGGGGTGTCAGAGTGTATCACTGGTGTGGCTGTGTTGC 512  
 QY 504 GAGATATCCCAAGCTGTTTATATACATTAATGACATGCTAGTGTATCCACTTTT 563  
 Db 513 TTCTGTCCAGGATCATCTTAAATGCCAGAAAGATTCGTTATGTCTGTG 572  
 QY 564 CCCCCGCTACCTAGACATCAATGAAGCATTTGATTCATGCTAGATCTGCATTGG 623  
 Db 573 CCCTTATTTCCAGAGATGATTAATTTCCACATATATAGAACATTT---TGGG 629  
 QY 624 ATTTGATGACCTTTCTTATATATGGGGGTGTGCTACTTTATACAGCAAGACACTCAT 683  
 Db 630 GCTGTCTGCTCCGCTGCTCATGTCATGCTGCTACTGCGAATCCTGAAACCTGTGT 689  
 QY 684 GAGATGCCAAGC---ATTAAATATCTGACCCCTTAAAGTTCTGCTACAGTCTTAT 740  
 Db 690 TCGGTGTGAAAGAGAGAGAGGATGAGGAGATGATCATCTTCAACATCATGAT 749  
 QY 741 AGTTTCAATGTCACTCACTGCTTATATACATTTGATCAAGTTCTGCGGACCATAGACAT 800  
 Db 750 TGTTCATTTCTCTTCTGAGCTCCCTATATATTTGATCTTCTGTAACCTTCCAGGA 809  
 QY 801 CATCTACTCCCTGATCAACAGCTGCAACATGAGCAAAACGATGAGATGCCATCCAGT 860  
 Db 810 ATTCTTGGGCTGAGTAACGTGAAAGACACAGTCAAC---TGGACCAAGCAGCAGAGT 866  
 QY 861 CACAGAAGCATGCACTTTTCAAGCTGCCCAACCCCATCTTATGTTTATGGG 920  
 Db 867 GAGAGAGACTCTTGGATGACTCACTGCTGATCAATCCATATATATGCTTGTGTGG 926  
 QY 921 AGCATCTTCAAAAACATA 938  
 Db 927 GGAGAGTTTCAGAAAGTA 944  
 RESULT 32  
 US-10-083-168-64  
 ; Sequence 64, Application US/10083168  
 ; Publication No. US20030023069A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liaw, Chen W.  
 ; APPLICANT: Chalmers, Derek T.  
 ; APPLICANT: Behan, Dominic P.  
 ; APPLICANT: Maciejewski-Lenior, Dominique  
 ; APPLICANT: Leonard, James N.  
 ; APPLICANT: Ortuno, Daniel  
 ; APPLICANT: Lin, I-Lin  
 ; TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Act  
 ; FILE REFERENCE: Recaptors  
 ; CURRENT APPLICATION NUMBER: US/10/083,168  
 ; CURRENT FILING DATE: 2002-02-26  
 ; NUMBER OF SEQ ID NOS: 102  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 64  
 ; LENGTH: 1029  
 ; TYPE: DNA  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: No. US20030023069A1el Sequence  
 US-10-083-168-64

Query Match 9.4%; Score 108; DB 9; Length 1029;  
 Best Local Similarity 49.0%; Pred. No. 1.4e-19;  
 Matches 430; Conservative 0; Mismatches 415; Indels 33; Gaps 4;  
 QY 101 AAGATGTGAGAAATTTCGAAAAGTTTCTCTGTTCTCTCAATAGTTTCTGTCA 160

Db 71 AAGCCTTCTGCAAGTTCAGCAAGGCTTTCTGCCCTGATCATCTGCTGTGTGTCT 130  
 QY 161 TTGACTTGACAGGCAATTCACATGATGAGCAATTTATGCTATTAACAAGAAACAGAA 220  
 Db 131 GTGTCTGTGGGAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 190  
 QY 221 CCAAAACAGATGTGATCTCTGAAATTTGGCTGATGAGATTTTACCTCTTATTCATC 280  
 Db 191 GCTGACCGATGTGTCTGTGTGAAACCTACCCCTGCTGACCTGTGTGTGTGTGTGTGT 250  
 QY 281 TGCCCTTTTGGGCTGTATATGACATGATGATGATGATGATGATGATGATGATGATGAT 340  
 Db 251 TGCCCTTTTGGGCTGTATATGACATGATGATGATGATGATGATGATGATGATGATGAT 310  
 QY 341 TAACCTTCACTTGTACACACTTAACTTTGCTGTGAAATGACATTTCTGCTGTATCA 400  
 Db 311 GCTTACGTGGGATCTACATCTTAACTTTTAACTTCAACGTGATCTTCACTGTGATCA 370  
 QY 401 GCATGACAGATATGTGCACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 460  
 Db 371 CTGTGATCTGTTTCAATGTATGTGTGTAAAG---CCACCAAGGCTTACACACAGACCA 427  
 QY 461 GGTGATCATCTGTTTCTGT 520  
 Db 428 AGAGATGACCTGGGGCAAGGTCAACGCTTGTCTCATCTGTGGTG---ATATCCCTGTGG 484  
 QY 521 TTTTATATACAGTAATGACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 571  
 Db 485 TTTCTTCCCTCCCAATATATGATGACATGCTTATATCTGCAAGCTCATATGTGTGT 544  
 QY 572 ACCTAGAACATGATGAAAGCATTTGATTTCAATGCTAGATCTGTGATTTGTAG 631  
 Db 545 ACATGACAGGCAATTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 604  
 QY 632 TACCTTCTTATATGAGGGGT 691  
 Db 605 TGCCACTGTCTACATGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 664  
 QY 692 CAATTAATATCTGCAACCCCTTAAAGTTTGTCTCACAGTGTGTATATGTTTCAATTG 751  
 Db 665 GAGCTTCCAGAGACAGATCAAAAAGATCATCTTCTGTGTGTGTGTGTGTGTGTGTGT 724  
 QY 752 TCACTCACTGCTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 811  
 Db 725 TGACCCAGATGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 784  
 QY 812 TGATCACAGCTGCAACATGAGCAACGATGACATGCACTGCACTGCACTGCACTGCACTG 871  
 Db 785 CCAATGACAGCT-----TTCACTAACATCATCATGATGATGATGATGATGATGATGATG 826  
 QY 872 TCGGACTCTTCACTGCTGCTCAACCCCATCTTATGTTTATGAGGACATCTTTCA 931  
 Db 827 TCGATATCTGAGGGCTGTGTTTAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 886  
 QY 932 AAAACTGATTATGAAAGTGGCAAGAAATATGAGTCC 969  
 Db 887 GAAAGAACTTCTGAAACTTGTGAAAGACATTTGTGC 924

RESULT 33  
 US-09-852-156-5  
 ; Sequence 5, Application US/09852156  
 ; Patent No. US2002007694A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Littman, Dan R.  
 ; Unutmaz, Derya  
 ; Deng, Hongkui  
 ; Ramani, Vineet N.K.  
 ; TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS  
 ; ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF  
 ; IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES  
 ; THEREOF

NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
FLOOR  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/852,156  
APPLICATION NUMBER: US/09/852,156  
FILING DATE: 09-May-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1049-1-009NCIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1029 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHEICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Pigtail macaque  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-852-156-5

Query Match 9.2%; Score 105.4; DB 10; Length 1029;  
Best Local Similarity 48.2%; Pred. No. 7e-19;  
Matches 424; Conservative 0; Mismatches 416; Indels 39; Gaps 3;

QY 101 AAGAGTCAGAGAAATTCAGAAAGTTTCCCTGCTATTCCTCACAATAGTTTCTGCA 160  
DB 71 AAGAGTCCTCAGATTGAGAGAGTCTTTTCCCTGCTATTCCTCACAATAGTTTCTGCT 130  
QY 161 TTGAGCTTGACGAGATTCATGCTAGTGGCAATTATGCTATTACAGAAACAGAGAA 220  
DB 131 GTGGCTGTGGGAGAACTCCTGGTGGTGCATATCCATCTTCTACCATTAAGCTGAGAA 190  
QY 221 CCAAAACAGATGTGATCATCTGAAATTTGGGTGAGAGATTTACTCCTTCTATTCATC 280  
DB 191 GCTGACGAGAGTGTCTGTGTGAACCTACCCCTGGCTGACCTGTGTGTGTGCTGACCTC 250  
QY 281 TGCCTTTTGGGCTGTATATGACATTCATGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 340  
DB 251 TGCCTTTTGGGCTGTATATGACATTCATGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 310  
QY 341 TAACTTACGCTTGTACACACTAACTTTGTCTGTGATGACATTTCTTGGCTTGATCA 400  
DB 311 CCTTACTGGGGGTCTACACTTATTAATCTTACATCCATGCTCATCTCACTGACATCA 370  
QY 401 GCATGAGAGATGTGCTAGTAAATGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 448  
DB 371 CTGTGATGCTTCTATTTAGTGGTAAAGGCGACAGGCGCTTACACAGGCAAGCCAGAA 430  
QY 449 TGGGAAACCATGTGATCATCTGTTCTGTGTGATGATGATGATGATGATGATGATGATGAT 508  
DB 431 GGATGATCTTGGGCAAGGTATCTGCTGCTGATCTGATCTGATCTGATCTGATCTGATCTG 490  
QY 509 TACCCAGCTGCTTTTATATACAGTAATGACATGCTAGGTGATGCTTCCATTTTCCCCC 568  
DB 491 TGCCCCAATATATATGAGCAATGTCTTAAATCTGGACAAAGCTCATATGTGTGT----- 543

QY 569 GCTACTAGAGAACATCAATGAAAGCATTTGATTAAGTCTAGAGATCTGATGATTTG 628  
DB 544 --TATCATGACAGAGAGATTTCCACTGTGGTCTTGGCCACCATGATGACACTGGGGTCT 601  
QY 629 TAGTACCTTTCTATTATATGAGGGGTGCTACTTTATTCAGACAGACACTCATGAGA 688  
DB 602 TCTTCCCACTGCTGCCCATGATGTGTCTGTATTCAGTCAATATCAAAACACTGTCTCATG 661  
QY 689 TGCCAAATATTAATATCTGACCCCTAAAGTTCTGCTCAGAGTGGTATGATTTTCA 748  
DB 662 CTGGAGCTTCCAGAGACACAGATTTCTTAAGATCATTTCTTGTATGAGCTGTCTCC 721  
QY 749 TTGTACTCAACTGCTTTATTAACATTTGCAATTTCTGCGGACCATAGACATCATCT 808  
DB 722 TGCTACCCAGACACCTTTCAACCTCGTGAAGCTCATCCGACAGACACTGGAGTACT 781  
QY 809 CCTGTATACCAAGCTGCAACATGAGCAAAAGCATGAGATGCGCATCCCAATTCACAGAA 868  
DB 782 ATGCCATGACGAGT-----TTCACTACACCATCATATGTCAGAGAG 823  
QY 869 GATGCACTCTTTACAGAGCTGCTCAACCCCATCTTTATGTTTATGGAGCATCTT 928  
DB 824 CCATGCAATACCTGAGGCTGCTTAACTCTGCTTATGCTTGTCTGATGCTTGTGAGCTGAG 883  
QY 929 TCAAAACTACGTTATGAAAGTGCCCAAGAAATATGAGT 967  
DB 884 TTGGAAGAACTTCTGGAACCTTGTGAAGGACATTTGGCT 922

RESULT 34  
US-10-106-623-19  
Sequence 19, Application US/10106623  
Patent No. US20020150888A1  
GENERAL INFORMATION:  
APPLICANT: Gray, Patrick W.  
Schweickart, Vicki L.  
Report, Carol J.  
TITLE OF INVENTION: Chemokine Receptor Materials and Methods  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/106,623  
FILING DATE: 26-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/771,276  
ATTORNEY/AGENT INFORMATION:  
NAME: No. US20020150888A1and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/33670  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1059 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1056  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-10-106-623-19

Query Match 9.2%; Score 105.2; DB 12; Length 1059;  
Best Local Similarity 47.8%; Pred. No. 8.1e-19;  
Matches 416; Conservative 0; Mismatches 433; Indels 21; Gaps 3;

QY 90 CTGATCAAGAAAGATGTCAGAGAAATTTGGCAAAAGTTTCTCCCTGATTTCTCCACAAAT 149  
DB 57 CTGCAAAAATCAATGATGAAACAAATGCAAGCCCGCTCCCTGCTCCGCTCACTACT 116  
QY 150 AGTTTGGTCAATGAGCTGAGGCAATTCATGATGATGATGATGATGATGATGATGATGAT 209  
DB 117 GGTGTTATCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 176  
QY 210 GAAACAGAAACCAAAACAGATGTCATCTGTAATTTGGCTGTTAGCAGATTTACTCT 269  
DB 177 AAGGCTGAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 236  
QY 270 TCTATTCATCTGCTCTTTTGGCTGTTAATGATGATGATGATGATGATGATGATGATGAT 329  
DB 237 CTTCTTACTGTCCTCTCTGCTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 296  
QY 330 AATGTCAGAAATTAATCTGAGCTGTCACACCTAACTTTGCTCTGGAATGAGTTCT 389  
DB 297 AATGTCAGATCTTTCAGAGGCTCTAATTTATGAGCTTTCTCTGGAATCTTTCTTCAAT 356  
QY 390 GGGTTGATCAGATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 434  
DB 357 CATCTCTGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 416  
QY 435 CAGGCAATCAGAGATGAGAAACCATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 494  
DB 417 CAGACAGTCACTTTGGGCTGTTGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 476  
QY 495 CATCTGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 554  
DB 477 CTCTCTCCAGAAATCACTTTTACAGATCTCAGAGAAAGTTTCAATTTACACCTGACAG 536  
QY 555 TCCCAATTTCCCGCTACCTGAGACATCAATGAAAGCAATGATGATGATGATGATGATGATGAT 614  
DB 537 CTCTCATTTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 596  
QY 615 CTGAT 674  
DB 597 CATCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 656  
QY 675 GACACTCATGAAAGATGCAAAAC--ATTAAATATCTGACCCCTTAAAGTTGCTGCTAC 721  
DB 657 AACTCTGCTTGGTGTGAAACGAAAGAAAGGACAGAGGCTGTGAGGCTTATCTTTAC 716  
QY 732 AGTGTATAGTTTCAATGTCATGCTCAATGCTTATTAATGATGATGATGATGATGATGATGATGAT 791  
DB 717 CATCATGAT 776  
QY 792 CATGAT 851  
DB 777 CTTCAGAGAAATCTTGGCTGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 833  
QY 852 CATCAAGTCAAGAAAGATGCAATCTTTCAGAGCTGCTCAACCCATCTTATGAT 911  
DB 834 CATCAAGTCAAGAGATCTTGGGATGACACATGCTGATCAACCCCATCTATGATG 893  
QY 912 TTTTATGAGAGATCTTTCAAAATCAAGT 941  
DB 894 CTTTGTGGGGAAGATTCAGAAATCACT 923

RESULT 35  
US-09-822-849A-256

Sequence 256, Application US/09822849A  
Patent No. US20020045170A1  
GENERAL INFORMATION:  
APPLICANT: Mong, Gordon G.  
APPLICANT: Clark, Hilary  
APPLICANT: Reche, Kim  
APPLICANT: Agostino, Michael J.  
APPLICANT: Howes, Steven H.  
APPLICANT: Resnick, Richard J.  
APPLICANT: Gulukota, Kamalakkar  
APPLICANT: Graham, James R.  
APPLICANT: Genetics Institute, Inc.  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
FILE REFERENCE: GIN 6403  
CURRENT APPLICATION NUMBER: US/09/822,849A  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/195,582  
PRIOR FILING DATE: 2000-04-06  
NUMBER OF SEQ ID NOS: 598  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 256  
LENGTH: 1896  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-822-849A-256

Query Match 8.9%; Score 102.6; DB 10; Length 1896;  
Best Local Similarity 52.2%; Pred. No. 5.6e-18;  
Matches 228; Conservative 0; Mismatches 299; Indels 0; Gaps 0;

QY 538 GACAAATGCTAGGTCATTTCCCTCCGCTACTAGGACATCAATGAAAGATG 597  
DB 89 GGCATGTCATGTCAGACCATGATTTTACCTGATGAGACCAACCAATGATGATGATGATGATGATGAT 148  
QY 598 ATTCAATGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 657  
DB 149 GCTTACCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 208  
QY 658 TACTTATCAGACAGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 717  
DB 209 TATACATGAT 268  
QY 718 AAGTTCGCTACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 777  
DB 269 AAGTACCATGAT 328  
QY 778 AAGTTCGCTACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 837  
DB 329 TGTGTCGACAGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 388  
QY 838 GGCATGACATGAT 897  
DB 389 AACATGAT 448  
QY 898 CCAATCTTTATGTTTATGAGAGATCTTTCAAAATCAAGTATGAAAGTGGCAAG 957  
DB 449 CCGTTCCTATGTTTGTGAGAGATTCGCGGAGATCTGAGAAACCTGTAAG 508  
QY 958 AATATAGGTCCTGAG 974  
DB 509 AACTTGGGTCATGAG 525

RESULT 36  
US-09-852-156-3  
Sequence 3, Application US/09852156  
Patent No. US2002007694A1  
GENERAL INFORMATION:  
APPLICANT: Littman, Dan R.  
APPLICANT: Deng, Hongkui  
APPLICANT: Unutmaz, Derya  
APPLICANT: Ramani, Vineet N.K.  
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS

ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF  
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES  
THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/852,156

FILING DATE: 09-May-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1049-1-009NCIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1037 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: African Green Monkey

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-852-156-3

Query Match 8.5%; Score 97.4; DB 10; Length 1037;

Best Local Similarity 48.1%; Pred. No. 1.1e-16;

Matches 420; Conservative 0; Mismatches 426; Indels 27; Gaps 4;

QY 101 AAGATGTCAGAGATTGGCAAAAGTTTCTCCCTGATTTCTCAATAGTTTCTCA 160  
DB 71 AGGACTTCTGCACTTCAAGCAAGTCTTCTGCTGATGATCTGATGATGATCT 130  
QY 161 TTGGACTTGGCAAGTTCATGATGATGATGATGATGATGATGATGATGATG 220  
DB 131 GTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 190  
QY 221 CCAAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 280  
DB 191 GGCTAGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 250  
QY 281 TGGCTTTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 340  
DB 251 TGGCTTTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 310  
QY 341 TAACTTCACTTGGATGATGATGATGATGATGATGATGATGATGATGATG 400  
DB 311 CCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 370  
QY 401 GCATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 458  
DB 371 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 430  
QY 459 A----TGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 514  
DB 431 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 490

QY 515 AGTGGTTTATATACATGATGATGATGATGATGATGATGATGATGATGATG 574  
DB 491 TGGCCAAATATATATGATGATGATGATGATGATGATGATGATGATGATG 547  
QY 575 TAGGAACATCATGATGATGATGATGATGATGATGATGATGATGATGATG 634  
DB 548 ATGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 607  
QY 635 CTTTCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATG 694  
DB 608 CACTGCTGGCATGATGATGATGATGATGATGATGATGATGATGATGATG 667  
QY 695 ACATTAATATATGATGATGATGATGATGATGATGATGATGATGATGATG 754  
DB 668 GCTTCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 727  
QY 755 CTAACTGCTTATATGATGATGATGATGATGATGATGATGATGATGATG 814  
DB 728 CCGAGACACCTTCAACCTGATGATGATGATGATGATGATGATGATGATG 787  
QY 815 TCACAGCTGCAACATGATGATGATGATGATGATGATGATGATGATGATG 874  
DB 788 TGACAGCT-----TTACATGACATGATGATGATGATGATGATGATG 829  
QY 875 CACTTTTACAGCTGCTTCAACCTTATGATGATGATGATGATGATGATGAT 934  
DB 830 CATACCTGAGAGGCTGCTTAACTGATGATGATGATGATGATGATGATG 889  
QY 935 ACTACCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 967  
DB 890 AGAATTTCTGGAATCTTGAAGAGATGATGATGATGATGATGATGATG 922

RESULT 37  
US-09-864-761-5709/C  
Sequence 5709, Application US/09864761  
Patent No. US2002048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30





QY 852 CATCAAGTCAAGAAAGCATGCACTCTTTCACAGCTGCTCAACCAATCCTTATGT 911  
 Db 860 TATGAGGTGACAGAGACTCTTGGATGACGACATGTCATCAACCCATCATCTATGTC 919  
 QY 912 TTTTATGGAGCATCTTCAAAAATCAGT 941  
 Db 920 CTTTGTGGGAGAAATTCAAAAATCACTCT 949

# RESULT 39 US-09-938-719-3

; Sequence 3, Application US/09938719  
 ; Patent No. US20020106742A1  
 ; GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL  
 PARMENTIER, MARC  
 VASSART, GILBERT

LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
 AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/938,719

FILING DATE: 24-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/626,939

FILING DATE: 27-JULY-2000

ATTORNEY/AGENT INFORMATION:  
 NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: <Unknown>

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1442 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 240..884

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-938-719-3

Query Match 8.2%; Score 93.8; DB 10; Length 1442;

Best Local Similarity 48.0%; Pired. No. 1.2e-15; Indels 23; Gaps 4;

Matches 410; Conservative 0; Mismatches 422;

QY 90 CTGATCAAGAAAGATGTCAGAGATTTGCAAAAGTTTCTCCCTGATATTCCTCACAAT 149  
 Db 296 CTGCAAAAATCAATGTAAGCAAAATGCAAGCCCGCTCTGCTCCGCTCACTACACT 355  
 QY 150 AGTTTGTCTATTGACTTGCAGGCAATTCATGATGATGAGCAATTTATGCCATTAACA 209  
 Db 356 GGTGTTCATCTTTGTTTGGGCAACATGCTGATCCTCATCTCTGATAAATGCA 415  
 QY 210 GAACAGAGAACCAACAGATGTCATTCCTGAATTTGGCTGTAGACAGATTACTCT 269  
 Db 416 AAGGTGAAGACATGATGATCTACTGCTCACTGCGCATCTCTGACCTGTTT 475

QY 270 TCTATTCACCTGCTCTTTTGGGCTGTTAATGCACTTCAATGCGGTTTAXGGAAAT 329  
 Db 476 CTTTCTTACCTGCTCTCTTCTGGGCTCACTATGCTGCCCGCACTTGGAAATAC 535  
 QY 330 AATGTCAAAATTAATCTTCAAGCTTGTGACACTAAACTTTGCTCGAATGCAATTTCT 389  
 Db 536 AATGTCACACTTTGACAGAGGCTCTATTATTAAGGCTTCTTCTGGAATCTTCTTCA 595  
 QY 390 GGCTTGTATCAGCATGACAGATATGTCAGTAACTAAAGTCCCAAGCAATCAGAGT 449  
 Db 596 CATCTCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 643  
 QY 450 GGGAAACCATGCTGATCATCTTTTCTGTCTGTCTGATGCTGCTGATGATGATGATGAT 509  
 Db 644 TGTCTTAAAGCAGGACGGTCACTTTGGGGTGTGAACAAGTGTATCACTTGGGTTGT 703  
 QY 510 ACCCCAGCTGTTTTTATACAGTAATGACAAATGCTAGTGCATTCCTATTTTCCCGG 569  
 Db 704 GGCTGTGTGCGCTCTCTCCAGAAATCATCTTTACCAATCTCAAAAGAAAGCTTTCA 763  
 QY 570 CTACCTAGAAATCAATGAAAGCAATGATTTCAATGCTAGAGATCTGATTTGATTTGT 629  
 Db 764 TTACACCTGACAGCTTCATTTTCCATACATTAAGATA-----GTCACTTGGGCTGTGT 818  
 QY 630 AGTACCTTTCTTATTAATGAGGCTGTCTACTTTATCAAGCAAGGACACTGAAGAT 689  
 Db 819 CTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878  
 QY 690 GCCAAATTAATAATATCTC---GACCCCTAAAGTTCTGCTCAGAGTGTATGATTTT 746  
 Db 879 TCGAATGAG 928  
 QY 747 CATGTGCTCACTGCTCTTATTAATGCTGCAAGTTCTGCGGACCATATGATCATCTTA 806  
 Db 939 TTTTCTTCTGCGCTCTCTCAACAACTTGTCTCTGAGACCTTCCAGAAATTTCT 988  
 QY 807 CTCCCTGATCAGAGCTGCAATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 866  
 Db 999 TGGCTGATTAATGCAATGCTGCTTACA---GATTGACCAAGCTATGAGGTGACAGA 1055  
 QY 867 AAGATCGCACTTTTCAAGCTGCTCAACCAATCCTTATGTTTATTTGAGAGATC 926  
 Db 1056 GACTCTTGAGATGAGCACTGCTGATCAACCCCATCATCTATGCTTGTGGGAGAA 1115  
 QY 927 TTTCAAAAATCAGT 941  
 Db 1116 GTTCAAAAATCACT 1130

## RESULT 40 US-09-939-226-3

; Sequence 3, Application US/09939226  
 ; Patent No. US20020110805A1  
 ; GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL  
 PARMENTIER, MARC  
 VASSART, GILBERT

LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
 AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/939,226  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/626,939  
FILING DATE: 2000-07-27  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: <Unknown>  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1442 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 240..884  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-939-226-3

Query Match 8.2%; Score 93.8; DB 10; Length 1442;  
Best Local Similarity 48.0%; Pred. No. 1.2e-15;  
Matches 410; Conservative 0; Mismatches 422; Indels 23; Gaps 4;

QY 90 CTGTATCAAGAAGATGCAAGAAATTTGCAAAAGTTTCTCCCTGATTCCTGACAAAT 149  
DB 296 CTGCCAAAATCAATGGAAGCAAAATGCGAGCCGCTCTGCTCCGCTACCTCACT 355  
QY 150 AGTTTGTGATTTGAGCTTGAGCAATTCATGAGTGTGAGCAATTTATGCTATTACA 209  
DB 356 GGTGTTATCTTTGTTTGGGCAACATGCTGATCTCTCATCTGATTAACAGCA 415  
QY 210 GAAACAGAAACCAAAACAGATGTGATCTGAAATTTGGCTGTAGCAATTTACTCT 269  
DB 416 AAGCTGAGAGCATGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 475  
QY 270 TCTATGCTGCTGCTTTTGGGCTGTAATGAGTTCATGAGGTTTGAAGAAAT 329  
DB 476 CTTTCTTACTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 535  
QY 330 AATGTGAAATTAATCTGAGCTTGTACACACTAACTTTGCTGTAATGCAATTTCT 389  
DB 536 AATGTGCACTTGTGACAGGCTCTATTTATAGGCTTCTCTGATCTTTCTTCT 595  
QY 390 GGTGTTATGAGTATGACAGATATGAGCAATTAAGTCCCAAGCAATCAGAGT 449  
DB 596 CATCTCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 643  
QY 450 GGGAAACCATGCTGATCATCTGTTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 509  
DB 644 TGTCTTAAAGCCAGAGAGCTGACCTTTGGGGTGTGACAGATGATCACTTTGGGTGT 703  
QY 510 ACCCGAGCTGTTTATACAGTAATGACAAATGCTAGGTCATTCATTTTCCCGG 569  
DB 704 GGTGTTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 763  
QY 570 CTACCTGAGAACTCAATGAAAGCTTGAATTCAAATGCTAGAGATCTGATTTGAT 629  
DB 764 TTACACCTGAGCTCTGATTTTCCATACATTAAGATA-----GTATCTTTGGGGCTGT 818  
QY 630 AGTACCTTTCTATTATGAGGGGTGCTCTTATCAAGCAAGACATCAATGAGAT 689  
DB 819 CTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878  
QY 690 GCCAAACATTAAATATCTC---GACCCCTAAAGTTTCTGCTCAGAGCTTATAGTTT 746  
DB 879 TCGAAATGAGAAAGAGGAGGAGGCTGTGAGGCTTATCTTACATCATGATTTGTTA 938  
QY 747 CATTTGCTCACTGCTGCTTATACATTTGCAAGTTCTGCCGAGCCATGACATCATCTA 806

DB 939 TTTTCTTTTGGGCTTCCCTACACATTTGCTTCTGAAACACCTTCCAGAAATCTT 998  
QY 807 CTCTGATCACCACTGCAATGAGCAAGCAATGAGCAATGAGCAATGAGCAATGAGCA 866  
DB 999 TGGCTGAATTAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1055  
QY 867 AAGATCGACTTTTCAAGCTGCTCAAGCAATCTTTATGTTTATGAGGAGCATC 926  
DB 1056 GACTCTTGGAGTGAAGGAGCACTGCTGATCAACCCCATCATATGCTTGTGAGGAGAA 1115  
QY 927 TTCAAAACTAGT 941  
DB 1116 GTTCAGAAACTACT 1130

Search completed: March 24, 2003, 11:18:43  
Job time : 602 secs